

AC AAV07431;
 XX 27-OCT-1998 (first entry)
 XX Synthetic peptide-labeled oligonucleotide primer.
 DE oligonucleotide; peptide; conjugate; release tag compound;
 KW mass spectrometry; detection; identification; diagnosis; primer; ss.
 XX Synthetic.
 OS
 XX WO9826095-A1.
 PN 18-JUN-1998.
 XX
 XX 10-DEC-1997; 97WO-US22639.
 PF
 XX 16-MAY-1997; 97US-0046719.
 PR 10-DEC-1996; 96US-0033037.
 XX
 XX (GENE-) GENETRACE SYSTEMS INC.
 PA
 XX Becker CH, Montforte JA, Pollart DJ, Shaler TA;
 PI WPI; 1998-348547/30.
 XX
 XX New release tag compounds for detecting target molecule(s) -
 PT comprising a reactive group, a release group and a releasable
 PT non-volatile mass label detectable by mass spectrometry
 XX
 XX Example 3; Page 92; 170pp; English.
 XX
 CC The sequence is that of an oligonucleotide primer which was produced
 CC as part of an oligonucleotide peptide conjugate as an example of
 CC a release tag compound (RTC). These comprise a reactive group, a
 CC release group and a non-volatile mass label comprising a
 CC synthetic polymer or biopolymer detectable by mass spectrometry.
 CC The RTCs can be used as probes for the detection of TMs.
 CC They can be used for e.g. identification of gene sequences,
 CC identification of non-coding nucleotide sequences, identification of
 CC mutations within a gene or protein sequence, detection of metals,
 CC detection of toxins, detection of receptors on an organism or a cell,
 CC characterisation of antibody-antigen interactions, enzyme-substrate
 CC interactions and characterisation of ligand interactions. Multiplex
 CC applications include multiple pathogen diagnostics, multigene genetic
 CC polymorphism screening, single nucleotide polymorphism (SNP)
 CC genotyping, clone and gene mapping, and gene expression analysis.
 CC The RTCs permit the ready detection of releasable mass labels by
 CC mass spectroscopy. The releasable mass labels permit the multiplexing
 CC of tens, hundreds and perhaps even thousands of different mass labels
 CC that can be used to uniquely identify each desired target.
 XX
 SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 other;
 Query Match 1.4%; Score 15; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1084 AAAAAAAAAAAAAA 1098
 DB 15 AAAAAAAAAAAAAA 1
 RESULT 720
 AAT86605/c
 ID AAT86605 standard; DNA; 15 BP.
 XX
 XX AAT86605;
 AC
 XX 04-JUN-1998 (first entry)
 DT
 DE Oligonucleotide separated by capillary affinity gel electrophoresis.
 XX

KW Capillary affinity gel electrophoresis; separation; polymer-gel;
 KW polyacrylamide; ss.
 XX Synthetic.
 XX WO9745721-A1.
 PN 04-DEC-1997.
 XX
 XX 23-MAY-1997; 97WO-EP02647.
 PF
 XX 24-MAY-1996; 96CH-0001320.
 PR
 XX (NOVS) NOVARTIS AG.
 PA
 XX Muscate A, Natt F, Paulus A;
 PI WPI; 1998-041763/04.
 XX
 XX Separation of electrically charged target molecules - by capillary
 PT affinity gel electrophoresis using polymer-gel to which receptors
 PT for target molecules are bound
 XX
 XX Example D3; Page 25; 41pp; English.
 XX
 CC A mixture of oligonucleotides (AAT86604-7) were separated by a new
 CC process using capillary affinity gel electrophoresis. The invention
 CC relates to selective separation of electrically charged target molecules
 CC in an analytical mixture. It comprises capillary affinity gel
 CC electrophoresis using a capillary tube which is at least partly filled
 CC with a polymer gel. Receptors for target molecules are covalently bound
 CC to the polymer. An electric field of at least 50 volts/cm is applied.
 CC The capillary tube is charged with the analytical mixture. In a first
 CC separation stage, the target molecules in the mixture are bound to the
 CC receptors and the remaining components are eluted, optionally whilst
 CC splitting open. In a second stage, the elution conditions are changed,
 CC the receptor is eliminated and the target molecules are eluted and
 CC detected, optionally whilst splitting open. The process is useful for
 CC selective separation and/or determination of charged organic compounds,
 CC such as oligonucleotides, peptides or carbohydrates. It may be used,
 CC e.g. for isolation of specific proteins and DNA molecules, purification
 CC of antibodies, analysis of anisense compounds or screening for enzyme
 CC inhibitors. The process achieves higher resolution and selectivity
 CC than prior art processes, especially in the case of complex biological
 CC analytical mixtures. It has high sensitivity, even with small amounts of
 CC samples. The derivatised polymers may be synthesised specifically using
 CC standard methods.
 XX
 SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 other;
 Query Match 1.4%; Score 15; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1084 AAAAAAAAAAAAAA 1098
 DB 15 AAAAAAAAAAAAAA 1
 RESULT 721
 AAT86675/c
 ID AAT86675 standard; DNA; 15 BP.
 XX
 XX AAT86675;
 AC
 XX 04-JUN-1998 (first entry)
 DT
 DE Oligonucleotide linked to polyacrylamide.
 XX
 KW Capillary affinity gel electrophoresis; separation; polymer-gel;
 KW polyacrylamide; ss.
 XX


```

OS Synthetic.
XX Key Location/Qualifiers
FH modified_base 1
FT /tag= a
FT /note= "Thymine at 5' end attached to a polyacrylamide
FT gel via a linking group"
XX WO9745721-A1.
XX 04-DEC-1997.
XX 23-MAY-1997; 97WO-EF02647.
XX 24-MAY-1996; 96CH-0001320.
XX (NOVS ) NOVARTIS AG.
XX Muscate A, Natt F, Paulus A;
XX WPI; 1998-041763/04.
XX Separation of electrically charged target molecules - by capillary
XX affinity gel electrophoresis using polymer-gel to which receptors
XX for target molecules are bound
XX Example A1; Page 22; 41pp; English.
XX This sequence represents an oligonucleotide receptor molecule covalently
XX bound to a polyacrylamide gel via a linking group. The invention relates
XX to selective separation of electrically charged target molecules in an
XX analytical mixture. It comprises capillary affinity gel electrophoresis
XX using a capillary tube which is at least partly filled with a polymer
XX gel. Receptors for target molecules are covalently bound to the
XX polymer. An electric field of at least 50 volts/cm is applied. The
XX capillary tube is charged with the analytical mixture. In a first
XX separation stage, the target molecules in the mixture are bound to the
XX receptors and the remaining components are eluted, optionally whilst
XX splitting open. In a second stage, the elution conditions are changed,
XX optionally in stages, so that the affinity of the target molecules for
XX the receptor is eliminated and the target molecules are eluted and
XX detected, optionally whilst splitting open. The process is useful for
XX selective separation and/or determination of charged organic compounds,
XX such as oligonucleotides, peptides or carbohydrates. It may be used,
XX e.g. for isolation of specific proteins and DNA molecules, purification
XX of antibodies, analysis of antisense compounds or screening for enzyme
XX inhibitors. The process achieves higher resolution and selectivity
XX than prior art processes, especially in the case of complex biological
XX analytical mixtures. It has high sensitivity, even with small amounts of
XX samples. The derivatised polymers may be synthesised specifically using
XX standard methods.
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 other;

Query Match 1.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1098
DB 15 AAAAAAAAAAAAAA 1

RESULT 722
AAAX00787/c
ID AAX00787 standard; DNA; 15 BP.
XX
AC AAX00787;
XX
DT 13-APR-1999 (first entry)
DE N3-P5 phosphoramidate oligonucleotide #3.
XX

Query Match 1.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1098
DB 15 AAAAAAAAAAAAAA 1

RESULT 723
AAAX00788
ID AAX00788 standard; DNA; 15 BP.
XX
AC AAX00788;
XX
DT 13-APR-1999 (first entry)
DE N3-P5 phosphoramidate oligonucleotide #4.
XX
KW Oligonucleotide; phosphoramidate; phosphoramidite; nucleoside; ss.
XX Synthetic.
XX Key Location/Qualifiers
FH misc_difference 1..15
FT /tag= a
FT /note= "contains internucleotide N3-P5 phosphoramidate
FT internucleotide linkages"
XX US5859233-A.
XX 12-JAN-1999.
XX 20-DEC-1996; 96US-0771789.
XX 20-DEC-1996; 96US-0771789.
XX 21-FEB-1996; 96US-0603566.
XX 14-JUN-1996; 96US-0663918.
XX (LYNX-) LYNX THERAPEUTICS INC.
XX Fearon KL, Gryaznov SM, Hirschbein BL, McCurdy SN;
XX Nelson JS, Schultz RG;
XX WPI; 1999-120007/10.
XX New 3'-protected-amino-nucleoside-5'-phosphoramidite monomers -
XX used in the synthesis of oligo-nucleotide(s)
XX Example 10; Column 33; 34pp; English.
XX This sequence represents an example of an oligonucleotide containing
XX novel 3'-amino-5'-phosphoramidite nucleoside of the invention. The
XX sequence is generated synthetically by using an amine-exchange reaction
XX of phosphoramidites in which a deprotected 3'-amino group of an
XX oligonucleotide chain is exchanged for the amino portion of a
XX 5'-phosphoramidite with a protected 3' amino group. The resulting
XX phosphoramidite internucleotide linkage is oxidised to form a stable
XX protected phosphoramidate linkage.
XX Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 other;

Query Match 1.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1098
DB 15 AAAAAAAAAAAAAA 1

RESULT 723
AAAX00788
ID AAX00788 standard; DNA; 15 BP.
XX
AC AAX00788;
XX
DT 13-APR-1999 (first entry)
DE N3-P5 phosphoramidate oligonucleotide #4.
XX
KW Oligonucleotide; phosphoramidate; phosphoramidite; nucleoside; ss.
XX Synthetic.
XX Key Location/Qualifiers
FH misc_difference 1..15
FT /tag= a
FT /note= "contains internucleotide N3-P5 phosphoramidate
FT internucleotide linkages"
XX US5859233-A.

```

XX 12-JAN-1999.
XX 20-DEC-1996; 96US-0771789.
XX 20-DEC-1996; 96US-0771789.
XX 21-FEB-1996; 96US-0603566.
XX 14-JUN-1996; 96US-0663918.
XX (LYNX-) LYNX THERAPEUTICS INC.
XX Fearon KL, Gryaznov SM, Hirschbein BL, McCurdy SN;
XX Nelson JS, Schultz RG;
XX WPI; 1999-120007/10.
XX New 3'-protected-amino-nucleoside-5'-phosphoramidite monomers
XX used in the synthesis of oligo-nucleotide(s)
XX Example 10; Column 33; 34pp; English.
XX This sequence represents an example of an oligonucleotide containing
XX novel 3'-amino-5'-phosphoramidite nucleoside of the invention. The
XX sequence is generated synthetically by using an amine-exchange reaction
XX of phosphoramidites in which a deprotected 3'-amino group of an
XX oligonucleotide chain is exchanged for the amino portion of a
XX 5'-phosphoramidite with a protected 3' amino group. The resulting
XX phosphoramidite internucleotide linkage is oxidized to form a stable
XX protected phosphoramidate linkage.
XX Sequence 15 BP; 15 A; 0 C; 0 G; 0 U; 0 other;
SQ Query Match 1.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1084 AAAAAAAAAAAAAA 1098
Db 1 AAAAAAAAAAAAAA 15
RESULT 724
AAA75048/C
ID AAA75048 standard; DNA; 15 BP.
AC AAA75048;
XX 15-JAN-2001 (first entry)
XX Primer used to reverse transcribe human RNA.
XX Human; heparanase; gene therapy; tumour; inflammation; autoimmunity;
XX heparin-binding growth factor; cytokine; neurodegenerative plaque;
XX wound healing; infection; burn; angiogenesis; restenosis;
XX atherosclerosis; inflammation; neurodegenerative disease;
XX Gerstmann-Straussler Syndrome; Creutzfeldt-Jakob disease; prion; ss.
XX Homo sapiens.
XX WO200052178-A1.
XX 08-SEP-2000.
XX 14-FEB-2000; 2000WO-US03542.
XX 01-MAR-1999; 99US-0258892.
XX (INST-) INSIGHT STRATEGY & MARKETING LTD.
XX (HADA-) HADASIT MEDICAL RES SERVICES & DEV.
XX (FRIE/) FRIEDMAN M M.
XX Pecker I, Vlodavsky I, Feinstein E;
XX

DR WPI; 2000-579289/54.
XX New polynucleotides encoding a polypeptide having heparanase activity,
XX useful in wound healing and in gene therapy, particularly in treating
XX tumour, inflammation, autoimmunity, neurodegenerative diseases
XX Disclosure; Page 44; 152pp; English.
XX The present primer was used to reverse transcribe human RNA, from
XX which a cDNA sequence encoding a protein with heparanase catalytic
XX activity was amplified. The heparanase (hpa) polynucleotide is useful
XX in gene therapy, particularly in treating tumour, inflammation or
XX autoimmunity. Particularly, the polynucleotide is useful in modulating
XX the bioavailability of heparin-binding growth factors, cellular responses
XX to heparin-binding growth factors (e.g. bFGF) and cytokines
XX (e.g. interleukin (IL)-8), cell interaction with plasma lipoproteins,
XX cellular susceptibility to certain viral and some bacterial and protozoa
XX infections, or disintegration of neurodegenerative plaques. The
XX polynucleotide is also useful in wound healing (e.g. thermal, chemical
XX or radiation burns), and in the treatment of angiogenesis, restenosis,
XX atherosclerosis, inflammation, neurodegenerative diseases (Gerstmann-
XX Straussler Syndrome or Creutzfeldt-Jakob disease), and some viral,
XX bacterial or protozoa infections.
XX Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 other;
SQ Query Match 1.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1084 AAAAAAAAAAAAAA 1098
Db 15 AAAAAAAAAAAAAA 1
RESULT 725
AAA62347/C
ID AAA62347 standard; DNA; 15 BP.
XX AAA62347;
XX 06-NOV-2000 (first entry)
XX Oligonucleotide #3 containing 3'-C-amino-5'(R)-C,3'-N-ethanothymidine.
XX Conformationally-locked oligonucleotide; antisense inhibitor;
XX bicyclic sugar nucleoside analogue; gene probe; ds.
XX Synthetic.
XX Key Location/Qualifiers
XX modified_base 1
XX /tag= a
XX /mod_base= OTHER
XX /note= "3'-C-amino-5'(R)-C,3'-N-ethanothymidine"
XX modified_base 3
XX /tag= b
XX /mod_base= OTHER
XX /note= "3'-C-amino-5'(R)-C,3'-N-ethanothymidine"
XX modified_base 5
XX /tag= c
XX /mod_base= OTHER
XX /note= "3'-C-amino-5'(R)-C,3'-N-ethanothymidine"
XX modified_base 9
XX /tag= d
XX /mod_base= OTHER
XX /note= "3'-C-amino-5'(R)-C,3'-N-ethanothymidine"
XX modified_base 11
XX /tag= e
XX /mod_base= OTHER
XX /note= "3'-C-amino-5'(R)-C,3'-N-ethanothymidine"
XX modified_base 13
XX /tag= f

```

FT      /mod_base= OTHER
FT      /note= "3'-C-amino-5'(R)-C,3'-N-ethanothymidine"
FT      15
FT      modified_base
FT      /*tag= g
FT      /mod_base= OTHER
FT      /note= "3'-C-amino-5'(R)-C,3'-N-ethanothymidine"
FT      15
PN      US6083482-A.
PD      04-JUL-2000.
XX      11-MAY-1999; 99US-0309742.
XX      11-MAY-1999; 99US-0309742.
XX      (ICNC ) ICN PHARM INC.
XX      Wang G;
XX      WPI; 2000-451496/39.
XX      New conformationally restricted 3',5'-bridged nucleosides and
FT      oligonucleotides useful as antisense therapeutics or as gene-specific
FT      diagnostics -
XX      Example 20; Column 15; 10pp; English.
XX      The present sequence is an oligonucleotide containing
CC      3'-C-amino-5'(R)-C,3'-N-ethanothymidine, a bicyclic-sugar nucleoside.
CC      All nucleotides in the sequence were incorporated by phosphoramidite
CC      chemistry using a DNA synthesiser. Bicyclic sugar nucleosides are
CC      conformationally restricted 3',5'-bridged nucleosides which can be used
CC      as building blocks for oligonucleotides. Oligonucleotides can be
CC      produced that have certain, desired, geometrical shapes and entropy
CC      advantages. They may have superior hybridisation to DNA and RNA, and
CC      excellent biological stability. The conformationally-modified
CC      oligonucleotides may be useful as antisense inhibitors of gene expression
CC      or as gene probes, and may therefore be used in antisense therapeutics or
CC      gene-specific diagnostics.
XX      SQ      Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 other;
XX      Query Match      1.4%; Score 15; DB 1; Length 15;
XX      Best Local Similarity 100.0%; Pred. No. 3.5e+02;
XX      Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1084 AAAAAAAAAAAAAA 1098
Db      15 AAAAAAAAAAAAAA 1

RESULT 726
AAAA62348/C
ID      AAA62348 standard; DNA; 15 BP.
XX      AC      AAA62348;
XX      DT      06-NOV-2000 (first entry)
XX      DE      Oligonucleotide #4 containing 3'-C-amino-5'(R)-C,3'-N-ethanothymidine.
XX      KW      Conformationally-locked oligonucleotide; antisense inhibitor;
XX      KW      bicyclic sugar nucleoside analogue; gene probe; ds.
XX      OS      Synthetic.
XX      FH      Key      Location/Qualifiers
FT      modified_base      7
FT      /*tag= a
FT      /mod_base= OTHER
FT      /note= "3'-C-amino-5'(R)-C,3'-N-ethanothymidine"
FT      modified_base      9
FT      /*tag= b
FT      /mod_base= OTHER
FT      /note= "3'-C-amino-5'(R)-C,3'-N-ethanothymidine"
FT      PN      US6083482-A.

```

```

FT      /mod_base= OTHER
FT      /note= "3'-C-amino-5'(R)-C,3'-N-ethanothymidine"
FT      15
FT      modified_base
FT      /*tag= g
FT      /mod_base= OTHER
FT      /note= "3'-C-amino-5'(R)-C,3'-N-ethanothymidine"
FT      15
PN      US6083482-A.
PD      04-JUL-2000.
XX      11-MAY-1999; 99US-0309742.
XX      11-MAY-1999; 99US-0309742.
XX      (ICNC ) ICN PHARM INC.
XX      Wang G;
XX      WPI; 2000-451496/39.
XX      New conformationally restricted 3',5'-bridged nucleosides and
FT      oligonucleotides useful as antisense therapeutics or as gene-specific
FT      diagnostics -
XX      Example 20; Column 15; 10pp; English.
XX      The present sequence is an oligonucleotide containing
CC      3'-C-amino-5'(R)-C,3'-N-ethanothymidine, a bicyclic-sugar nucleoside.
CC      All nucleotides in the sequence were incorporated by phosphoramidite
CC      chemistry using a DNA synthesiser. Bicyclic sugar nucleosides are
CC      conformationally restricted 3',5'-bridged nucleosides which can be used
CC      as building blocks for oligonucleotides. Oligonucleotides can be
CC      produced that have certain, desired, geometrical shapes and entropy
CC      advantages. They may have superior hybridisation to DNA and RNA, and
CC      excellent biological stability. The conformationally-modified
CC      oligonucleotides may be useful as antisense inhibitors of gene expression
CC      or as gene probes, and may therefore be used in antisense therapeutics or
CC      gene-specific diagnostics.
XX      SQ      Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 other;
XX      Query Match      1.4%; Score 15; DB 1; Length 15;
XX      Best Local Similarity 100.0%; Pred. No. 3.5e+02;
XX      Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1084 AAAAAAAAAAAAAA 1098
Db      15 AAAAAAAAAAAAAA 1

RESULT 727
AAAA62350/C
ID      AAA62350 standard; DNA; 15 BP.
XX      AC      AAA62350;
XX      DT      06-NOV-2000 (first entry)
XX      DE      Oligonucleotide #2 containing 3'-C-amino-5'(S)-C,3'-N-ethanothymidine.
XX      KW      Conformationally-locked oligonucleotide; antisense inhibitor;
XX      KW      bicyclic sugar nucleoside analogue; gene probe; ds.
XX      OS      Synthetic.
XX      FH      Key      Location/Qualifiers
FT      modified_base      7
FT      /*tag= a
FT      /mod_base= OTHER
FT      /note= "3'-C-amino-5'(S)-C,3'-N-ethanothymidine"
FT      modified_base      9
FT      /*tag= b
FT      /mod_base= OTHER
FT      /note= "3'-C-amino-5'(S)-C,3'-N-ethanothymidine"
FT      PN      US6083482-A.

```

XX PD 04-JUL-2000.
 XX PF 11-MAY-1999; 99US-0309742.
 XX PR 11-MAY-1999; 99US-0309742.
 XX PA (ICNC) ICN PHARM INC.
 XX PI Wang G;
 XX DR WPI; 2000-451496/39.
 XX PT New conformationally restricted 3',5'-bridged nucleosides and
 PT oligonucleotides useful as antisense therapeutics or as gene-specific
 PT diagnostics -
 XX PS Example 20; Column 16; 10pp; English.
 XX CC The present sequence is an oligonucleotide containing
 CC 3'-C-amino-5'(S)-C,3'-N-ethanochymidine, a bicyclic-sugar nucleoside.
 CC All nucleotides in the sequence were incorporated by phosphoramidite
 CC chemistry using a DNA synthesizer. Bicyclic sugar nucleosides are
 CC conformationally restricted 3',5'-bridged nucleosides which can be used
 CC as building blocks for oligonucleotides. Oligonucleotides can be
 CC produced that have certain, desired, geometrical shapes and entropy
 CC advantages. They may have superior hybridisation to DNA and RNA, and
 CC excellent biological stability. The conformationally-modified
 CC oligonucleotides may be useful as antisense inhibitors of gene expression
 CC or as gene probes, and may therefore be used in antisense therapeutics or
 CC gene-specific diagnostics.
 XX SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 other;
 Query Match 1.4%; Score 15; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1084 AAAAAAAAAAAAAA 1098
 DB 15 AAAAAAAAAAAAAA 1
 RESULT 728
 AAA46502/c
 ID AAA46502 standard; cDNA; 15 BP.
 XX AC AAA46502;
 XX DT 04-SEP-2000 (first entry)
 XX DE PCR primer used to amplify DNA encoding an endo-beta-mannanase.
 XX KW Hydrolysis; polysaccharide; mannan; coffee; endo-beta-mannanase;
 XX KW PCR primer; ss.
 XX OS Coffea arabica.
 XX PN WO200028046-A1.
 XX PD 18-MAY-2000.
 XX PF 28-OCT-1999; 99WO-EF08314.
 XX PR 11-NOV-1998; 98EP-0203742.
 XX PA (NEST) SOC PROD NESTLE SA.
 XX PI Marraccini P, Rogers J;
 XX PR WPI; 2000-399535/34.
 XX PT New DNA encoding endo-beta-mannanase from coffee, used e.g. in

PT pharmaceutical, cosmetic or food compositions to hydrolyze polymannans
 PT
 XX
 XX PS Disclosure; Page 32; 41pp; French.
 XX CC PCR primers AAA46501-02 were used to amplify DNA encoding an
 CC endo-beta-mannanase enzyme, which is involved in the hydrolysis of
 CC polysaccharides that consist of molecules of mannan, either simple
 CC or branched, linked together by beta(1-4) bonds. The mannanase
 CC polynucleotide sequence is used for in vivo modification
 CC of the coffee endo-beta-mannanase gene. It is also used to produce
 CC transgenic plant cells (especially coffee cells) which have modified
 CC properties of mannan polysaccharide, and thus altered flavour or
 CC structure. The enzyme is used for modification, degradation or synthesis
 CC of mannan polysaccharides in vitro, particularly to treat coffee beans
 CC to increase the percentage of dry matter extraction, and thus reduce the
 CC quantity of sediment.
 XX SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 other;
 Query Match 1.4%; Score 15; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1084 AAAAAAAAAAAAAA 1098
 DB 15 AAAAAAAAAAAAAA 1
 RESULT 729
 AAA07788/c
 ID AAA07788 standard; DNA; 15 BP.
 XX AC AAA07788;
 XX DT 23-JUN-2000 (first entry)
 XX DE Nucleic acid sequence of ODN-a.
 XX KW Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
 XX KW viral infection; inflammatory response; cellular proliferation;
 XX KW psoriasis; duplex; ss.
 XX OS Synthetic.
 XX PN WO200011013-A1.
 XX PD 02-MAR-2000.
 XX PF 20-AUG-1999; 99WO-US19029.
 XX PR 22-AUG-1998; 98US-0097712.
 XX PA (UYNE-) UNIV NEBRASKA.
 XX PI Gold B;
 XX DR WPI; 2000-246530/21.
 XX PT Modified nucleomonomers, used in physiologically stable, non-toxic
 PT oligomers used to inhibit expression of nucleic acids and in gene
 PT regulation, antisense technology and diagnostics -
 XX PS Disclosure; Page 20; 42pp; English.
 XX CC The invention provides modified nucleomonomers of specified formula and
 CC their pharmaceutically acceptable salts. The nucleomonomers are used as
 CC monomers in oligomers, which are used in pharmaceutical compositions to
 CC inhibit expression of nucleic acid molecules including DNA and RNA in
 CC cells such as bacterial, fungal, yeast, mammalian, cancer and virally-
 CC infected cells. They are used in oligomers for gene regulation,
 CC antisense technology, diagnostic applications to detect target sequences
 CC in biological samples such as those containing pathogenic bacteria,

CC fungi and viruses, oncogenes, growth hormones and enzymes, to target
 CC genes or encoded RNAs that encode enzymes, hormones, serum proteins,
 CC adhesion molecules, receptor molecules, cytokines, oncogenes, growth
 CC factors and interleukins associated with pathological conditions such as
 CC inflammatory conditions, cardiovascular disorders, immune reactions,
 CC cancer, viral infections and bacterial infections (see AAA07786 for
 CC details of other uses for which the oligomers are suitable for).
 CC Oligomers comprising the nucleomonomers exhibit increased duplex DNA
 CC stability when hybridizing to target nucleic acid sequences, are
 CC physiologically stable, non-toxic and able to penetrate into cells while
 CC maintaining stringent base pair fidelity for target DNA sequences. The
 CC oligomers demonstrate significant single- or double-stranded target
 CC nucleic acid binding activity to form duplexes, triplexes or other forms
 CC of stable association. Sequences AAA07788-803 represent oligonucleotides
 CC forming a third strand along with the duplex sequences.

XX
 SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 other;
 Query Match 1.4%; Score 15; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1098
 DB 15 AAAAAAAAAAAAAA 1

RESULT 730
 AAA07789/C
 ID AAA07789 standard; DNA; 15 BP.
 AC AAA07789;
 XX
 XX 23-JUN-2000 (first entry)
 DE Nucleic acid sequence of ODN-b.
 XX Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
 KW viral infection; inflammatory response; cellular proliferation;
 KW psoriasis; duplex; ss.
 XX Synthetic.
 OS
 XX WO200011013-A1.
 PN 02-MAR-2000.
 XX
 PD 20-AUG-1999; 99WO-US19029.
 XX
 PF 22-AUG-1998; 98US-0097712.
 XX
 PR (UYNE-) UNIV NEBRASKA.
 PA Gold B;
 XX
 PI WPI; 2000-246530/21.
 XX
 DR Modified nucleomonomers, used in physiologically stable, non-toxic
 XX oligomers used to inhibit expression of nucleic acids and in gene
 PT regulation, antisense technology and diagnostics
 XX
 PS Disclosure; Page 20; 42pp; English.

CC The invention provides modified nucleomonomers of specified formula and
 CC their pharmaceutically acceptable salts. The nucleomonomers are used as
 CC monomers in oligomers, which are used in pharmaceutical compositions to
 CC inhibit expression of nucleic acid molecules including DNA and RNA in
 CC cells such as bacterial, fungal, yeast, mammalian, cancer and virally-
 CC infected cells. They are used in oligomers for gene regulation,
 CC antisense technology, diagnostic applications to detect target sequences
 CC in biological samples such as those containing pathogenic bacteria,
 CC fungi and viruses, oncogenes, growth hormones and enzymes, to target
 CC genes or encoded RNAs that encode enzymes, hormones, serum proteins,
 CC factors and interleukins associated with pathological conditions such as

CC adhesion molecules, receptor molecules, cytokines, oncogenes, growth
 CC factors and interleukins associated with pathological conditions such as
 CC inflammatory conditions, cardiovascular disorders, immune reactions,
 CC cancer, viral infections and bacterial infections (see AAA07786 for
 CC details of other uses for which the oligomers are suitable for).
 CC Oligomers comprising the nucleomonomers exhibit increased duplex DNA
 CC stability when hybridizing to target nucleic acid sequences, are
 CC physiologically stable, non-toxic and able to penetrate into cells while
 CC maintaining stringent base pair fidelity for target DNA sequences. The
 CC oligomers demonstrate significant single- or double-stranded target
 CC nucleic acid binding activity to form duplexes, triplexes or other forms
 CC of stable association. Sequences AAA07788-803 represent oligonucleotides
 CC forming a third strand along with the duplex sequences.

XX
 SQ Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 1 U; 0 other;
 Query Match 1.4%; Score 15; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1098
 DB 15 AAAAAAAAAAAAAA 1

RESULT 731
 AAA07790/C
 ID AAA07790 standard; DNA; 15 BP.
 AC AAA07790;
 XX
 XX 23-JUN-2000 (first entry)
 DE Nucleic acid sequence of ODN-c.
 XX Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
 KW viral infection; inflammatory response; cellular proliferation;
 KW psoriasis; duplex; ss.
 XX Synthetic.
 OS
 XX WO200011013-A1.
 PN 02-MAR-2000.
 XX
 PD 20-AUG-1999; 99WO-US19029.
 XX
 PF 22-AUG-1998; 98US-0097712.
 XX
 PR (UYNE-) UNIV NEBRASKA.
 PA Gold B;
 XX
 PI WPI; 2000-246530/21.
 XX
 DR Modified nucleomonomers, used in physiologically stable, non-toxic
 XX oligomers used to inhibit expression of nucleic acids and in gene
 PT regulation, antisense technology and diagnostics
 XX
 PS Disclosure; Page 20; 42pp; English.

CC The invention provides modified nucleomonomers of specified formula and
 CC their pharmaceutically acceptable salts. The nucleomonomers are used as
 CC monomers in oligomers, which are used in pharmaceutical compositions to
 CC inhibit expression of nucleic acid molecules including DNA and RNA in
 CC cells such as bacterial, fungal, yeast, mammalian, cancer and virally-
 CC infected cells. They are used in oligomers for gene regulation,
 CC antisense technology, diagnostic applications to detect target sequences
 CC in biological samples such as those containing pathogenic bacteria,
 CC fungi and viruses, oncogenes, growth hormones and enzymes, to target
 CC genes or encoded RNAs that encode enzymes, hormones, serum proteins,
 CC adhesion molecules, receptor molecules, cytokines, oncogenes, growth
 CC factors and interleukins associated with pathological conditions such as

Sequence 15 BP: 0 A; 0 C; 0 G; 11 T; 4 U; 0 other;

```
Query Match      1.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 15: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

Qy      1084 AAAAAAAAAAAAAAAAAA 1098
         |||||
Db      15  AAAAAAAAAAAAAAAAAA 1

```

RESULT 733
AAA07792/c
ID AAA07792 standard: DNA: 15 BP.

DT 23 - JUN - 20

DT 23-JUN-2000 (first entry)

DE Nucleic acid sequence of ODN-e.

KW Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
 KW viral infection; inflammatory response; cellular proliferation;
 KW psoriasis; duplex: ss.

OS Synthetic.

PN WO200011013-A1.

02-MAR-2000.

AA 20-AUG-1999; 99WO-US19029.
PF

PR 22-AUG-1998; 98US-0097712.

PA (UYNE-) UNIV NEBRASKA.

PI Gold B:

DR WPI: 2000-246530/21.

Modified nucleomonomers, used in physiologically stable, non-toxic oligomers used to inhibit expression of nucleic acids and in gene regulation, antisense technology and diagnostics -

PS Disclosure; Page 20; 42pp; English

The invention provides modified nucleomonomers of specified formula and their pharmaceutically acceptable salts. The nucleomonomers are used as monomers in oligomers, which are used in pharmaceutical compositions to inhibit expression of nucleic acid molecules including DNA and RNA in cells such as bacterial, fungal, yeast, mammalian, cancer and virally-infected cells. They are used in oligomers for gene regulation, antisense technology, diagnostic applications to detect target sequences in biological samples such as those containing pathogenic bacteria, fungi and viruses, oncogenes, growth hormones and enzymes, to target genes or encoded RNAs that encode enzymes, hormones, serum proteins, adhesion molecules, receptor molecules, cytokines, oncogenes, growth factors and interleukins associated with pathological conditions such as inflammatory conditions, cardiovascular disorders, immune reactions, cancer, viral infections and bacterial infections (see AAA07796 for details of other uses for which the oligomers are suitable for). Oligomers comprising the nucleomonomers exhibit increased duplex DNA

CC stability when hybridizing to target nucleic acid sequences, are
CC physiologically stable, non-toxic and able to penetrate into cells while
CC maintaining stringent base pair fidelity for target DNA sequences. The
CC oligomers demonstrate significant single- or double-stranded target
CC nucleic acid binding activity to form duplexes, triplexes or other forms
CC of stable association. Sequences AAA07788-803 represent oligonucleotides
CC forming a third strand along with the duplex sequences.
XX

SQ Sequence 15 BP; 0 A; 0 C; 0 G; 13 T; 2 U; 0 other;

Query Match 1.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1098
DB 15 AAAAAAAAAAAAAA 1

RESULT 734
AAA07793/c
ID AAA07793 standard; DNA; 15 BP.

XX AC AAA07793;

XX DT 23-JUN-2000 (first entry)

XX DE Nucleic acid sequence of ODN-f.

XX KW Nucleonome; cancer; gene regulation; antisense technology; leukemia;
XX KW viral infection; inflammatory response; cellular proliferation;
XX KW psoriasis; duplex; ss.

XX OS Synthetic.

XX PN WO200011013-A1.

XX PD 02-MAR-2000.

XX PF 20-AUG-1999; 99WO-US19029.

XX PR 22-AUG-1998; 98US-0097712.

XX PA (UYNE-) UNIV NEBRASKA.

XX PI Gold B;

XX WPI; 2000-246530/21.

XX Modified nucleonome, used in physiologically stable, non-toxic
XX oligomers used to inhibit expression of nucleic acids and in gene
XX regulation, antisense technology and diagnostics -

XX Disclosure; Page 20; 42pp; English.

XX The invention provides modified nucleonome of specified formula and
XX their pharmaceutically acceptable salts. The nucleonome are used as
XX monomers in oligomers, which are used in pharmaceutical compositions to
XX inhibit expression of nucleic acid molecules including DNA and RNA in
XX cells such as bacterial, fungal, yeast, mammalian, cancer and virally-
XX infected cells. They are used in oligomers for gene regulation,
XX antisense technology, diagnostic applications to detect target sequences
XX in biological samples such as those containing pathogenic bacteria,
XX fungi and viruses, oncogenes, growth hormones and enzymes, to target
XX genes or encoded RNAs that encode enzymes, hormones, serum proteins,
XX adhesion molecules, receptor molecules, cytokines, oncogenes, growth
XX factors and interleukins associated with pathological conditions such as
XX inflammatory conditions, cardiovascular disorders, immune reactions,
XX cancer, viral infections and bacterial infections (see AAA07786 for
XX details of other uses for which the oligomers are suitable for).
XX Oligomers comprising the nucleonome exhibit increased duplex DNA
XX stability when hybridizing to target nucleic acid sequences, are
XX physiologically stable, non-toxic and able to penetrate into cells while

CC maintaining stringent base pair fidelity for target DNA sequences. The
CC oligomers demonstrate significant single- or double-stranded target
CC nucleic acid binding activity to form duplexes, triplexes or other forms
CC of stable association. Sequences AAA07788-803 represent oligonucleotides
CC forming a third strand along with the duplex sequences.
XX

SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 U; 0 other;

Query Match 1.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1098
DB 15 AAAAAAAAAAAAAA 1

RESULT 735
AAA07794/c
ID AAA07794 standard; DNA; 15 BP.

XX AC AAA07794;

XX DT 23-JUN-2000 (first entry)

XX DE Nucleic acid sequence of ODN-g.

XX KW Nucleonome; cancer; gene regulation; antisense technology; leukemia;
XX KW viral infection; inflammatory response; cellular proliferation;
XX KW psoriasis; duplex; ss.

XX OS Synthetic.

XX PN WO200011013-A1.

XX PD 02-MAR-2000.

XX PF 20-AUG-1999; 99WO-US19029.

XX PR 22-AUG-1998; 98US-0097712.

XX PA (UYNE-) UNIV NEBRASKA.

XX PI Gold B;

XX WPI; 2000-246530/21.

XX Modified nucleonome, used in physiologically stable, non-toxic
XX oligomers used to inhibit expression of nucleic acids and in gene
XX regulation, antisense technology and diagnostics -

XX Disclosure; Page 20; 42pp; English.

XX The invention provides modified nucleonome of specified formula and
XX their pharmaceutically acceptable salts. The nucleonome are used as
XX monomers in oligomers, which are used in pharmaceutical compositions to
XX inhibit expression of nucleic acid molecules including DNA and RNA in
XX cells such as bacterial, fungal, yeast, mammalian, cancer and virally-
XX infected cells. They are used in oligomers for gene regulation,
XX antisense technology, diagnostic applications to detect target sequences
XX in biological samples such as those containing pathogenic bacteria,
XX fungi and viruses, oncogenes, growth hormones and enzymes, to target
XX genes or encoded RNAs that encode enzymes, hormones, serum proteins,
XX adhesion molecules, receptor molecules, cytokines, oncogenes, growth
XX factors and interleukins associated with pathological conditions such as
XX inflammatory conditions, cardiovascular disorders, immune reactions,
XX cancer, viral infections and bacterial infections (see AAA07786 for
XX details of other uses for which the oligomers are suitable for).
XX Oligomers comprising the nucleonome exhibit increased duplex DNA
XX stability when hybridizing to target nucleic acid sequences, are
XX physiologically stable, non-toxic and able to penetrate into cells while
XX maintaining stringent base pair fidelity for target DNA sequences. The
XX oligomers demonstrate significant single- or double-stranded target

CC nucleic acid binding activity to form duplexes, triplexes or other forms
CC of stable association. Sequences AAA07788-803 represent oligonucleotides
CC forming a third strand along with the duplex sequences.
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 1 U; 0 other;
Query Match 1.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1084 AAAAAAAAAAAAAA 1098
|||||
DB 15 AAAAAAAAAAAAAA 1
RESULT 736
AAA07795/C
ID AAA07795 standard; DNA; 15 BP.
XX
AC AAA07795;
XX
DT 23-JUN-2000 (first entry)
XX
DE Nucleic acid sequence of ODN-h.
XX
DE Nucleonome; cancer; gene regulation; antisense technology; leukemia;
KW viral infection; inflammatory response; cellular proliferation;
KW psoriasis; duplex; ss.
XX
OS Synthetic.
XX
PN WO200011013-A1.
XX
PD 02-MAR-2000.
XX
PF 20-AUG-1999; 99WO-US19029.
XX
PR 22-AUG-1998; 98US-0097712.
XX
PA (UYNE-) UNIV NEBRASKA.
XX
PI Gold B;
XX
DR WPI; 2000-246530/21.
XX
PT Modified nucleomoners, used in physiologically stable, non-toxic
PT oligomers used to inhibit expression of nucleic acids and in gene
PT regulation, antisense technology and diagnostics -
XX
PS Disclosure; Page 20; 42pp; English.
XX
CC The invention provides modified nucleomoners of specified formula and
CC their pharmaceutically acceptable salts. The nucleomoners are used as
CC monomers in oligomers, which are used in pharmaceutical compositions to
CC inhibit expression of nucleic acid molecules including DNA and RNA in
CC cells such as bacterial, fungal, yeast, mammalian, cancer and virally-
CC infected cells. They are used in oligomers for gene regulation,
CC antisense technology, diagnostic applications to detect target sequences
CC in biological samples such as those containing pathogenic bacteria,
CC fungi and viruses, oncogenes, growth hormones and enzymes, to target
CC genes or encoded RNAs that encode enzymes, hormones, serum proteins,
CC adhesion molecules, receptor molecules, cytokines, oncogenes, growth
CC factors and interleukins associated with pathological conditions such as
CC inflammatory conditions, cardiovascular disorders, immune reactions,
CC cancer, viral infections and bacterial infections (see AAA07786 for
CC details of other uses for which the oligomers are suitable for).
CC Oligomers comprising the nucleomoners exhibit increased duplex DNA
CC stability when hybridizing to target nucleic acid sequences, are
CC physiologically stable, non-toxic and able to penetrate into cells while
CC maintaining stringent base pair fidelity for target DNA sequences. The
CC oligomers demonstrate significant single- or double-stranded target
CC nucleic acid binding activity to form duplexes, triplexes or other forms
CC of stable association. Sequences AAA07788-803 represent oligonucleotides
XX

CC forming a third strand along with the duplex sequences.
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 13 T; 2 U; 0 other;
Query Match 1.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1084 AAAAAAAAAAAAAA 1098
|||||
DB 15 AAAAAAAAAAAAAA 1
RESULT 737
AAA07796/C
ID AAA07796 standard; DNA; 15 BP.
XX
AC AAA07796;
XX
DT 23-JUN-2000 (first entry)
XX
DE Nucleic acid sequence of ODN-i.
XX
DE Nucleonome; cancer; gene regulation; antisense technology; leukemia;
KW viral infection; inflammatory response; cellular proliferation;
KW psoriasis; duplex; ss.
XX
OS Synthetic.
XX
PN WO200011013-A1.
XX
PD 02-MAR-2000.
XX
PF 20-AUG-1999; 99WO-US19029.
XX
PR 22-AUG-1998; 98US-0097712.
XX
PA (UYNE-) UNIV NEBRASKA.
XX
PI Gold B;
XX
DR WPI; 2000-246530/21.
XX
PT Modified nucleomoners, used in physiologically stable, non-toxic
PT oligomers used to inhibit expression of nucleic acids and in gene
PT regulation, antisense technology and diagnostics -
XX
PS Disclosure; Page 20; 42pp; English.
XX
CC The invention provides modified nucleomoners of specified formula and
CC their pharmaceutically acceptable salts. The nucleomoners are used as
CC monomers in oligomers, which are used in pharmaceutical compositions to
CC inhibit expression of nucleic acid molecules including DNA and RNA in
CC cells such as bacterial, fungal, yeast, mammalian, cancer and virally-
CC infected cells. They are used in oligomers for gene regulation,
CC antisense technology, diagnostic applications to detect target sequences
CC in biological samples such as those containing pathogenic bacteria,
CC fungi and viruses, oncogenes, growth hormones and enzymes, to target
CC genes or encoded RNAs that encode enzymes, hormones, serum proteins,
CC adhesion molecules, receptor molecules, cytokines, oncogenes, growth
CC factors and interleukins associated with pathological conditions such as
CC inflammatory conditions, cardiovascular disorders, immune reactions,
CC cancer, viral infections and bacterial infections (see AAA07786 for
CC details of other uses for which the oligomers are suitable for).
CC Oligomers comprising the nucleomoners exhibit increased duplex DNA
CC stability when hybridizing to target nucleic acid sequences, are
CC physiologically stable, non-toxic and able to penetrate into cells while
CC maintaining stringent base pair fidelity for target DNA sequences. The
CC oligomers demonstrate significant single- or double-stranded target
CC nucleic acid binding activity to form duplexes, triplexes or other forms
CC of stable association. Sequences AAA07788-803 represent oligonucleotides
XX

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1098
 DB 15 AAAAAAAAAAAAAA 1

RESULT 740
 AAA07799/c
 ID AAA07799 standard; DNA; 15 BP.
 XX
 AC AAA07799;
 XX
 DT 23-JUN-2000 (first entry)
 XX
 DE Nucleic acid sequence of ODN-1.
 XX
 DE Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
 KW viral infection; inflammatory response; cellular proliferation;
 KW psoriasis; duplex; ss.
 XX
 OS Synthetic.
 XX
 PN WO200011013-A1.
 XX
 PD 02-MAR-2000.
 XX
 PF 20-AUG-1999; 99WO-US19029.
 XX
 PR 22-AUG-1998; 98US-0097712.
 XX
 PA (UYNE-) UNIV NEBRASKA.
 XX
 PI Gold B;
 XX
 WPI; 2000-246530/21.
 XX
 DR Modified nucleomonomers, used in physiologically stable, non-toxic
 PT oligomers used to inhibit expression of nucleic acids and in gene
 PT regulation, antisense technology and diagnostics -
 XX
 PS Disclosure; Page 20; 42pp; English.
 XX
 CC The invention provides modified nucleomonomers of specified formula and
 CC their pharmaceutically acceptable salts. The nucleomonomers are used as
 CC monomers in oligomers, which are used in pharmaceutical compositions to
 CC inhibit expression of nucleic acid molecules including DNA and RNA in
 CC cells such as bacterial, fungal, yeast, mammalian, cancer and virally-
 CC infected cells. They are used in oligomers for gene regulation,
 CC antisense technology, diagnostic applications to detect target sequences
 CC in biological samples such as those containing pathogenic bacteria,
 CC fungi and viruses, oncogenes, growth hormones and enzymes, to target
 CC genes or encoded RNAs that encode enzymes, hormones, serum proteins,
 CC adhesion molecules, receptor molecules, cytokines, oncogenes, growth
 CC factors and interleukins associated with pathological conditions such as
 CC inflammatory conditions, cardiovascular disorders, immune reactions,
 CC cancer, viral infections and bacterial infections (see AAA07786 for
 CC details of other uses for which the oligomers are suitable for).
 CC Oligomers comprising the nucleomonomers exhibit increased duplex DNA
 CC stability when hybridizing to target nucleic acid sequences, are
 CC physiologically stable, non-toxic and able to penetrate into cells while
 CC maintaining stringent base pair fidelity for target DNA sequences. The
 CC oligomers demonstrate significant single- or double-stranded target
 CC nucleic acid binding activity to form duplexes, triplexes or other forms
 CC of stable association. Sequences AAA07788-803 represent oligonucleotides
 CC forming a third strand along with the duplex sequences.
 XX
 SQ Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 1 U; 0 other;

Query Match 1.4%; Score 15; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1098
 DB 15 AAAAAAAAAAAAAA 1

RESULT 741
 AAA07800/c
 ID AAA07800 standard; DNA; 15 BP.
 XX
 AC AAA07800;
 XX
 DT 23-JUN-2000 (first entry)
 XX
 DE Nucleic acid sequence of ODN-m.
 XX
 DE Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
 KW viral infection; inflammatory response; cellular proliferation;
 KW psoriasis; duplex; ss.
 XX
 OS Synthetic.
 XX
 PN WO200011013-A1.
 XX
 PD 02-MAR-2000.
 XX
 PF 20-AUG-1999; 99WO-US19029.
 XX
 PR 22-AUG-1998; 98US-0097712.
 XX
 PA (UYNE-) UNIV NEBRASKA.
 XX
 PI Gold B;
 XX
 WPI; 2000-246530/21.
 XX
 DR Modified nucleomonomers, used in physiologically stable, non-toxic
 PT oligomers used to inhibit expression of nucleic acids and in gene
 PT regulation, antisense technology and diagnostics -
 XX
 PS Disclosure; Page 20; 42pp; English.
 XX
 CC The invention provides modified nucleomonomers of specified formula and
 CC their pharmaceutically acceptable salts. The nucleomonomers are used as
 CC monomers in oligomers, which are used in pharmaceutical compositions to
 CC inhibit expression of nucleic acid molecules including DNA and RNA in
 CC cells such as bacterial, fungal, yeast, mammalian, cancer and virally-
 CC infected cells. They are used in oligomers for gene regulation,
 CC antisense technology, diagnostic applications to detect target sequences
 CC in biological samples such as those containing pathogenic bacteria,
 CC fungi and viruses, oncogenes, growth hormones and enzymes, to target
 CC genes or encoded RNAs that encode enzymes, hormones, serum proteins,
 CC adhesion molecules, receptor molecules, cytokines, oncogenes, growth
 CC factors and interleukins associated with pathological conditions such as
 CC inflammatory conditions, cardiovascular disorders, immune reactions,
 CC cancer, viral infections and bacterial infections (see AAA07786 for
 CC details of other uses for which the oligomers are suitable for).
 CC Oligomers comprising the nucleomonomers exhibit increased duplex DNA
 CC stability when hybridizing to target nucleic acid sequences, are
 CC physiologically stable, non-toxic and able to penetrate into cells while
 CC maintaining stringent base pair fidelity for target DNA sequences. The
 CC oligomers demonstrate significant single- or double-stranded target
 CC nucleic acid binding activity to form duplexes, triplexes or other forms
 CC of stable association. Sequences AAA07788-803 represent oligonucleotides
 CC forming a third strand along with the duplex sequences.
 XX
 SQ Sequence 15 BP; 0 A; 0 C; 0 G; 13 T; 2 U; 0 other;

Query Match 1.4%; Score 15; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 15 AAAAAAAAAAAAAA 1

RESULT 742
AAA07801/c
ID AAA07801 standard; DNA; 15 BP.

XX AC AAA07801;
XX DT 23-JUN-2000 (first entry)
XX DE Nucleic acid sequence of ODN-n.
XX KW Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
XX KW viral infection; inflammatory response; cellular proliferation;
XX KW psoriasis; duplex; ss.
XX OS Synthetic.
XX PN W0200011013-A1.
XX PD 02-MAR-2000.
XX PF 20-AUG-1999; 99WO-US19029.
XX PR 22-AUG-1998; 98US-0097712.
XX PA (UYNE-) UNIV NEBRASKA.
XX PI Gold B;
XX DR WPI; 2000-246530/21.
XX PT Modified nucleomonomers, used in physiologically stable, non-toxic
XX PT oligomers used to inhibit expression of nucleic acids and in gene
XX PT regulation, antisense technology and diagnostics -
XX PS Disclosure; Page 20; 42pp; English.

XX CC The invention provides modified nucleomonomers of specified formula and
XX CC their pharmaceutically acceptable salts. The nucleomonomers are used as
XX CC monomers in oligomers, which are used in pharmaceutical compositions to
XX CC inhibit expression of nucleic acid molecules including DNA and RNA in
XX CC cells such as bacterial, fungal, yeast, mammalian, cancer and virally-
XX CC infected cells. They are used in oligomers for gene regulation,
XX CC antisense technology, diagnostic applications to detect target sequences
XX CC in biological samples such as those containing pathogenic bacteria,
XX CC fungi and viruses, oncogenes, growth hormones and enzymes, to target
XX CC genes or encoded RNAs that encode enzymes, hormones, serum proteins,
XX CC adhesion molecules, receptor molecules, cytokines, oncogenes, growth
XX CC factors and interleukins associated with pathological conditions such as
XX CC inflammatory conditions, cardiovascular disorders, immune reactions,
XX CC cancer, viral infections and bacterial infections (see AAA07786 for
XX CC details of other uses for which the oligomers are suitable for).
XX CC Oligomers comprising the nucleomonomers exhibit increased duplex DNA
XX CC stability when hybridizing to target nucleic acid sequences, are
XX CC physiologically stable, non-toxic and able to penetrate into cells while
XX CC maintaining stringent base pair fidelity for target DNA sequences. The
XX CC oligomers demonstrate significant single- or double-stranded target
XX CC nucleic acid binding activity to form duplexes, triplexes or other forms
XX CC of stable association. Sequences AAA07788-803 represent oligonucleotides
XX CC forming a third strand along with the duplex sequences.

XX SQ Sequence 15 BP; 0 A; 0 C; 0 G; 11 T; 4 U; 0 other;
Query Match 1.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1098
DB 15 AAAAAAAAAAAAAA 1

RESULT 743
AAA07802/c
ID AAA07802 standard; DNA; 15 BP.

XX AC AAA07802;
XX DT 23-JUN-2000 (first entry)
XX DE Nucleic acid sequence of ODN-0.
XX KW Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
XX KW viral infection; inflammatory response; cellular proliferation;
XX KW psoriasis; duplex; ss.
XX OS Synthetic.
XX PN W0200011013-A1.
XX PD 02-MAR-2000.
XX PF 20-AUG-1999; 99WO-US19029.
XX PR 22-AUG-1998; 98US-0097712.
XX PA (UYNE-) UNIV NEBRASKA.
XX PI Gold B;
XX DR WPI; 2000-246530/21.
XX PT Modified nucleomonomers, used in physiologically stable, non-toxic
XX PT oligomers used to inhibit expression of nucleic acids and in gene
XX PT regulation, antisense technology and diagnostics -
XX PS Disclosure; Page 20; 42pp; English.

XX CC The invention provides modified nucleomonomers of specified formula and
XX CC their pharmaceutically acceptable salts. The nucleomonomers are used as
XX CC monomers in oligomers, which are used in pharmaceutical compositions to
XX CC inhibit expression of nucleic acid molecules including DNA and RNA in
XX CC cells such as bacterial, fungal, yeast, mammalian, cancer and virally-
XX CC infected cells. They are used in oligomers for gene regulation,
XX CC antisense technology, diagnostic applications to detect target sequences
XX CC in biological samples such as those containing pathogenic bacteria,
XX CC fungi and viruses, oncogenes, growth hormones and enzymes, to target
XX CC genes or encoded RNAs that encode enzymes, hormones, serum proteins,
XX CC adhesion molecules, receptor molecules, cytokines, oncogenes, growth
XX CC factors and interleukins associated with pathological conditions such as
XX CC inflammatory conditions, cardiovascular disorders, immune reactions,
XX CC cancer, viral infections and bacterial infections (see AAA07786 for
XX CC details of other uses for which the oligomers are suitable for).
XX CC Oligomers comprising the nucleomonomers exhibit increased duplex DNA
XX CC stability when hybridizing to target nucleic acid sequences, are
XX CC physiologically stable, non-toxic and able to penetrate into cells while
XX CC maintaining stringent base pair fidelity for target DNA sequences. The
XX CC oligomers demonstrate significant single- or double-stranded target
XX CC nucleic acid binding activity to form duplexes, triplexes or other forms
XX CC of stable association. Sequences AAA07788-803 represent oligonucleotides
XX CC forming a third strand along with the duplex sequences.

XX SQ Sequence 15 BP; 0 A; 0 C; 0 G; 13 T; 2 U; 0 other;
Query Match 1.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1098
DB 15 AAAAAAAAAAAAAA 1

RESULT 744

```

AAA07803/c
ID AAA07803 standard; DNA; 15 BP.
XX AC
XX AA07803;
XX DT
XX 23-JUN-2000 (first entry)
XX DE
XX Nucleic acid sequence of ON-p.
XX Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
KW viral infection; inflammatory response; cellular proliferation;
KW psoriasis; duplex; ss.
XX OS
XX Synthetic.
XX PN
XX WO200011013-A1.
XX PD
XX 02-MAR-2000.
XX PF
XX 20-AUG-1999; 99WO-US19029.
XX PR
XX 22-AUG-1998; 98US-0097712.
XX PA
XX (UYNE-) UNIV NEBRASKA.
XX PI
XX Gold B;
XX DR
XX WPI; 2000-246530/21.
XX PT
XX Modified nucleomonomers, used in physiologically stable, non-toxic
PT oligomers used to inhibit expression of nucleic acids and in gene
PT regulation, antisense technology and diagnostics -
XX PT
XX Disclosure; Page 20; 42pp; English.
XX CC
XX The invention provides modified nucleomonomers of specified formula and
CC their pharmaceutically acceptable salts. The nucleomonomers are used as
CC monomers in oligomers, which are used in pharmaceutical compositions to
CC inhibit expression of nucleic acid molecules including DNA and RNA in
CC cells such as bacterial, fungal, yeast, mammalian, cancer and virally-
CC infected cells. They are used in oligomers for gene regulation,
CC antisense technology, diagnostic applications to detect target sequences
CC in biological samples such as those containing pathogenic bacteria,
CC fungi and viruses, oncogenes, growth hormones and enzymes, to target
CC genes or encoded RNAs that encode enzymes, hormones, serum proteins,
CC adhesion molecules, receptor molecules, cytokines, oncogenes, growth
CC factors and interleukins associated with pathological conditions such as
CC inflammatory conditions, cardiovascular disorders, immune reactions,
CC cancer, viral infections and bacterial infections (see AAA07786 for
CC details of other uses for which the oligomers are suitable for).
CC Oligomers comprising the nucleomonomers exhibit increased duplex DNA
CC stability when hybridizing to target nucleic acid sequences, are
CC physiologically stable, non-toxic and able to penetrate into cells while
CC maintaining stringent base pair fidelity for target DNA sequences. The
CC oligomers demonstrate significant single- or double-stranded target
CC nucleic acid binding activity to form duplexes, triplexes or other forms
CC of stable association. Sequences AAA0788-803 represent oligonucleotides
CC forming a third strand along with the duplex sequences.
XX CC
XX Sequence 15 BP; 0 A; 0 C; 0 G; 15 U; 0 other;
SQ Query Match 1.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1098
DB 15 AAAAAAAAAAAAAA 1

RESULT 745
AAA07825/c
ID AAA07825 standard; DNA; 15 BP.
XX AC

```

```
XX DT 23-JUN-2000 (first entry)
XX DE Nucleic acid sequence of a strand of triplex oligomer 15.
XX KW Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
XX KW viral infection; inflammatory response; cellular proliferation;
XX KW psoriasis; duplex; triplex; ss.
XX OS Synthetic.
XX PN WO200011013-A1.
XX PD 02-MAR-2000.
XX PF 20-AUG-1999; 99WO-US19029.
XX PR 22-AUG-1998; 98US-0097712.
XX PA (UYNE-) UNIV NEBRASKA.
XX PI Gold B;
XX DR WPI; 2000-246530/21.
XX PT Modified nucleomonomers, used in physiologically stable, non-toxic
XX PT oligomers used to inhibit expression of nucleic acids and in gene
XX PT regulation, antisense technology and diagnostics -
XX PS Disclosure; Page 30; 42pp; English.
XX CC The invention provides modified nucleomonomers of specified formula and
XX CC their pharmaceutically acceptable salts. The nucleomonomers are used as
XX CC monomers in oligomers, which are used in pharmaceutical compositions to
XX CC inhibit expression of nucleic acid molecules including DNA and RNA in
XX CC cells such as bacterial, fungal, yeast, mammalian, cancer and virally-
XX CC infected cells. They are used in oligomers for gene regulation,
XX CC antisense technology, diagnostic applications to detect target sequences
XX CC in biological samples such as those containing pathogenic bacteria,
XX CC fungi and viruses, oncogenes, growth hormones and enzymes, to target
XX CC genes or encoded RNAs that encode enzymes, cytokines, oncogenes, growth
XX CC adhesion molecules, receptor molecules, hormones, serum proteins,
XX CC factors and interleukins associated with pathological conditions such as
XX CC inflammatory conditions, cardiovascular disorders, immune reactions,
XX CC cancer, viral infections and bacterial infections (see AAA07786 for
XX CC details of other uses for which the oligomers are suitable for).
XX CC Oligomers comprising the nucleomonomers exhibit increased duplex DNA
XX CC stability when hybridizing to target nucleic acid sequences, are
XX CC physiologically stable, non-toxic and able to penetrate into cells while
XX CC maintaining stringent base pair fidelity for target DNA sequences. The
XX CC oligomers demonstrate significant single- or double-stranded target
XX CC nucleic acid binding activity to form duplexes, triplexes or other forms
XX CC of stable association. Sequences AAA07820-834 represent sequences forming
XX CC triplex oligomers.
XX SQ Sequence 15 BP; 0 A; 0 C; 0 G; 13 T; 2 U; 0 other;
XX
XX Query Match 1.4%; Score 15; DB 1; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 3.5e+02;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1084 AAAAAAAAAAAAAA 1098
XX Db 15 AAAAAAAAAAAAAA 1
XX
XX RESULT 747
XX AAA07831/c
XX ID AAA07831 standard; DNA; 15 BP.
XX XX
XX AC AAA07831;
XX XX
XX DT 23-JUN-2000 (first entry)
```

```
XX DE Nucleic acid sequence of a strand of triplex oligomer 16.
XX KW Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
XX KW viral infection; inflammatory response; cellular proliferation;
XX KW psoriasis; duplex; triplex; ss.
XX OS Synthetic.
XX PN WO200011013-A1.
XX PD 02-MAR-2000.
XX PF 20-AUG-1999; 99WO-US19029.
XX PR 22-AUG-1998; 98US-0097712.
XX PA (UYNE-) UNIV NEBRASKA.
XX PI Gold B;
XX DR WPI; 2000-246530/21.
XX PT Modified nucleomonomers, used in physiologically stable, non-toxic
XX PT oligomers used to inhibit expression of nucleic acids and in gene
XX PT regulation, antisense technology and diagnostics -
XX PS Disclosure; Page 30; 42pp; English.
XX CC The invention provides modified nucleomonomers of specified formula and
XX CC their pharmaceutically acceptable salts. The nucleomonomers are used as
XX CC monomers in oligomers, which are used in pharmaceutical compositions to
XX CC inhibit expression of nucleic acid molecules including DNA and RNA in
XX CC cells such as bacterial, fungal, yeast, mammalian, cancer and virally-
XX CC infected cells. They are used in oligomers for gene regulation,
XX CC antisense technology, diagnostic applications to detect target sequences
XX CC in biological samples such as those containing pathogenic bacteria,
XX CC fungi and viruses, oncogenes, growth hormones and enzymes, to target
XX CC genes or encoded RNAs that encode enzymes, cytokines, oncogenes, growth
XX CC adhesion molecules, receptor molecules, hormones, serum proteins,
XX CC factors and interleukins associated with pathological conditions such as
XX CC inflammatory conditions, cardiovascular disorders, immune reactions,
XX CC cancer, viral infections and bacterial infections (see AAA07786 for
XX CC details of other uses for which the oligomers are suitable for).
XX CC Oligomers comprising the nucleomonomers exhibit increased duplex DNA
XX CC stability when hybridizing to target nucleic acid sequences, are
XX CC physiologically stable, non-toxic and able to penetrate into cells while
XX CC maintaining stringent base pair fidelity for target DNA sequences. The
XX CC oligomers demonstrate significant single- or double-stranded target
XX CC nucleic acid binding activity to form duplexes, triplexes or other forms
XX CC of stable association. Sequences AAA07820-834 represent sequences forming
XX CC triplex oligomers.
XX SQ Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 1 U; 0 other;
XX
XX Query Match 1.4%; Score 15; DB 1; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 3.5e+02;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1084 AAAAAAAAAAAAAA 1098
XX Db 15 AAAAAAAAAAAAAA 1
XX
XX RESULT 748
XX AAA07834/c
XX ID AAA07834 standard; DNA; 15 BP.
XX XX
XX AC AAA07834;
XX XX
XX DT 23-JUN-2000 (first entry)
XX DE Nucleic acid sequence of a strand of triplex oligomer 17.
```

XX Nucleonome; cancer; gene regulation; antisense technology; leukemia;
 KW viral infection; inflammatory response; cellular proliferation;
 KW psoriasis; duplex; triplex; ss.
 XX Synthetic.
 XX WO200011013-A1.
 PN 02-MAR-2000.
 XX 20-AUG-1999; 99WO-US19029.
 PF 22-AUG-1998; 98US-0097712.
 PR (UYNE-) UNIV NEBRASKA.
 XX Gold B;
 XX WPI; 2000-246530/21.
 DR Modified nucleonome, used in physiologically stable, non-toxic
 PT oligomers used to inhibit expression of nucleic acids and in gene
 PT regulation, antisense technology and diagnostics -
 XX Disclosure; Page 30; 42pp; English.
 XX The invention provides modified nucleonome of specified formula and
 CC their pharmaceutically acceptable salts. The nucleonome are used as
 CC monomers in oligomers, which are used in pharmaceutical compositions to
 CC inhibit expression of nucleic acid molecules including DNA and RNA in
 CC cells such as bacterial, fungal, yeast, mammalian, cancer and virally-
 CC infected cells. They are used in oligomers for gene regulation,
 CC antisense technology, diagnostic applications to detect target sequences
 CC in biological samples such as those containing pathogenic bacteria,
 CC fungi and viruses, oncogenes, growth hormones and enzymes, to target
 CC genes or encoded RNAs that encode enzymes, hormones, serum proteins,
 CC adhesion molecules, receptor molecules, cytokines, oncogenes, growth
 CC factors and interleukins associated with pathological conditions such as
 CC inflammatory conditions, cardiovascular disorders, immune reactions,
 CC cancer, viral infections and bacterial infections (see AAA07786 for
 CC details of other uses for which the oligomers are suitable for).
 CC Oligomers comprising the nucleonome exhibit increased duplex DNA
 CC stability when hybridizing to target nucleic acid sequences, are
 CC physiologically stable, non-toxic and able to penetrate into cells while
 CC maintaining stringent base pair fidelity for target DNA sequences. The
 CC oligomers demonstrate significant single- or double-stranded target
 CC nucleic acid binding activity to form duplexes, triplexes or other forms
 CC of stable association. Sequences AAA07820-834 represent sequences forming
 CC triplex oligomers.
 XX
 SQ Sequence 15 BP; 0 A; 0 C; 0 G; 13 T; 2 U; 0 other;
 Query Match 1.4%; Score 15; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1084 AAAAAAAAAAAAAA 1098
 DB 15 AAAAAAAAAAAAAA 1
 RESULT 749
 AAZ61854/C
 ID AAZ61854 standard; RNA; 15 BP.
 XX AAZ61854;
 AC
 XX 28-MAR-2000 (first entry)
 DT
 XX HCV 3' non core region substrate for Hammerhead ribozyme HCV.3-118.
 DE Enzymatic nucleic acid; hammerhead ribozyme; virus replication; cleavage;
 KW Enzymatic nucleic acid; hammerhead ribozyme; virus replication; cleavage;

KW cirrhosis; liver failure; hepatocellular carcinoma; interferon; cancer;
 KW autoimmune disease; ss.
 XX Hepatitis C virus.
 XX WO9955847-A2.
 PN 04-NOV-1999.
 PD 26-APR-1999; 99WO-US09027.
 XX 27-APR-1998; 98US-0083217.
 PR 18-SEP-1998; 98US-0100842.
 PR 25-FEB-1999; 99US-0257608.
 PR 23-MAR-1999; 99US-0274553.
 XX (RIBO-) RIBOZYME PHARM INC.
 XX Blatt L, McSwiggen JA, Roberts E, Pavco PA, Macejak D;
 PI WPI; 2000-062023/05.
 XX Novel ribozymes for the treatment of diseases and conditions related to
 PT hepatitis C infection -
 PT Claim 1; Page 49; 123pp; English.
 PS The present sequence represents the preferred target sequence of an
 CC enzymatic nucleic acid, especially a hammerhead ribozyme, which cleaves
 CC the Hepatitis C virus (HCV) RNA sequence in the 3' non-core region.
 CC The HCV sequence was screened for optimal ribozyme target sites using
 CC a computer folding algorithm and regions of the mRNA which did not form
 CC secondary folding structures and contained potential ribozyme cleavage
 CC sites were identified. Ribozymes were synthesized to target these sites
 CC and their activities optimized by either varying the length of the
 CC binding arms or by modification to prevent degradation by nucleases.
 CC The ribozymes of the invention inhibit gene expression and/or viral
 CC replication, and are used to treat diseases associated with Hepatitis C
 CC virus (HCV) infection, e.g. cirrhosis, liver failure and hepatocellular
 CC carcinoma. The ribozymes may be used in combination with interferon to
 CC treat HCV infection, other infectious diseases, autoimmune diseases, and
 CC cancer.
 XX Sequence 15 BP; 0 A; 0 C; 0 G; 15 U; 0 other;
 SQ
 Query Match 1.4%; Score 15; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1084 AAAAAAAAAAAAAA 1098
 DB 15 AAAAAAAAAAAAAA 1
 RESULT 750
 AAZ64910/C
 ID AAZ64910 standard; RNA; 15 BP.
 XX AAZ64910;
 AC
 XX 28-MAR-2000 (first entry)
 DT
 XX Substrate for HH ribozyme HCV.3-118 which cleaves HCV at nt. 9418.
 DE Enzymatic nucleic acid; hammerhead ribozyme; virus replication; cleavage;
 KW cirrhosis; liver failure; hepatocellular carcinoma; interferon; cancer;
 KW autoimmune disease; ss.
 XX Hepatitis C virus.
 OS WO9955847-A2.
 PN 04-NOV-1999.
 PD


```

PN DE10051726-A1.
XX 10-MAY-2001.
XX 18-OCT-2000; 2000DE-1051726.
XX PF
XX 30-OCT-1999; 99DE-1052376.
XX PR
XX (MERE ) MERCK PATENT GMBH.
XX PA
XX Seliger H, Sobkowski M, Hinz M;
XX PI
XX WPI; 2001-336414/36.
XX DR
XX Intermediate for oligonucleotide synthesis comprises partially
XX PT hydrolysed cross-linked vinyl acetate copolymer loaded with nucleotide
XX PT derivative
XX PS
XX Example 2; Page 5; 8pp; German.
XX
XX This invention describes a novel chemical product comprising a partially
XX CC hydrolysed cross-linked vinyl acetate copolymer carrier material loaded
XX CC with nucleotide derivative(s). The product is an intermediate for the
XX CC large (gram) scale solid phase synthesis of modified oligonucleotides
XX CC useful e.g. as clinical diagnostics and therapeutics, e.g. for the
XX CC treatment of AIDS and cancers. The presence of the partially hydrolysed
XX CC copolymer facilitates the synthesis of larger amounts of oligonucleotides
XX CC compared with the use of Merckogel (RTM; macroporous polyvinyl acetate)
XX CC described in Nucleic Acid Res. Sympo. Ser. 31, p. 153, 1994.
XX CC Oligonucleotides are obtained in very good quality and high yields. Also,
XX CC the nucleosides do not display the reduced activity seen in some prior
XX CC art procedures, less carrier material, reagents and solvent are required.
XX CC Further, the carrier material is biodegradable and thus does not present
XX CC disposal problems. It also swells uniformly in a range of solvents, which
XX CC obviates expansion or contraction during use or solvent exchange.
XX CC AAH20510-AAH20513 represent oligonucleotides containing modified
XX CC deoxynucleotides which are used to illustrate the method of the
XX CC invention.
XX SQ
XX Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 other;
XX
XX Query Match 1.4%; Score 15; DB 1; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 3.5e+02;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1084 AAAAAAAAAAAAAA 1098
XX Db 15 AAAAAAAAAAAAAA 1
XX
XX RESULT 753
XX AAF53331/c
XX ID AAF53331 standard; DNA; 15 BP.
XX AC
XX AAF53331;
XX DT 30-MAR-2001 (first entry)
XX DE
XX IGF-I oligonucleotide #4291.
XX
XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
XX KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
XX KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
XX KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
XX KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
XX KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
XX KW hyperneovascular condition; hyperplasia; kidney disease;
XX KW neovascular condition of the retina; ss.
XX
XX Homo sapiens.
XX OS
XX WO200078341-A1.
XX PN
XX 28-DEC-2000.
XX
XX 21-JUN-2000; 2000WO-AU00693.
XX XX

```

28-DEC-2000.

21-JUN-2000; 2000WO-AU00693.

21-JUN-1999; 99US-0140345.

(MURD-) MURDOCH CHILDRENS RES INST.

Wraight CJ, Werther GA, Edmondson SR;

WPI; 2001-041421/05.

Ameliorating the effects of a disorder, e.g. psoriasis, by administering UV (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or inflammation -

Example 8; Page 88; 201pp; English.

The present invention relates to a method for ameliorating the effects of skin disorders. The method comprises contacting the skin with an antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1 receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of inhibiting or reducing growth factor mediated cell proliferation, inflammation and/or other disorders. The present sequence is an oligonucleotide which can be used to design the antisense oligonucleotide of the present invention (see AAF45151 and AAF45153-FA5161). The method is useful for ameliorating the effects of psoriasis, ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis, neoplasias, scleroderma, warts, benign growths, cancers of the skin, a hyperneovascular condition such as a neovascular condition of the retina, brain or skin, growth factor-mediated malignancies, other sclerotic diseases, kidney disease, hyperproliferation of the inside of blood vessels or any other hyperplasia.

Sequence 15 BP; 3 A; 5 C; 3 G; 4 T; 0 other;

Query Match 1.4%; Score 15; DB 1; Length 15;

Best Local Similarity 100.0%; Pred. No. 3.5e+02;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 320 CTGCAGAGAAGCTGT 334

Db 15 CTGCAGAGAAGCTGT 1

RESULT 754

AAF53332/c

ID AAF53332 standard; DNA; 15 BP.

AC

AAF53332;

DT 30-MAR-2001 (first entry)

DE

IGF-I oligonucleotide #4292.

Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic; cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid; skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis; IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris; growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba; keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease; hyperneovascular condition; hyperplasia; kidney disease; neovascular condition of the retina; ss.

Homo sapiens.

WO200078341-A1.

28-DEC-2000.

21-JUN-2000; 2000WO-AU00693.

PR 21-JUN-1999; 99US-0140345.
 XX (MURD-) MURDOCH CHILDRENS RES INST.
 XX Wright CJ, Werther GA, Edmondson SR;
 XX WPI; 2001-041421/05.
 XX
 XX Ameliorating the effects of a disorder, e.g. psoriasis, by
 PT administering UV (ultra-violet) treatment (optional) and an antisense
 PT nucleic acid that inhibits or reduces growth factor mediated cell
 PT proliferation and/or inflammation -
 XX
 XX Example 8; Page 88; 201pp; English.
 XX
 XX The present invention relates to a method for ameliorating the effects
 CC of skin disorders. The method comprises contacting the skin with an
 CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
 CC inhibiting or reducing growth factor mediated cell proliferation,
 CC inflammation and/or other disorders. The present invention is an
 CC oligonucleotide which can be used to design the antisense
 CC oligonucleotides of the present invention (see AAF45151 and
 CC AAF45153-F45161). The method is useful for ameliorating the effects of
 CC psoriasis, ichthyosis, pityriasis, ruba, pilaris, seborrheoa, keloids,
 CC keratosis, neoplasias, scleroderma, warts, benign growths, cancers of the
 CC skin, a hyperneovascular condition such as a neovascular condition of the
 CC retina, brain or skin, growth factor-mediated malignancies, other
 CC sclerotic disease, kidney disease, hyperproliferation of the inside of
 CC blood vessels or any other hyperplasia.
 XX
 XX Sequence 15 BP; 2 A; 5 C; 3 G; 5 T; 0 other;
 SQ
 Query Match 1.4%; Score 15; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 319 ACTGCAGAGAGCTG 333
 Db 15 ACTGCAGAGAGCTG 1
 RESULT 755
 AAF16603
 ID AAF16603 standard; DNA; 15 BP.
 XX
 AC AAF16603;
 XX
 DT 13-MAR-2001 (first entry)
 XX
 DE Gastric acid production inhibiting oligonucleotide SEQ ID NO: 90.
 XX
 KW Gastric acid disturbance; gastric reflux; gastritis; dyspepsia;
 KW stomach ulcer; duodenal ulcer; Helicobacter pylori; antisense;
 KW DNA-RNA hybrid; ss.
 XX
 OS Homo sapiens.
 XX
 FN WO200071164-A1.
 XX
 PD 30-NOV-2000.
 XX
 PF 24-MAY-2000; 2000WO-AU00498.
 XX
 PR 24-MAY-1999; 99AU-0000510.
 XX
 PA (TACH/) TACHAS G.
 XX
 PI Tachas G;
 XX
 DR WPI; 2001-025093/03.
 XX
 PT Treating gastric acid disturbance by administering an oligonucleotide

PT which modulates the activity of a polypeptide involved in gastric acid
 PT production or secretion -
 XX
 XX Example 3; Page 148; 164pp; English.
 XX
 XX The present invention provides oligonucleotides, and methods for their
 CC use, which are useful in modulating the action of proteins involved in
 CC gastric acid production. The target protein is preferably the histamine
 CC H2 receptor or one of the proteins which form part of the gastric proton
 CC pump. The sequences and methods of the invention are useful in the
 CC treatment of gastric reflux, gastritis, dyspepsia, stomach ulcers,
 CC duodenal ulcers and other gastric acid disturbances, most of which are
 CC caused by Helicobacter pylori.
 XX
 XX Sequence 15 BP; 14 A; 0 C; 0 G; 1 T; 0 other;
 SQ
 Query Match 1.4%; Score 15; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1083 TAAAAAATAAAAAA 1097
 Db 1 TAAAAAATAAAAAA 15
 RESULT 756
 AAF30882/C
 ID AAF30882 standard; DNA; 15 BP.
 XX
 AC AAF30882;
 XX
 DT 09-JUL-2001 (first entry)
 XX
 DE Oligonucleotide portion of ODN-MGB-LF conjugate.
 XX
 KW ODN-MGB-LF; oligonucleotide; minor groove binder;
 KW latent fluorophore; hybridisation; detection; fluorescence; probe;
 KW ss.
 XX
 OS Synthetic.
 XX
 FN WO200131063-A1.
 XX
 PD 03-MAY-2001.
 XX
 PF 26-OCT-2000; 2000WO-US29786.
 XX
 PR 26-OCT-1999; 99US-0428236.
 XX
 PA (EPOC-) EPOCH BIOSCIENCES INC.
 XX
 PI Dempcy RO, Afonina IA, Vermeulen NMJ;
 XX
 DR WPI; 2001-328656/34.
 XX
 PT Conjugate of oligonucleotide, minor groove binder and latent
 PT fluorophore, useful for detecting specific nucleic acids, e.g. for
 PT single-nucleotide mismatch discrimination -
 XX
 XX Disclosure: Page 58; 105pp; English.
 XX
 XX The present sequence is that of the oligonucleotide (ODN) component
 CC of an ODN-MGB (minor groove binder)-LF (latent fluorophore)
 CC conjugate of the invention. MGBs bind in a non-intercalating
 CC manner to the minor groove of non-single-stranded DNA, RNA or their
 CC hybrids, while a LF binds similarly but in an intercalating manner,
 CC or lies in the minor groove, or is oriented in some other way to
 CC the DNA molecule by MGB, such that it becomes fluorescent (or its
 CC fluorescent properties change detectably). The conjugates are used
 CC as hybridisation probes and amplification primers for fluorescent
 CC detection of specifically hybridising sequences, for analysis or
 CC diagnosis, especially (real-time) PCR, for single-nucleotide
 CC mismatch discrimination, target or signal amplification,

CC array-based assays and sequencing, including detection of
 CC double-stranded DNA by triplex formation. Many different targets
 CC can be detected at a single reaction vessel. The present ODN-MGB-LF
 CC conjugate was used to demonstrate hybridisation-triggered
 CC fluorescence. Upon hybridisation to the complementary target
 CC sequence there was an increase in fluorescence yield, measured as
 CC the ratio of the fluorescence emitted by the hybrid between the
 CC ODN-MGB-LF conjugate and its target sequence to the fluorescence
 CC emitted by unhybridised (i.e. single-stranded) ODN-MGB-LF, of 8.3.
 XX
 SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 other;
 Query Match 1.4%; Score 15; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1084 AAAAAAAAAAAAAA 1098
 Db 15 AAAAAAAAAAAAAA 1
 RESULT 757
 AAH49243/c
 ID AAH49243 standard; DNA; 15 BP.
 XX
 AC AAH49243;
 XX
 DT 26-NOV-2001 (first entry)
 DE
 DE PNA-forming oligonucleotide #7.
 XX
 KW Polyamide-oligonucleotide derivative; anticancer; antiproliferative;
 KW antiviral; hepatotropic; vasotropic; antisense inhibition; ribozyme;
 KW integrin; cell-cell adhesion; cancer; restenosis; stability; PNA;
 KW peptide nucleic acid; ss.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT modified_base 9
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "t-but"
 FT modified_base 15
 FT /*tag= b
 FT /mod_base= OTHER
 FT /note= "t-hex"
 XX
 PN EP1113021-A2.
 XX
 PD 04-JUL-2001.
 XX
 PF 08-MAR-1995; 2001EP-0104012.
 XX
 PR 14-MAR-1994; 94DE-4408528.
 PR 08-MAR-1995; 95EP-0103332.
 XX
 PA (AVET) AVENTIS PHARMA DEUT GMBH.
 XX
 PI Uhlmann E, Breipohl G;
 XX
 DR WPI; 2001-591267/67.
 XX
 PT New DNA-peptide nucleic acid chimeras, useful e.g. as antisense agents
 PT for treating e.g. cancer, also as diagnostic probes and primers
 XX
 XX Example 26; Page 40; 54pp; German.
 XX
 CC This invention describes novel polyamide-oligonucleotide derivatives (I)
 CC and their physiologically acceptable salts of formula
 CC F((DNA)-Li) q(PNA-Li) r(DNA-Li) s(PNA) t) xF, where q, r, s, t = 0 or 1,
 CC with the sum of two or more adjacent letters at least 2; x = 1-20; DNA
 CC = nucleic acid (such as DNA or RNA or their known derivatives); Li =

CC covalent linkage between DNA and PNA, i.e. a bond or a residue containing
 CC at least one atom of carbon, nitrogen, oxygen or sulfur; PNA = polyamide
 CC structure containing at least one nucleobase different from thymine; and
 CC F, F' = end groups and/or are connected through a covalent bond. The
 CC products of the invention have anticancer, antiproliferative, antiviral,
 CC hepatotropic and vasotropic activity and can be used for the inhibition
 CC of gene expression by antisense, ribozyme, sense, or triple-helix
 CC methods, or by binding to proteins (aptamers). (I) are used for treating
 CC diseases caused by viruses (human immune deficiency, herpes simplex,
 CC influenza, vesicular stomatitis, hepatitis B or papilloma), or mediated
 CC by integrins or cell-cell adhesion reactions, for treating cancer, or
 CC for inhibiting restenosis, particularly as antisense reagents. They are
 CC also useful in heterogeneous or homogeneous assays, as primers or probes,
 CC particularly where the target is amplified before being detected by
 CC hybridization, for diagnosis of genetic, malignant or pathogen-related
 CC diseases. (I) retain the increased affinity for complementary strands and
 CC better stability in serum, associated with conventional peptide nucleic
 CC acids (PNA), but lack the disadvantages, i.e. have improved cellular
 CC uptake, do not aggregate in aqueous solution, and have reduced affinity
 CC for purification materials, reduced cytotoxicity, better sequence
 CC specificity. They are more active than either DNA or PNA oligomers. When
 CC used as probes, (I) show different responses to base-pair mismatches in
 CC the DNA and PNA segments, allowing better discrimination between
 CC pathogenic and non-pathogenic conditions such as the transition from
 CC proto-oncogene to oncogene, also, when used as primers, with the PNA
 CC segment at the 5'-end, they produce amplicons resistant to
 CC 5'-exonuclease, allowing this enzyme to be used to eliminate RNA or DNA
 CC primers. The DNA component allows additional reactions not possible with
 CC PNA alone, e.g. 3'-tailing and (I) may be incorporated into a gene.
 CC AAH49208-AAH49264 represent oligonucleotides used to illustrate the
 CC method of the invention.
 XX
 SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 other;
 Query Match 1.4%; Score 15; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1084 AAAAAAAAAAAAAA 1098
 Db 15 AAAAAAAAAAAAAA 1
 RESULT 758
 ABX00240/c
 ID ABX00240 standard; RNA; 15 BP.
 XX
 AC ABX00240;
 XX
 DT 23-DEC-2002 (first entry)
 XX
 DE Hepatitis C virus substrate #22 for HCV hammerhead ribozyme #22.
 XX
 KW Enzymatic nucleic acid; RNA cleavage; Hepatitis C virus infection;
 KW HCV ribozyme; HCV expression; HCV replication; cirrhosis; virucide;
 KW liver failure; hepatocellular carcinoma; HCV infection; drug therapy;
 KW type I interferon; interferon alpha; interferon beta; cytosstatic;
 KW interferon gamma; consensus interferon; hepatotropic; antiinflammatory;
 KW substrate; hammerhead ribozyme; H1 ribozyme; ss.
 XX
 OS Hepatitis C virus.
 XX
 PN US2002082225-A1.
 XX
 PD 27-JUN-2002.
 XX
 XX 23-MAR-1999; 99US-0274553.
 XX
 PR 23-MAR-1999; 99US-0274553.
 XX
 XX (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGGEN J A.
 PA (ROBE/) ROBERTS B.

PA (PAVC/) PAVCO P A.
 XX (MACE/) MACEJACK D.
 PI Blatt L, McSwiggen JA, Roberts B, Pavco PA, Macejack D;
 XX WPI; 2002-617759/66.
 DR
 XX
 XX New ribozymes targeting RNA derived from hepatitis C virus inhibit
 PT viral replication and are useful to treat hepatitis C virus infections
 PT and cirrhosis, liver failure or hepatocellular carcinoma -
 XX
 XX
 PS Claim 1; Page 21; 80pp; English.
 XX
 XX The present invention relates to enzymatic nucleic acids which
 CC specifically cleave RNA derived from Hepatitis C virus (HCV). The
 CC enzymatic nucleic acid or ribozyme is in a hammerhead (HH) or
 CC hairpin (HP) motif where the binding arms comprise sequences
 CC complementary to one of the substrate sequences defined in the
 CC specification. The HCV ribozymes are useful for modulating the
 CC expression and/or replication of HCV. They can be used to treat
 CC cirrhosis, liver failure and/or hepatocellular carcinoma. The HCV
 CC ribozymes are also useful for treating a condition associated with
 CC HCV infection in conjunction with one or more other drug therapies,
 CC particularly type I interferon, especially interferon alpha, beta or
 CC gamma or consensus interferon. The present sequence represents a
 CC substrate for a HCV hammerhead (HH) ribozyme.
 CC Note: Some of the sequence data for this patent did not form part of
 CC the printed specification. The complete sequence data for this patent
 CC was obtained in electronic format directly from the USPTO web site
 CC at seqdata.uspto.gov/psipdIDEntry.html.
 XX
 SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 U; 0 other;

Query Match 1.4%; Score 15; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1084 AAAAAAAAAAAAAA 1098
 Db 15 AAAAAAAAAAAAAA 1

RESULT 759
 ABX03406/C
 ID ABX03406 standard; RNA; 15 BP.
 XX
 AC ABX03406;
 XX
 DT 24-DEC-2002 (first entry)
 XX
 DE Hepatitis C virus substrate #1319 for HCV hammerhead ribozyme #1319.
 XX
 KW Enzymatic nucleic acid; RNA cleavage; Hepatitis C virus infection;
 KW HCV ribozyme; HCV expression; HCV replication; cirrhosis; virucide;
 KW liver failure; hepatocellular carcinoma; HCV infection; drug therapy;
 KW type I interferon; interferon alpha; interferon beta; cytosstatic;
 KW interferon gamma; consensus interferon; hepatotropic; antiinflammatory;
 KW substrate; hammerhead ribozyme; HH ribozyme; ss.
 XX
 OS Hepatitis C virus.
 XX
 XX US2002082225-A1.
 XX
 XX 27-JUN-2002.
 XX
 XX 23-MAR-1999; 99US-0274553.
 XX
 XX 23-MAR-1999; 99US-0274553.
 XX
 XX (BLAT/) BLATT L.
 XX (MCSW/) MCSWIGGEN J A.
 XX (ROBE/) ROBERTS B.
 XX (PAVC/) PAVCO P A.

PA (MACE/) MACEJACK D.
 XX
 PI Blatt L, McSwiggen JA, Roberts B, Pavco PA, Macejack D;
 XX WPI; 2002-617759/66.
 DR
 XX
 XX New ribozymes targeting RNA derived from hepatitis C virus inhibit
 PT viral replication and are useful to treat hepatitis C virus infections
 PT and cirrhosis, liver failure or hepatocellular carcinoma -
 XX
 XX
 PS Claim 1; Page 64; 80pp; English.
 XX
 XX The present invention relates to enzymatic nucleic acids which
 CC specifically cleave RNA derived from Hepatitis C virus (HCV). The
 CC enzymatic nucleic acid or ribozyme is in a hammerhead (HH) or
 CC hairpin (HP) motif where the binding arms comprise sequences
 CC complementary to one of the substrate sequences defined in the
 CC specification. The HCV ribozymes are useful for modulating the
 CC expression and/or replication of HCV. They can be used to treat
 CC cirrhosis, liver failure and/or hepatocellular carcinoma. The HCV
 CC ribozymes are also useful for treating a condition associated with
 CC HCV infection in conjunction with one or more other drug therapies,
 CC particularly type I interferon, especially interferon alpha, beta or
 CC gamma or consensus interferon. The present sequence represents a
 CC substrate for a HCV hammerhead (HH) ribozyme.
 CC Note: Some of the sequence data for this patent did not form part of
 CC the printed specification. The complete sequence data for this patent
 CC was obtained in electronic format directly from the USPTO web site
 CC at seqdata.uspto.gov/psipdIDEntry.html.
 XX
 SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 U; 0 other;

Query Match 1.4%; Score 15; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1084 AAAAAAAAAAAAAA 1098
 Db 15 AAAAAAAAAAAAAA 1

RESULT 760
 ABQ82140
 ID ABQ82140 standard; DNA; 15 BP.
 XX
 AC ABQ82140;
 XX
 DT 11-DEC-2002 (first entry)
 XX
 DE Acceptor vector pHELLSGATE 4 nucleotide sequence SEQ ID NO:23.
 XX
 KW Chimeric nucleic acid construct; recombinational cloning; silencing;
 KW recombination site; double stranded RNA; plant; ds.
 XX
 OS Synthetic.
 XX
 XX WO200259294-A1.
 XX
 XX 01-AUG-2002.
 XX
 XX 24-JAN-2002; 2002WO-AU00073.
 XX
 XX 26-JAN-2001; 2001US-264067P.
 XX
 XX 29-NOV-2001; 2001US-333743P.
 XX
 XX (CSIR) COMMONWEALTH SCI & IND RES ORG.
 XX
 XX Wesley S, Waterhouse P, Helliwell C;
 PI
 XX WPI; 2002-682669/73.
 DR
 XX
 XX New vectors comprising operably linked DNA fragments having an origin
 PT of replication, a selectable marker and a chimeric DNA construct,

PT useful for silencing target nucleic acids and for producing large
PT amounts of double-stranded RNA -
XX
PS Claim 14; Page 74; 104pp; English.
XX
CC The present invention describes a vector (I) comprising operably linked
CC DNA fragments having: (a) origin of replication allowing replication in a
CC recipient cell, preferably in bacteria such as *Escherichia coli*;
CC (b) selectable marker region capable of being expressed in the recipient
CC cell; and (c) a chimeric DNA construct comprising: (i) promoter or
CC promoter region capable of being recognized by RNA polymerase of a
CC eukaryotic cell or by prokaryotic RNA polymerase; (ii) first, second,
CC third and fourth recombination sites; (iii) 3' transcription terminating
CC and polyadenylation region functional in the eukaryotic cell. The first
CC and fourth recombination sites, or the second and third recombination
CC sites are capable of reacting with a same recombination site, and
CC preferably are identical. The first and second recombination sites, or
CC the third and fourth recombination sites, do not recombine with each
CC other or with a same recombination site. The vector is useful for
CC producing large amounts of double-stranded RNA which can be used for
CC silencing target nucleic acid sequences. The vectors can also be used to
CC convert a DNA fragment into an inverted repeat structure. Plants
CC transformed with a vector from the present invention can be used in a
CC conventional breeding scheme to produce more plants with the same
CC characteristics or to introduce a chimeric gene for reduction of the
CC phenotypic expression of nucleic acids. The present sequence represents
CC an acceptor vector nucleotide sequence from the present invention.

SQ Sequence 15 BP; 15 A; 0 C; 0 G; 0 U; 0 other;
Query Match 1.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1098
Db 1 AAAAAAAAAAAAAA 15

RESULT 761
AAL49453
ID AAL49453 standard; DNA; 15 BP.
AC AAL49453;
XX
XX
DT 14-NOV-2002 (first entry)
XX
DE Mutation detection method tag peptide coding sequence SEQ ID NO: 1.
XX
KW Mutation detection; primer; mutant; tag; tumour suppressor gene;
KW protein production; cancer; ds.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT CDS 1..15
FT /*tag= a
FT /product= "tag peptide"
FT /partial
FT /note= "no start or stop"
XX
XX WO200266675-A2.
PN
XX
XX 29-AUG-2002.
PD
XX
XX 15-FEB-2002; 2002WO-EP01651.
PF
XX
XX 16-FEB-2001; 2001DE-1007317.
PR
XX
XX (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
PA Kahmann S, Mueller O;
XX
XX WPI; 2002-674959/72.
PI P-PSDB; AAO19056.
XX

DR WPI; 2002-674959/72.
DR P-PSDB; AAO19054.
XX
PT Detecting mutations in nucleic acid, useful for diagnosis and
PT characterization of tumors, by amplification, in vitro transcription
PT and translation, then protein detection -
XX
XX Claim 11; Fig 5; 62pp; German.

XX
CC The present invention relates to a method of detecting mutations in a
CC nucleic acid by amplifying the nucleic acid to produce a double-stranded
CC amplicon, in vitro transcription and translation of this amplicon, and
CC detection of the translated protein. The primers used for amplification
CC are designed to produce an amplicon that is translatable and allows
CC differentiation between translation products of wild-type and mutated
CC nucleic acids. The method is used to detect mutations in tumour
CC suppressor genes, for (early) diagnosis, monitoring and characterisation
CC of tumours (especially of bladder and intestines) and in the germ line
CC (using nucleic acids from embryos or blood cells). A new multi-tag vector
CC is used to detect or verify the reading frame of a nucleic acid cloned in
CC it, and to determine the suitability of detectable peptides for analysis
CC and/or purification of a recombinant protein, expressed from a sequence
CC cloned in the vector. The present sequence encodes a tag peptide and was
CC used in the invention.

SQ Sequence 15 BP; 15 A; 0 C; 0 G; 0 U; 0 other;

Query Match 1.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1098
Db 1 AAAAAAAAAAAAAA 15

RESULT 762
AAL49455
ID AAL49455 standard; DNA; 15 BP.
AC AAL49455;
XX
XX 14-NOV-2002 (first entry)
XX
DE Mutation detection method tag peptide coding sequence SEQ ID NO: 3.
XX
KW Mutation detection; primer; mutant; tag; tumour suppressor gene;
KW protein production; cancer; ds.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT CDS 1..15
FT /*tag= a
FT /product= "tag peptide"
FT /partial
FT /note= "no start or stop"
XX
XX WO200266675-A2.
PN
XX
XX 29-AUG-2002.
PD
XX
XX 15-FEB-2002; 2002WO-EP01651.
PF
XX
XX 16-FEB-2001; 2001DE-1007317.
PR
XX
XX (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
PA Kahmann S, Mueller O;
XX
XX WPI; 2002-674959/72.
PI P-PSDB; AAO19056.
XX

PT Detecting mutations in nucleic acid, useful for diagnosis and
PT characterization of tumors, by amplification, in vitro transcription
PT and translation, then protein detection
XX
PS Claim 11; Fig 5; 62pp; German.
XX
CC The present invention relates to a method of detecting mutations in a
CC nucleic acid by amplifying the nucleic acid to produce a double-stranded
CC amplicon, in vitro transcription and translation of this amplicon, and
CC detection of the translated protein. The primers used for amplification
CC are designed to produce an amplicon that is translatable and allows
CC differentiation between translation products of wild-type and mutated
CC nucleic acids. The method is used to detect mutations in tumour
CC suppressor genes, for (early) diagnosis, monitoring and characterisation
CC of tumours (especially of bladder and intestines) and in the germ line
CC (using nucleic acids from embryos or blood cells). A new multi-tag vector
CC is used to detect or verify the reading frame of a nucleic acid cloned in
CC it, and to determine the suitability of detectable peptides for analysis
CC and/or purification of a recombinant protein, expressed from a sequence
CC cloned in the vector. The present sequence encodes a tag peptide and was
CC used in the invention.
XX
SQ Sequence 15 BP; 15 A; 0 C; 0 G; 0 U; 0 other;

Query Match 1.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1084 AAAAAAAAAAAAAA 1098
Db 1 AAAAAAAAAAAAAA 15

RESULT 763
ABK98141/c
ID ABK98141 standard; DNA; 15 BP.
AC ABK98141;
XX
XX 07-OCT-2002 (first entry)
XX
XX Triple helix forming associated oligonucleotide #26.
DE
DE Triple-helix formation; purine-rich target sequence; double-helix DNA;
KW Gene expression; regulatory sequence; pathogenic double-stranded DNA;
KW pathogenic bacteria; virus; replication; virulence; cancer;
KW oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.
XX
XX Synthetic.
XX
XX US6403302-B1.
XX
XX 11-JUN-2002.
XX
XX 16-DEC-1993; 93US-0168920.
XX
XX 17-SEP-1992; 92US-0946976.
XX
XX (CALY) CALIFORNIA INST OF TECHNOLOGY.
XX
XX Dervan PB, Beal PA;
XX
XX WPI; 2002-536030/57.
XX
XX A triple-helix comprising a double helical nucleic acid (DHNA) and an
XX oligonucleotide which binds in parallel and antiparallel orientation,
XX respectively, for targetting sequences on alternate strands of DHNA to
XX control gene expression -
XX
XX Example 1; Fig 3B; 108pp; English.
XX
XX The present invention relates to methods and oligonucleotides for
XX forming a triple-helix comprising a double helical nucleic acid

CC comprising first and second substantially complementary strands, and
CC an oligonucleotide bound to a purine-rich target sequence within the
CC double helical nucleic acid, where the oligonucleotide binds in a
CC parallel and antiparallel orientation, respectively, to target
CC sequences on alternate strands of the double helical nucleic acid.
CC The method has therapeutic applications, where gene expression is
CC controlled by selective triple-helix formation within expression
CC regulatory sequences of a target gene. The oligonucleotides can be
CC used to form triple-helices, and are useful to detect the presence or
CC absence of specific sequences within genomic DNA for diagnostic and
CC therapeutic purposes. The oligonucleotides can be selected to
CC specifically bind to pathogenic double-stranded DNA including specific
CC sequences required by pathogenic bacteria or viruses for replication or
CC virulence, reducing their pathogenicity. Alternatively, the
CC oligonucleotide can be chosen to target a unique sequence of the
CC pathogen which is not found in the genome of pathogen's host. The
CC oligonucleotides can be used in cancer treatment by way of triple-helix
CC suppression of specific oncogenes including those of endogenous or
CC viral origin. Such therapeutic oligonucleotides are capable of forming
CC triple-helices with such sequences in cancerous cells containing the
CC activated oncogene, so preferentially killing or repressing the cancer
CC causing cell. The present sequence represents an oligonucleotide
CC used in the methods of the present invention.
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 other;
Query Match 1.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1084 AAAAAAAAAAAAAA 1098
Db 15 AAAAAAAAAAAAAA 1
RESULT 764
ABK98184/c
ID ABK98184 standard; DNA; 15 BP.
XX
XX ABK98184;
XX
XX 07-OCT-2002 (first entry)
XX
XX Triple helix forming associated oligonucleotide #48.
DE
DE Triple-helix formation; purine-rich target sequence; double-helix DNA;
KW Gene expression; regulatory sequence; pathogenic double-stranded DNA;
KW pathogenic bacteria; virus; replication; virulence; cancer;
KW oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.
XX
XX Synthetic.
XX
XX US6403302-B1.
XX
XX 11-JUN-2002.
XX
XX 16-DEC-1993; 93US-0168920.
XX
XX 17-SEP-1992; 92US-0946976.
XX
XX (CALY) CALIFORNIA INST OF TECHNOLOGY.
XX
XX Dervan PB, Beal PA;
XX
XX WPI; 2002-536030/57.
XX
XX A triple-helix comprising a double helical nucleic acid (DHNA) and an
XX oligonucleotide which binds in parallel and antiparallel orientation,
XX respectively, for targetting sequences on alternate strands of DHNA to
XX control gene expression -
XX
XX Example 7; Fig 24A; 108pp; English.

CC The present invention relates to methods and oligonucleotides for
 CC forming a triple-helix comprising a double helical nucleic acid
 CC comprising first and second substantially complementary strands, and
 CC an oligonucleotide bound to a purine-rich target sequence within the
 CC double helical nucleic acid, where the oligonucleotide binds in a
 CC parallel and antiparallel orientation, respectively, to target
 CC sequences on alternate strands of the double helical nucleic acid.
 CC The method has therapeutic applications, where gene expression is
 CC controlled by selective triple-helix formation within expression
 CC regulatory sequences of a target gene. The oligonucleotides can be
 CC used to form triple-helices, and are useful to detect the presence or
 CC absence of specific sequences within genomic DNA for diagnostic and
 CC therapeutic purposes. The oligonucleotides can be selected to
 CC specifically bind to pathogenic double-stranded DNA including specific
 CC sequences required by pathogenic bacteria or viruses for replication or
 CC virulence, reducing their pathogenicity. Alternatively, the
 CC oligonucleotide can be chosen to target a unique sequence of the
 CC pathogen which is not found in the genome of pathogen's host. The
 CC oligonucleotides can be used in cancer treatment by way of triple-helix
 CC suppression of specific oncogenes including those of endogenous or
 CC viral origin. Such therapeutic oligonucleotides are capable of forming
 CC triple-helices with such sequences in cancerous cells containing the
 CC activated oncogene, so preferentially killing or repressing the cancer
 CC causing cell. The present sequence represents an oligonucleotide
 CC used in the methods of the present invention.

XX SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 other;
 Query Match 1.4%; Score 15; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1098
 DB 15 AAAAAAAAAAAAAA 1

RESULT 765
 ABL57054/c
 ID ABL57054 standard; DNA; 15 BP.
 XX AC ABL57054;
 XX DT 22-JUL-2002 (first entry)
 XX DE Hydrazide phosphoramidite oligonucleotide O9.
 XX KW Macromolecule; hydrazide; immobilisation; ss.
 XX OS Synthetic.
 FH Key Location/Qualifiers
 FT modified_base 1 /*tag= a
 FT /mod_base= "OTHER"
 FT /note= "6-((2Cyanethoxy)(diisopropylamino)
 FT phosphanyloxy)-N'-tritylhexanohydrazide"
 FT modified_base 1.15
 FT /*tag= b
 FT /mod_base= "OTHER"
 FT /note= "phosphoramidite linkage"
 WO200214558-A2.
 XX DT 21-FEB-2002.
 XX PF 10-AUG-2001; 2001WO-US41663.
 XX PR 11-AUG-2000; 2000WO-US22205.
 XX PA (NANO-) NANOGEN INC.
 XX Raddatz S, Mueller-Ibeler J, Schweitzer M, Bruecher C, Windhab N;
 PI Havens JR, Onofrey TJ, Greef CH, Wang D;

XX WPI; 2002-401666/43.
 XX Compound for binding macromolecule to substrate surface or conjugation
 XX targets, contains phosphorus containing reactive group, hydrazide
 XX protecting group and benzene ring, and has predefined formula -
 XX Example 2; Page 40; 120pp; English.
 XX The present sequence is of a trityl deprotected hydrazide
 XX phosphoramidite 15-mer, designated oligo O9, which was produced in
 XX an example from the invention. The invention describes an improved
 XX process for immobilisation of macromolecules including DNA, RNA,
 XX peptide nucleic acids, pyranosyl-RNA and peptides, especially
 XX macromolecules containing multiple reactive sites, to a substrate
 XX surface or other conjugation target. It also describes the
 XX preparation of oligos containing one or more hydrazides, which can
 XX be used for conjugation to surface binding moieties, or for other
 XX conjugation reactions. The process is useful e.g. in nucleic acid
 XX hybridisation based assays, DNA chip technology and biosensor
 XX applications.
 XX SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 other;
 Query Match 1.4%; Score 15; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1098
 DB 15 AAAAAAAAAAAAAA 1

RESULT 766
 ABL57056/c
 ID ABL57056 standard; DNA; 15 BP.
 XX AC ABL57056;
 XX DT 22-JUL-2002 (first entry)
 XX DE Hydrazide phosphoramidite oligonucleotide O31.
 XX KW Macromolecule; hydrazide; immobilisation; ss.
 XX OS Synthetic.
 FH Key Location/Qualifiers
 FT modified_base 1 /*tag= a
 FT /mod_base= "OTHER"
 FT /note= "6-((2Cyanethoxy)(diisopropylamino)
 FT phosphanyloxy)-N'-tritylhexanohydrazide"
 FT modified_base 1.15
 FT /*tag= b
 FT /note= "phosphoramidite linkage"
 FT modified_base 15
 FT /*tag= c
 FT /mod_base= "OTHER"
 FT /note= "3' Cy3 dye"
 WO200214558-A2.
 XX DT 21-FEB-2002.
 XX PF 10-AUG-2001; 2001WO-US41663.
 XX PR 11-AUG-2000; 2000WO-US22205.
 XX PA (NANO-) NANOGEN INC.
 XX Raddatz S, Mueller-Ibeler J, Schweitzer M, Bruecher C, Windhab N;
 PI Havens JR, Onofrey TJ, Greef CH, Wang D;

```
XX DR WPI; 2002-401666/43.
XX FT Compound for binding macromolecule to substrate surface or conjugation
XX PT targets, contains phosphorous containing reactive group, hydrazide
XX FT protecting group and benzene ring, and has predefined formula
XX PS Example 2; Page 40; 120pp; English.
XX CC The present sequence is of a trityl deprotected hydrazide
XX CC phosphoramidite 15-mer, designated oligo O31, which was produced in
XX CC an example from the invention. The invention describes an improved
XX CC process for immobilisation of macromolecules including DNA, RNA,
XX CC peptide nucleic acids, pyranosyl-RNA and peptides, especially
XX CC macromolecules containing multiple reactive sites, to a substrate
XX CC surface or other conjugation target. It also describes the
XX CC preparation of oligos containing one or more hydrazides, which can
XX CC be used for conjugation to surface binding moieties, or for other
XX CC conjugation reactions. The process is useful e.g. in nucleic acid
XX CC hybridisation based assays, DNA chip technology and biosensor
XX CC applications.
XX SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 other;

Query Match 1.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1084 AAAAAAAAAAAAAA 1098
Db 15 AAAAAAAAAAAAAA 1

RESULT 767
ABL57059/C
ID ABL57059 standard; DNA; 15 BP.
XX AC ABL57059;
XX DT 22-JUL-2002 (first entry)
XX DE Hydrazide precursor phosphoramidite oligonucleotide O33.
XX KW Macromolecule; hydrazide; immobilisation; ss.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT modified_base 1
XX FT /*tag= a
XX FT /mod_base= "OTHER"
XX FT /note= "4-((2-cyanoethyl)-(diisopropylamino)
XX FT phospharyloxymethyl)-benzoic acid methyl
XX FT ester"
XX FT modified_base 1..15
XX FT /*tag= b
XX FT /note= "phosphoramidite linkage"
XX FT modified_base 15
XX FT /*tag= c
XX FT /mod_base= "OTHER"
XX FT /note= "3, Cy3 dye"
XX PN WO200214558-A2.
XX PD 21-FEB-2002.
XX PF 10-AUG-2001; 2001WO-US41663.
XX PR 11-AUG-2000; 2000WO-US22205.
XX PA (NANO-) NANOGEN INC.
XX PI Raddatz S, Mueller-Ibeler J, Schweitzer M, Bruecher C, Windhab N;
```

```
PI XX Havens JR, Onofrey TJ, Greef CH, Wang D;
XX DR WPI; 2002-401666/43.
XX FT Compound for binding macromolecule to substrate surface or conjugation
XX PT targets, contains phosphorous containing reactive group, hydrazide
XX FT protecting group and benzene ring, and has predefined formula
XX PS Example 3; Page 43; 120pp; English.
XX CC The present sequence is of a hydrazine treated hydrazide precursor
XX CC phosphoramidite 15-mer, designated oligo O33, which was produced in
XX CC an example from the invention. The invention describes an improved
XX CC process for immobilisation of macromolecules including DNA, RNA,
XX CC peptide nucleic acids, pyranosyl-RNA and peptides, especially
XX CC macromolecules containing multiple reactive sites, to a substrate
XX CC surface or other conjugation target. It also describes the
XX CC preparation of oligos containing one or more hydrazides, which can
XX CC be used for conjugation to surface binding moieties, or for other
XX CC conjugation reactions. The process is useful e.g. in nucleic acid
XX CC hybridisation based assays, DNA chip technology and biosensor
XX CC applications.
XX SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 other;

Query Match 1.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1084 AAAAAAAAAAAAAA 1098
Db 15 AAAAAAAAAAAAAA 1

RESULT 768
ABL57060/C
ID ABL57060 standard; DNA; 15 BP.
XX AC ABL57060;
XX DT 22-JUL-2002 (first entry)
XX DE Hydrazide precursor phosphoramidite oligonucleotide O34.
XX KW Macromolecule; hydrazide; immobilisation; ss.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT modified_base 1
XX FT /*tag= a
XX FT /mod_base= "OTHER"
XX FT /note= "Diethyl 5-(((2-cyanoethoxy)(diisopropylamino)
XX FT phosphanyloxy)methyl)isophthalate"
XX FT modified_base 1..15
XX FT /*tag= b
XX FT /note= "phosphoramidite linkage"
XX FT modified_base 15
XX FT /*tag= c
XX FT /mod_base= "OTHER"
XX FT /note= "3, Cy3 dye"
XX PN WO200214558-A2.
XX PD 21-FEB-2002.
XX PF 10-AUG-2001; 2001WO-US41663.
XX PR 11-AUG-2000; 2000WO-US22205.
XX PA (NANO-) NANOGEN INC.
XX PI Raddatz S, Mueller-Ibeler J, Schweitzer M, Bruecher C, Windhab N;
```

PI Havens JR, Onofrey TJ, Greef CH, Wang D;
XX WPI; 2002-401666/43.
XX
XX Compound for binding macromolecule to substrate surface or conjugation
PT targets, contains phosphorous containing reactive group, hydrazide
PT protecting group and benzene ring, and has predefined formula -
XX
PS Example 3; Page 43; 120pp; English.
XX
XX The present sequence is of a hydrazine treated hydrazide precursor
CC phosphoramidite 15-mer, designated oligo O34, which was produced in
CC an example from the invention. The invention describes an improved
CC process for immobilisation of macromolecules including DNA, RNA,
CC peptide nucleic acids, pyranosyl-RNA and peptides, especially
CC macromolecules containing multiple reactive sites, to a substrate
CC surface or other conjugation target. It also describes the
CC preparation of oligos containing one or more hydrazides, which can
CC be used for conjugation to surface binding moieties, or for other
CC conjugation reactions. The process is useful e.g. in nucleic acid
CC hybridisation based assays, DNA chip technology and biosensor
CC applications.
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 other;
Query Match 1.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1084 AAAAAAAAAAAAAA 1098
Db |||||||
15 AAAAAAAAAAAAAA 1
RESULT 769
ABL57061/C
ID ABL57061 standard; DNA; 15 BP.
XX AC ABL57061;
XX
XX 22-JUL-2002 (first entry)
XX
XX Hydrazide precursor phosphoramidite oligonucleotide O37.
XX
XX Macromolecule; hydrazide; immobilisation; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FT modified_base 1 /*tag= a
FT /mod_base= "OTHER"
FT /note= "1,3-Bis-(3',5'-bis(ethyloxycarbonyl)
FT phenylcarbonylamido)-2-((2',-cyanoethyloxy)
FT (diisopropyl)amino)-phosphanyloxy)-propane"
FT modified_base 1..15
FT /*tag= b
FT /note= "phosphoramidite linkage"
FT modified_base 15
FT /*tag= c
FT /mod_base= "OTHER"
FT /note= "3' Cy3 dye"
XX
XX WC200214558-A2.
XX
XX 21-FEB-2002.
XX
XX 10-AUG-2001; 2001WO-US41663.
XX
XX 11-AUG-2000; 2000WO-US22205.
XX
XX (NANO-) NANOGEN INC.
XX
XX PA

PI Raddatz S, Mueller-Ibeler J, Schweitzer M, Bruecher C, Windhab N;
PI Havens JR, Onofrey TJ, Greef CH, Wang D;
XX WPI; 2002-401666/43.
XX
XX Compound for binding macromolecule to substrate surface or conjugation
PT targets, contains phosphorous containing reactive group, hydrazide
PT protecting group and benzene ring, and has predefined formula -
XX
PS Example 3; Page 43; 120pp; English.
XX
XX The present sequence is of a hydrazine treated hydrazide precursor
CC phosphoramidite 15-mer, designated oligo O37, which was produced in
CC an example from the invention. The invention describes an improved
CC process for immobilisation of macromolecules including DNA, RNA,
CC peptide nucleic acids, pyranosyl-RNA and peptides, especially
CC macromolecules containing multiple reactive sites, to a substrate
CC surface or other conjugation target. It also describes the
CC preparation of oligos containing one or more hydrazides, which can
CC be used for conjugation to surface binding moieties, or for other
CC conjugation reactions. The process is useful e.g. in nucleic acid
CC hybridisation based assays, DNA chip technology and biosensor
CC applications.
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 other;
Query Match 1.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1084 AAAAAAAAAAAAAA 1098
Db |||||||
15 AAAAAAAAAAAAAA 1
RESULT 770
ABL57063/C
ID ABL57063 standard; DNA; 15 BP.
XX AC ABL57063;
XX
XX 22-JUL-2002 (first entry)
XX
XX Hydrazide precursor phosphoramidite oligonucleotide O39.
XX
XX Macromolecule; hydrazide; immobilisation; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FT modified_base 1 /*tag= a
FT /mod_base= "OTHER"
FT /note= "1,3-Bis-(3',5'-bis(ethyloxycarbonyl)
FT benzyloxy)-5-((2'-cyanoethyl)(diisopropylamino)
FT phosphanyloxy)-benzene"
FT modified_base 1..15
FT /*tag= b
FT /note= "phosphoramidite linkage"
FT modified_base 15
FT /*tag= c
FT /mod_base= "OTHER"
FT /note= "3' Cy3 dye"
XX
XX WC200214558-A2.
XX
XX 21-FEB-2002.
XX
XX 10-AUG-2001; 2001WO-US41663.
XX
XX 11-AUG-2000; 2000WO-US22205.
XX
XX (NANO-) NANOGEN INC.
XX
XX PA


```

XX Raddatz S, Mueller-Ibeler J, Schweitzer M, Bruecher C, Windhab N;
PI Havens JR, Onofrey TJ, Greef CH, Wang D;
XX WPI; 2002-401666/43.
XX
XX Compound for binding macromolecule to substrate surface or conjugation
PT targets, contains phosphorous containing reactive group, hydrazide
PT protecting group and benzene ring, and has predefined formula -
XX
XX Example 3; Page 43; 120pp; English.
XX
XX The present sequence is of a hydrazine treated hydrazide precursor
CC phosphoramidite 15-mer, designated oligo O39, which was produced in
CC an example from the invention. The invention describes an improved
CC process for immobilisation of macromolecules including DNA, RNA,
CC peptide nucleic acids, pyranosyl-RNA and peptides, especially
CC macromolecules containing multiple reactive sites, to a substrate
CC surface or other conjugation target. It also describes the
CC preparation of oligos containing one or more hydrazides, which can
CC be used for conjugation to surface binding moieties, or for other
CC conjugation reactions. The process is useful e.g. in nucleic acid
CC hybridisation based assays, DNA chip technology and biosensor
XX applications.
XX
XX Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 other;
SQ
Query Match 1.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1084 AAAAAAAAAAAAAA 1098
Db 15 AAAAAAAAAAAAAA 1
RESULT 771
ABL57064/C
ID ABL57064 standard; DNA; 15 BP.
XX
XX ABL57064;
XX
XX 22-JUL-2002 (first entry)
XX
XX Hydrazide precursor phosphoramidite oligonucleotide O35.
XX
XX Macromolecule; hydrazide; immobilisation; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FH modified_base 1 /tag= a
FT /mod_base= "OTHER"
FT /note= "Diethyl 5-(((2-cyanoethoxy)(diisopropylamino)
FT phosphanyloxy)methyl)isophthalate, synthetic
FT branching amide"
FT modified_base 1..15
FT /tag= b
FT /note= "phosphoramidite linkage"
FT modified_base 15
FT /tag= c
FT /mod_base= "OTHER"
FT /note= "3, Cy3 dye"
XX
XX WO200214558-A2.
PN
XX
XX 21-FEB-2002.
PD
XX
XX 10-AUG-2001; 2001WO-US41663.
PF
XX
XX 11-AUG-2000; 2000WO-US22205.
PR
XX
XX (NANO-) NANOGEN INC.
PA
XX
XX Raddatz S, Mueller-Ibeler J, Schweitzer M, Bruecher C, Windhab N;

```

```

PA (NANO-) NANOGEN INC.
XX
XX Raddatz S, Mueller-Ibeler J, Schweitzer M, Bruecher C, Windhab N;
PI Havens JR, Onofrey TJ, Greef CH, Wang D;
XX WPI; 2002-401666/43.
XX
XX Compound for binding macromolecule to substrate surface or conjugation
PT targets, contains phosphorous containing reactive group, hydrazide
PT protecting group and benzene ring, and has predefined formula -
XX
XX Example 4; Page 44; 120pp; English.
XX
XX The present sequence is of a hydrazine treated hydrazide precursor
CC phosphoramidite 15-mer, designated oligo O35, which was produced in
CC an example from the invention and which includes a synthetic
CC branching amide compound. The invention describes an improved
CC process for immobilisation of macromolecules including DNA, RNA,
CC peptide nucleic acids, pyranosyl-RNA and peptides, especially
CC macromolecules containing multiple reactive sites, to a substrate
CC surface or other conjugation target. It also describes the
CC preparation of oligos containing one or more hydrazides, which can
CC be used for conjugation to surface binding moieties, or for other
CC conjugation reactions. The process is useful e.g. in nucleic acid
CC hybridisation based assays, DNA chip technology and biosensor
XX applications.
XX
XX Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 other;
SQ
Query Match 1.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1084 AAAAAAAAAAAAAA 1098
Db 15 AAAAAAAAAAAAAA 1

```

```

RESULT 772
ABL57066/C
ID ABL57066 standard; DNA; 15 BP.
XX
XX ABL57066;
XX
XX 22-JUL-2002 (first entry)
XX
XX Amino-C6-modified and Cy3 labeled T15 oligonucleotide.
XX
XX Macromolecule; hydrazide; immobilisation; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FH modified_base 1 /tag= a
FT /mod_base= "OTHER"
FT /note= "Amino-C6 modification"
FT modified_base 15
FT /tag= b
FT /mod_base= "OTHER"
FT /note= "3, Cy3 dye"
XX
XX WO200214558-A2.
PN
XX
XX 21-FEB-2002.
PD
XX
XX 10-AUG-2001; 2001WO-US41663.
PF
XX
XX 11-AUG-2000; 2000WO-US22205.
PR
XX
XX (NANO-) NANOGEN INC.
PA
XX
XX Raddatz S, Mueller-Ibeler J, Schweitzer M, Bruecher C, Windhab N;

```

PI Havens JR, Onofrey TJ, Greef CH, Wang D;
 DR WPI; 2002-401666/43.
 XX
 PT Compound for binding macromolecule to substrate surface or conjugation
 PT targets, contains phosphorous containing reactive group, hydrazide
 PT protecting group and benzene ring, and has predefined formula -
 XX
 PS Example 12; Page 57; 120pp; English.
 XX
 CC The present sequence is of an amino-C6-modified and Cy3 dye
 CC labeled T15 oligonucleotide that was used in a comparison of
 CC hydrazine and amine attachment moieties on active ester surfaces
 CC in an example from the invention. The invention describes an
 CC improved process for immobilisation of macromolecules including DNA,
 CC RNA, peptide nucleic acids, pyranosyl-RNA and peptides, especially
 CC macromolecules containing multiple reactive sites, to a substrate
 CC surface or other conjugation target. It also describes the
 CC preparation of oligos containing one or more hydrazides, which can
 CC be used for conjugation to surface binding moieties, or for other
 CC conjugation reactions. The process is useful e.g. in nucleic acid
 CC hybridisation based assays, DNA chip technology and biosensor
 CC applications.
 XX
 SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 other;
 Query Match 1.4%; Score 15; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1084 AAAAAAAAAAAAAA 1098
 DB 15 AAAAAAAAAAAAAA 1
 RESULT 773
 ABL40743/C
 ID ABL40743 standard; DNA; 15 BP.
 XX
 AC ABL40743;
 XX
 DT 03-JUL-2002 (first entry)
 XX
 DE Chicken heparanase (hpa) cDNA cloning oligo dt(15) primer.
 XX
 KW Heparanase; catalytic; cytosolic; antiviral; antibacterial; enzyme;
 KW anti-protozoan; neuroprotective; heparin; hpa; chicken; PCR primer; ss.
 XX
 OS Gallus gallus.
 XX
 FN US2002034810-A1.
 XX
 PD 21-MAR-2002.
 XX
 PF 16-AUG-2001; 2001US-0930218.
 XX
 PR 20-SEP-2000; 2000US-0666390.
 XX
 PA (INSI-) INSIGHT STRATEGY & MARKETING LTD.
 XX
 PI Goldshmidt O, Pecker I, Vlodavsky I, Michal I, Zcharia E;
 XX
 DR WPI; 2002-338926/37.
 XX
 CC Nucleic acid encoding avian and reptile heparanase polypeptide is
 CC useful to treat various heparin-related disorders and the signal
 CC peptide is useful in production of membrane-targeted or secreted
 CC recombinant proteins -
 XX
 PS Disclosure; Page 13; 39pp; English.
 XX
 CC The invention relates to an isolated avian and reptile nucleic acid,
 CC encoding a polypeptide with heparanase catalytic activity. The signal

CC peptide of the nucleic acid can be used to express membrane-associated or
 CC secreted proteins in heterologous expression systems. The encoded
 CC polypeptides can be used to prevent tumour angiogenesis, metastasis and
 CC invasion, and to intervene with pathologies associated with impaired
 CC heparin-binding growth factors, cellular responses to heparin-binding
 CC growth factors and cytokines, cell interaction with plasma lipoproteins,
 CC cellular susceptibility to viral, protozoan and bacterial infections or
 CC disintegration of neurodegenerative plaques. The present sequence
 CC represents a chicken heparanase (hpa) cDNA cloning oligo dt(15) primer.
 XX
 SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 other;
 Query Match 1.4%; Score 15; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1084 AAAAAAAAAAAAAA 1098
 DB 15 AAAAAAAAAAAAAA 1
 RESULT 774
 ABA97403/C
 ID ABA97403 standard; DNA; 15 BP.
 XX
 AC ABA97403;
 XX
 DT 18-JUN-2002 (first entry)
 XX
 DE Nucleotide sequence of oligomer # 10 used to compare mismatches.
 XX
 KW Protein nucleic acid molecule; PNA; ds.
 XX
 OS Synthetic.
 XX
 FN WO200168673-A1.
 XX
 PD 20-SEP-2001.
 XX
 PF 13-MAR-2001; 2001WO-US08111.
 XX
 PR 14-MAR-2000; 2000US-189190P.
 PR 30-NOV-2000; 2000US-250334P.
 XX
 PA (ACTI-) ACTIVE MOTIF.
 XX
 PI Efimov V, Fernandez J, Archdeacon D, Archdeacon J;
 PI Chakhmakhcheu O, Buryakova A, Choob M, Hondorp K;
 XX
 DR WPI; 2002-041177/05.
 XX
 CC Oligonucleotides analogues useful in detection, separation and
 CC purification of nucleic acid molecules, comprise monomers, dimers and
 CC oligomers -
 XX
 PS Example 20; Page 123; 197pp; English.
 XX
 CC This invention relates to oligonucleotide analogues comprising a protein
 CC nucleic acid molecule (PNA) monomer. They are used in the detection and
 CC separation of nucleic acid molecules and as probes, primers, linkers,
 CC adaptors and antisense agents on solid supports. Modifications enhance
 CC their use as capture and detection probes e.g. by the incorporation of
 CC biotin, digoxigenin, radioisotopes, fluorescent labels such as
 CC fluorescein and reporter molecules such as alkaline phosphatase.
 CC They are also used for enhancing or inhibiting the activity of an enzyme
 CC or cellular activity. The compounds are stable to nucleases and
 CC proteases, have high affinity, binding specificity and solubility. The
 CC polyamide backbone of PNAs is resistant to both nucleases and proteases.
 CC PNAs bind nucleic acid molecules with greater affinity than DNA or RNA
 CC concentration. The compounds are relatively simple to synthesize and
 CC are used in a wide variety of applications. This sequence
 CC represents a DNA oligomer which is used to represent the effect of
 CC single base mismatches on oligonucleotides.

```

XX SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 other;
Query Match 1.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1098
DB 15 AAAAAAAAAAAAAA 1

RESULT 775
AAD29506/c
ID AAD29506 standard; DNA; 15 BP.
XX AC AAD29506;
XX DT 17-MAY-2002 (first entry)
XX DE Primer used for the expression of adipocytes in human preadipose cells.
XX KW Pre-adipose cell line; white adipocyte; food ingredient; obesity; lipid;
XX KW diabetes; cardiovascular disease; reverse transcription; RT-PCR primer;
XX KW ss.
XX OS Unidentified.
XX PN WO200206450-A1.
XX PD 24-JAN-2002.
XX PF 13-JUL-2001; 2001WO-EP08165.
XX PR 18-JUL-2000; 2000EP-0115489.
XX PA (NEST ) SOC PROD NESTLE SA.
XX PI Darimont C, Mace K, Pfeifer A;
XX DR WPI; 2002-188539/24.
XX The present invention relates to new human pre-adipose cell lines capable
CC to differentiate to white adipose cells, exhibiting essentially the same
CC cellular properties of normal white adipose cells. The human pre-adipose
CC cell lines are useful for the identification of substances controlling
CC the regulation of lipid uptake and release by human white adipocytes,
CC and substances controlling the differentiation of preadipocytes into
CC mature adipocytes. They are useful for screening compounds capable to
CC regulate the secretion of any metabolites or hormones from human white
CC adipocytes. Sequences of the invention are useful for developing drugs,
CC food ingredients and supplements against obesity, diabetes and cardio-
CC vascular diseases. The present DNA sequence is a reverse transcription
CC (RT)-PCR primer which is used for the expression of adipocytes in
CC differentiated immortalised human preadipose cells. This primer is
CC used in the exemplification of the invention.
XX SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 other;
Query Match 1.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1098
DB 15 AAAAAAAAAAAAAA 1

XX SQ Sequence 15 BP; 0 A; 0 C; 0 G; 0 U; 0 other;
Query Match 1.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1098
DB 1 AAAAAAAAAAAAAA 15

RESULT 776
AAD22531
ID AAD22531 standard; RNA; 15 BP.
XX AC AAD22531;
XX DT 12-FEB-2002 (first entry)
XX DE Retroviral reverse transcriptase inhibitor DNP-poly [A] RNA fragment.
XX KW RNase inhibitor; anti-HIV; cytostatic; hepatotropic; antiinflammatory;
XX KW virucide; oncogene; cancer; transcription; translation; leukaemia virus;
XX KW hepatitis virus; human immunodeficiency virus; retroviral; DNP-poly [A];
XX KW poly-2'-O-(2,4-dinitrophenyl)-poly [A]; viral reverse transcriptase; ss.
XX OS Retrovirus.
XX PN US6291438-B1.
XX PD 18-SEP-2001.
XX PF 06-OCT-1998; 98US-0167375.
XX PR 24-FEB-1993; 93US-0022055.
XX PR 23-FEB-1994; 94US-0200650.
XX PR 22-FEB-1996; 96US-0604871.
XX PA (WANG/) WANG J H.
XX PI Wang JH;
XX DR WPI; 2002-009339/01.
XX Derivatized antisense oligoribonucleotide useful to inhibit e.g. viral
PT reverse transcriptase comprises at the 2'-O position of the
PT oligoribonucleotide, a hydrophobic carrier reagent containing a poly
PT substituted phenyl compound -
XX Example 3; Column 24; 56pp; English.
XX The invention relates to derivatised antisense oligoribonucleotides with
CC enhanced membrane permeability and stability. The derivatised antisense
CC oligoribonucleotide complementary to a sequence of nucleotides found
CC in a virus or a cell is useful for inhibiting e.g., viral reverse
CC transcriptase. Derivatized antisense oligoribonucleotide is conjugated at
CC the 2'-O position with a hydrophobic carrier reagent containing a poly
CC substituted phenyl compound. The derivatised oligoribonucleotides are
CC used to decrease the expression of oncogenes and thereby decrease the
CC phenotypic and pathological properties. The oligoribonucleotides are also
CC used for increasing the effectiveness of antisense oligonucleotide
CC targeted to a gene associated with a disease or a condition in an
CC animal. To alter gene transcription and/or translation for any gene or
CC gene segment responsible for expression, to inhibit viral reverse
CC transcriptase, to inhibit the expression of leukaemia virus, hepatitis
CC virus, oncogenes and human immunodeficiency virus. The present sequence
CC is retroviral reverse transcriptase inhibitor DNP-poly [A] RNA fragment
CC which is used in the treatment of moloney murine leukaemia virus (MuLV)
CC in mammals.
XX SQ Sequence 15 BP; 15 A; 0 C; 0 G; 0 U; 0 other;
Query Match 1.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1098
DB 1 AAAAAAAAAAAAAA 15

RESULT 777

```


DB 15 AAAAAAAAAAAAAA 1

RESULT 779
ABV74141/c

ID ABV74141 standard; DNA; 15 BP.

XX
AC ABV74141;

XX
DT 23-JAN-2003 (first entry)

XX
DE Oligonucleotide used in cDNA library array.

XX
KW G-protein coupled receptor; odourant; receptor; olfaction; array;
KW microarray; anosmia; attractant; aromatic; pesticide; PCR; primer;
KW ss.

XX
OS Synthetic.

XX
FH Key Location/Qualifiers

FT modified_base 1

FT /*tag= a

FT /mod_base= OTHER

FT /note= "5, polylinker"

XX
PN WO200277200-A2.

XX
PD 03-OCT-2002.

XX
PF 26-MAR-2002; 2002WO-US09559.

XX
PR 27-MAR-2001; 2001US-279168P.

PR 31-JAN-2002; 2002US-353392P.

XX
PA (INSC-) INSCENT INC.

XX
PI Woods D, Dimitratos S;

XX
DR WPI; 2003-029930/02.

XX
PT Identifying nucleic acid encoding novel sex-linked-tissue-linked
PT receptors, useful for isolating odourant binding proteins or pesticide
PT alternatives, by analyzing sequences from a male- and female-specific
PT nucleic acid library -

XX
PS Disclosure; Fig 5; 83pp; English.

XX
CC The present sequence is that of a poly-T oligonucleotide used in a
CC method designed to rapidly array and normalize a complex cDNA library
CC obtained from a target species. Clones are arrayed into multi-well
CC plates. Each well contains 16 oligonucleotides with a 5' polylinker,
CC a poly-T run capable of binding cDNAs by their poly-A tail and a
CC unique 3' sequence, which allows an anchored oligonucleotide in each
CC well to selectively hybridise only to those cDNA clones with a
CC complementary 5' end. The unique 3' key sequences are designed to
CC give a comprehensive level of degeneracy since they are diverse and
CC numerous enough to ensure that every possible cDNA sequence can be
CC bound by an individual, specific oligonucleotide in a single well.
CC The cDNA library is heated to denature the clones into single
CC stranded DNA, and an aliquot is added to every well. The anchored
CC oligonucleotide serves as the 3' primer in PCR, and the common 5'
CC region present in every cDNA clone serves as the 5' priming site.
CC Denaturing and washing leave anchored cDNA in each well. The library
CC is now arrayed and normalised. The method was used to identify and
CC isolate clones encoding G-protein coupled receptors, especially
CC odourant receptors, and active effectors involved in the olfactory
CC pathway of invertebrates and vertebrates, e.g. odourant binding
CC proteins, or other olfactory or neuronal proteins. The identified
CC receptors and proteins are useful for identifying compounds that
CC reduce a target animal's sensitivity to odours, for manufacturing
CC compounds or devices that mask odours, or trapping invertebrates with
CC odourants. Semi-chemicals (e.g. aromatics or pheromone mimetics) can
CC be developed with desirable effects on specific species, for the

CC development of pest monitoring systems or non-toxic, species-specific
CC pesticide alternatives, for controlling insect feeding and breeding
CC behaviour, detecting the presence of small air-borne molecules, etc.

XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 other;

Query Match 1.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1098
|||||

Db 15 AAAAAAAAAAAAAA 1

RESULT 780
ABV74142

ID ABV74142 standard; DNA; 15 BP.

XX
AC ABV74142;

XX
DT 23-JAN-2003 (first entry)

XX
DE 5' End of cDNA library clone.

XX
KW G-protein coupled receptor; odourant; receptor; olfaction; array;
KW microarray; anosmia; attractant; aromatic; pesticide; ss.

XX
OS Synthetic.

XX
PN WO200277200-A2.

XX
PD 03-OCT-2002.

XX
PF 26-MAR-2002; 2002WO-US09559.

XX
PR 27-MAR-2001; 2001US-279168P.

PR 31-JAN-2002; 2002US-353392P.

XX
PA (INSC-) INSCENT INC.

XX
PI Woods D, Dimitratos S;

XX
DR WPI; 2003-029930/02.

XX
PT Identifying nucleic acid encoding novel sex-linked-tissue-linked
PT receptors, useful for isolating odourant binding proteins or pesticide
PT alternatives, by analyzing sequences from a male- and female-specific
PT nucleic acid library -

XX
PS Disclosure; Fig 5; 83pp; English.

XX
CC The present sequence is that of the 5' end of a cDNA clone
CC isolated from a cDNA library e.g. a mosquito antenna library. A
CC clone was isolated using a method designed to rapidly array and
CC normalize a complex cDNA library obtained from a target species.
CC Clones are arrayed into multi-well plates. Each well contains 16
CC oligonucleotides (see ABV74137) with a 5' polylinker, a poly-T run
CC capable of binding cDNAs by their poly-A tail and a unique 3'
CC sequence, which allows an anchored oligonucleotide in each well to
CC selectively hybridise only to those cDNA clones with a complementary
CC 5' end. The unique 3' key sequences are designed to give a
CC comprehensive level of degeneracy since they are diverse and
CC numerous enough to ensure that every possible cDNA sequence can be
CC bound by an individual, specific oligonucleotide in a single well.
CC The cDNA library is heated to denature the clones into single
CC stranded DNA, and an aliquot is added to every well. The anchored
CC oligonucleotide serves as the 3' primer in PCR, and the common 5'
CC region present in every cDNA clone serves as the 5' priming site.
CC Denaturing and washing leave anchored cDNA in each well. The library
CC is now arrayed and normalised. The method was used to identify and
CC isolate clones encoding G-protein coupled receptors, especially
CC odourant receptors, and active effectors involved in the olfactory

CC pathway of invertebrates and vertebrates, e.g. odourant binding
CC proteins, or other olfactory or neuronal proteins. The identified
CC receptors and proteins are useful for identifying compounds that
CC reduce a target animal's sensitivity to odours, for manufacturing
CC compounds or devices that mask odours, or trapping invertebrates with
CC odourants. Semiochemicals (e.g. aromatics or pheromone mimetics) can
CC be developed with desirable effects on specific species, for the
CC development of pest monitoring systems or non-toxic, species-specific
CC pesticide alternatives, for controlling insect feeding and breeding
CC behaviour, detecting the presence of small air-borne molecules, etc.
XX

SQ Sequence 15 BP; 15 A; 0 C; 0 G; 0 U; 0 other;

Query Match 1.4%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1098
Db 1 AAAAAAAAAAAAAA 15

RESULT 781
AAK18368/c
ID AAK18368 standard; DNA; 16 BP.

AC AAK18368;

DT 11-MAY-1999 (first entry)

RT-PCR primer of the invention SEQ ID 9.

RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.

OS Synthetic.

PN JP11032765-A.

PD 09-FEB-1999.

PF 18-JUL-1997; 97JP-0208312.

PR 18-JUL-1997; 97JP-0208312.

PA (TAKI) TAKARA SHUZO CO LTD.

DR WPI; 1999-183822/16.

PT Peptides having at least two new nucleotides - useful as primers in
RT-PCR

PS Disclosure; Page 10; 19pp; Japanese.

CC This sequence represents a primer of the invention. The invention relates
to sequences of at least two nucleotides of formula:

(X)m5'-(alpha)n-beta-N3'; or (X)m5'-(gamma)k-delta-N3'; where

X = a labelled compound and/or a nucleotide with voluntary sequence;

m = 0 or 1; alpha = thymine; n = natural number indicating the repetition

of alpha; beta, delta = V or N; V = adenine, guanine or cytosine;

N = adenine, guanine, cytosine or thymine; gamma = thymine;

k = natural number of 3 or over indicating the repetition of gamma, in

which thymine expressed by gamma is composed of 1/3 or less of adenine,

guanine and/or cytosine. The new nucleotides are useful as primers for

RT-PCR and determination of base sequences. The new sequences allow for

reproductive and highly efficient analysis of gene sequences.

SQ Sequence 16 BP; 1 A; 0 C; 1 G; 14 T; 0 other;

Query Match 1.4%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAAAAAAAAA 1097

Db 15 TAAAAAAAAAAAAA 1

RESULT 782

AAK18369/c

ID AAK18369 standard; DNA; 16 BP.

AC AAK18369;

DT 11-MAY-1999 (first entry)

RT-PCR primer of the invention SEQ ID 10.

RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.

OS Synthetic.

PN JP11032765-A.

PD 09-FEB-1999.

PF 18-JUL-1997; 97JP-0208312.

PR 18-JUL-1997; 97JP-0208312.

PA (TAKI) TAKARA SHUZO CO LTD.

DR WPI; 1999-183822/16.

PT Peptides having at least two new nucleotides - useful as primers in
RT-PCR

PS Disclosure; Page 10; 19pp; Japanese.

CC This sequence represents a primer of the invention. The invention relates
to sequences of at least two nucleotides of formula:

(X)m5'-(alpha)n-beta-N3'; or (X)m5'-(gamma)k-delta-N3'; where

X = a labelled compound and/or a nucleotide with voluntary sequence;

m = 0 or 1; alpha = thymine; n = natural number indicating the repetition

of alpha; beta, delta = V or N; V = adenine, guanine or cytosine;

N = adenine, guanine, cytosine or thymine; gamma = thymine;

k = natural number of 3 or over indicating the repetition of gamma, in

which thymine expressed by gamma is composed of 1/3 or less of adenine,

guanine and/or cytosine. The new nucleotides are useful as primers for

RT-PCR and determination of base sequences. The new sequences allow for

reproductive and highly efficient analysis of gene sequences.

SQ Sequence 16 BP; 1 A; 1 C; 0 G; 14 T; 0 other;

Query Match 1.4%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAAAAAAAAA 1097

Db 15 TAAAAAAAAAAAAA 1

RESULT 783

ABL57075

ID ABL57075 standard; DNA; 16 BP.

AC ABL57075;

DT 22-JUL-2002 (first entry)

Molecular beacon target sequence.

Molecular beacon; fluorophore; nanoparticle; nucleic acid detection;

ss.

OS Synthetic.

PA (RIBO-) RIBOZYME PHARM INC.
XX Escobedo J, McSwiggen J, Pavco P, Stinchcomb D;
XX WPI; 1997-259017/23.
XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or
PT mRNA stability - useful for treating e.g. tumour angiogenesis,
PT psoriasis, rheumatoid arthritis, etc., in a human patient
XX
PS Claim 4; Page 79; 218pp; English.
XX
CC The present invention describes nucleic acid molecules which modulate
CC the synthesis, expression and/or stability of a mRNA encoding 1 or more
CC receptors of vascular endothelial growth factor (VEGF). A patient
CC (preferably human) having a condition associated with the level of the
CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC receptor (KOR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can
CC be treated by administering the nucleic acid molecule or the expression
CC vector to the patient. AAX67275 to AAX75752 represent specific examples
CC of nucleic acid molecules from the present invention.
XX
SQ Sequence 17 BP; 0 A; 2 C; 0 G; 15 U; 0 other;
Query Match 1.4%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1084 AAAAAAAAAAAAAA 1098
DB 15 AAAAAAAAAAAAAA 1
RESULT 786
AAV37934/C
ID AAV37934 standard; cDNA; 17 BP.
XX
XX AAV37934;
XX
XX 05-OCT-1998 (first entry)
XX
DE Primer of the specification.
XX
XX Leukocyte; Iga nephropathy; diagnosis; treatment; PCR primer; ss.
XX
XX Synthetic.
XX
XX WO9824815-A1.
XX
XX 11-JUN-1998.
XX
XX 05-DEC-1997; 97WO-JP04469.
XX
XX 05-DEC-1996; 96JP-0325752.
XX
XX (KAZU-) KAZUSA DNA RES INST FOUND.
XX (KIOW) KIOWA HAKKO KOGYO KK.
XX
XX Ishiwata T, Kuga T, Nagase T, Nakagawa S, Nishi T;
XX Nishimura A, Nomura N, Sakurada M, Sawada S, Takei M;
XX WPI; 1998-333259/29.
XX
XX Protein from leukocytes and DNA encoding it - useful as reagents for
PT diagnosing and treating Iga nephropathy
XX
XX Example 2; Page 33; 41pp; Japanese.
XX
CC PCR primers AAV37933-39 are used in the course of the invention. The
CC specification describes a novel protein isolated from leukocytes of
CC patients with Iga nephropathy. Oligonucleotides based on the DNA
CC sequence encoding this protein are useful as reagents for diagnosing

CC and treating Iga nephropathy.
XX
SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 other;
Query Match 1.4%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1084 AAAAAAAAAAAAAA 1098
DB 16 AAAAAAAAAAAAAA 2
RESULT 787
AAV19118/C
ID AAV19118 standard; DNA; 17 BP.
XX
XX AAV19118;
XX
XX 28-AUG-1998 (first entry)
XX
XX Anchored oligo(T) primer.
XX
XX Secreted apoptosis-related protein; SARP; msARPI; mouse;
KW prostate cancer; breast cancer; diagnosis; gene therapy; PCR;
KW primer; ss.
XX
XX Synthetic.
XX
XX WO9813493-A2.
XX
XX 02-APR-1998.
XX
XX 24-SEP-1997; 97WO-US17154.
XX
XX 11-OCT-1996; 96US-0028363.
XX
XX 24-SEP-1996; 96US-0026603.
XX
XX (LXRB-) LXR BIOTECHNOLOGY INC.
XX
XX Melkonyan H, Umansky S;
XX
XX WPI; 1998-230704/20.
XX
XX New secreted apoptosis-related proteins - useful for modulating
PT apoptosis, particularly for treatment of prostatic or breast cancer,
PT also for diagnosis and monitoring of disease
XX
XX Example 1; Page 30; 101pp; English.
XX
XX This oligo(T) synthetic oligonucleotide was used for first strand
CC cDNA synthesis from total RNA isolated from either logarithmically
CC growing or quiescent 10T1/2 mouse fibroblast cells. It was also
CC used with an arbitrary d(N10) primer in PCR. The PCR products
CC were used in a differential display to identify the msARPI gene
CC (see AAV19112) that codes for novel murine secreted apoptosis-related
CC protein msARPI (see AAW37814). The invention relates to SARP
CC polynucleotides (see also AAV19113-15) and polypeptides (see also
CC AAW37815-17), antibodies specific for SARP, and use of such
CC polynucleotides and antibodies in diagnostic and therapeutic
CC methods, and methods for treating diseases related to the
CC regulation of SARP expression in tissue and body fluid samples,
CC including cancers.
XX
SQ Sequence 17 BP; 0 A; 0 C; 0 G; 15 T; 2 other;
Query Match 1.4%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1084 AAAAAAAAAAAAAA 1098
DB 15 AAAAAAAAAAAAAA 1


```
RESULT 788
AAC64162/c
ID AAC64162 standard; DNA; 17 BP.
XX
AC AAC64162;
XX
DT 21-FEB-2001 (first entry)
XX
DE PCR anchor primer, SEQ ID NO:3, used in human gene 581 isolation.
XX
KW Human; pollinosis-associated gene 581; IgE; immunoglobulin E;
KW cedar pollen allergy; T-cell; reduced expression; detection;
KW diagnosis; drug screening; allergic disease; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO200065048-A1.
XX
PD 02-NOV-2000.
XX
PF 26-APR-2000; 2000WO-JP02732.
XX
PR 27-APR-1999; 99JP-0120492.
XX
PA (GENO-) GENOX RES INC.
XX
PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
DR WPI; 2000-687341/67.
XX
PT Pollenosis-associated gene 581 undergoing significantly low expression
PT in subjects with high cedar pollen-specific IgE levels; useful in
PT diagnosis of allergic diseases and screening drug candidates -
XX
PS Example 6; Page 40; 69pp; Japanese.
XX
CC The invention relates to the human pollinosis-associated gene 581 which
CC exhibits significantly reduced expression in the T-cells of individuals
CC with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene
CC was isolated from T-cells from individuals allergic to cedar pollen using
CC the differential display method. The invention also relates also relates
CC to the protein encoded by pollinosis-associated gene 581; to expression
CC constructs and host cells comprising pollinosis-associated gene 581
CC nucleic acids; pollinosis-associated gene 581 primers and probes;
CC antibodies against the protein encoded by the gene; methods of detection
CC of pollinosis-associated gene 581 nucleic acids; and a method of
CC diagnosis of allergic diseases via the detection of pollinosis-associated
CC gene 581 nucleic acids. The invention additionally encompasses methods of
CC screening drug candidates for the treatment of allergic disease by
CC measuring the expression of pollinosis-associated gene 581 in pollen
CC antigen-stimulated T-cells in the presence of a test compound relative
CC to a control. Pollinosis-associated gene 581 is useful in the diagnosis
CC of allergic diseases and in the screening of drug candidates for the
CC treatment of such diseases. The present sequence represents a PCR primer
CC used in the isolation of human pollinosis-associated gene 581 cDNA.
XX
SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 other;
Query Match 1.4%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1084 AAAAAAAAAAAAAA 1098
Db 16 AAAAAAAAAAAAAA 2
RESULT 789
AAC64163/c
ID AAC64163 standard; DNA; 17 BP.
XX
AC AAC64163;
XX
DT 21-FEB-2001 (first entry)
XX
DE PCR anchor primer, SEQ ID NO:4, used in human gene 581 isolation.
XX
KW Human; pollinosis-associated gene 581; IgE; immunoglobulin E;
KW cedar pollen allergy; T-cell; reduced expression; detection;
KW diagnosis; drug screening; allergic disease; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO200065048-A1.
XX
PD 02-NOV-2000.
XX
PF 26-APR-2000; 2000WO-JP02732.
XX
PR 27-APR-1999; 99JP-0120492.
XX
PA (GENO-) GENOX RES INC.
XX
PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
DR WPI; 2000-687341/67.
XX
PT Pollenosis-associated gene 581 undergoing significantly low expression
PT in subjects with high cedar pollen-specific IgE levels; useful in
PT diagnosis of allergic diseases and screening drug candidates -
XX
PS Example 6; Page 40; 69pp; Japanese.
XX
CC The invention relates to the human pollinosis-associated gene 581 which
CC exhibits significantly reduced expression in the T-cells of individuals
CC with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene
CC was isolated from T-cells from individuals allergic to cedar pollen using
CC the differential display method. The invention also relates also relates
CC to the protein encoded by pollinosis-associated gene 581; to expression
CC constructs and host cells comprising pollinosis-associated gene 581
CC nucleic acids; pollinosis-associated gene 581 primers and probes;
CC antibodies against the protein encoded by the gene; methods of detection
CC of pollinosis-associated gene 581 nucleic acids; and a method of
CC diagnosis of allergic diseases via the detection of pollinosis-associated
CC gene 581 nucleic acids. The invention additionally encompasses methods of
CC screening drug candidates for the treatment of allergic disease by
CC measuring the expression of pollinosis-associated gene 581 in pollen
CC antigen-stimulated T-cells in the presence of a test compound relative
CC to a control. Pollinosis-associated gene 581 is useful in the diagnosis
CC of allergic diseases and in the screening of drug candidates for the
CC treatment of such diseases. The present sequence represents a PCR primer
CC used in the isolation of human pollinosis-associated gene 581 cDNA.
XX
SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 other;
Query Match 1.4%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1084 AAAAAAAAAAAAAA 1098
Db 16 AAAAAAAAAAAAAA 2
RESULT 790
AAC64172/c
ID AAC64172 standard; DNA; 17 BP.
XX
AC AAC64172;
XX
DT 21-FEB-2001 (first entry)
```

```
XX
AC AAC64163;
XX
DT 21-FEB-2001 (first entry)
XX
DE PCR anchor primer, SEQ ID NO:4, used in human gene 581 isolation.
XX
KW Human; pollinosis-associated gene 581; IgE; immunoglobulin E;
KW cedar pollen allergy; T-cell; reduced expression; detection;
KW diagnosis; drug screening; allergic disease; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO200065048-A1.
XX
PD 02-NOV-2000.
XX
PF 26-APR-2000; 2000WO-JP02732.
XX
PR 27-APR-1999; 99JP-0120492.
XX
PA (GENO-) GENOX RES INC.
XX
PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
DR WPI; 2000-687341/67.
XX
PT Pollenosis-associated gene 581 undergoing significantly low expression
PT in subjects with high cedar pollen-specific IgE levels; useful in
PT diagnosis of allergic diseases and screening drug candidates -
XX
PS Example 6; Page 40; 69pp; Japanese.
XX
CC The invention relates to the human pollinosis-associated gene 581 which
CC exhibits significantly reduced expression in the T-cells of individuals
CC with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene
CC was isolated from T-cells from individuals allergic to cedar pollen using
CC the differential display method. The invention also relates also relates
CC to the protein encoded by pollinosis-associated gene 581; to expression
CC constructs and host cells comprising pollinosis-associated gene 581
CC nucleic acids; pollinosis-associated gene 581 primers and probes;
CC antibodies against the protein encoded by the gene; methods of detection
CC of pollinosis-associated gene 581 nucleic acids; and a method of
CC diagnosis of allergic diseases via the detection of pollinosis-associated
CC gene 581 nucleic acids. The invention additionally encompasses methods of
CC screening drug candidates for the treatment of allergic disease by
CC measuring the expression of pollinosis-associated gene 581 in pollen
CC antigen-stimulated T-cells in the presence of a test compound relative
CC to a control. Pollinosis-associated gene 581 is useful in the diagnosis
CC of allergic diseases and in the screening of drug candidates for the
CC treatment of such diseases. The present sequence represents a PCR primer
CC used in the isolation of human pollinosis-associated gene 581 cDNA.
XX
SQ Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 other;
Query Match 1.4%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1084 AAAAAAAAAAAAAA 1098
Db 16 AAAAAAAAAAAAAA 2
RESULT 790
AAC64172/c
ID AAC64172 standard; DNA; 17 BP.
XX
AC AAC64172;
XX
DT 21-FEB-2001 (first entry)
```

DE PCR anchor primer, SEQ ID NO:3, used in human gene 513 isolation.
 XX Human; pollinosis-associated gene 513; IgE; immunoglobulin E;
 KW cedar pollen allergy; T-cell; reduced expression; detection;
 KW diagnosis; drug screening; allergic disease; PCR primer; ss.
 XX Synthetic.
 OS
 XX WO200065049-A1.
 PN
 XX
 XX 02-NOV-2000.
 PD
 XX
 XX 26-APR-2000; 2000WO-JP02733.
 PF
 XX
 XX 27-APR-1999; 99JP-0120491.
 PR
 XX
 XX (GENO-) GENOX RES INC.
 PA
 XX
 XX Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
 PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
 PI
 XX WPI; 2000-687342/67.
 DR
 XX
 XX Pollinosis-associated gene 513 undergoing significantly low expression
 PT in subjects with high cedar pollen-specific IgE levels, useful in
 PT diagnosis of allergic diseases and screening drug candidates -
 PT
 XX Example 6; Page 38; 46pp; Japanese.
 PS
 XX The invention relates to the human pollinosis-associated gene 513 which
 CC exhibits significantly reduced expression in the T-cells of individuals
 CC with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene
 CC was isolated from T-cells from individuals allergic to cedar pollen
 CC using the differential display method. The invention also relates
 CC to methods of detection of pollinosis-associated gene 513 nucleic acids;
 CC a method of diagnosis of allergic diseases via the detection of
 CC pollinosis-associated gene 513 nucleic acids; and methods of screening
 CC drug candidates for the treatment of allergic disease by measuring the
 CC expression of pollinosis-associated gene 513 in pollen antigen-stimulated
 CC T-cells in the presence of a test compound relative to a control.
 CC Pollinosis-associated gene 513 is useful in the diagnosis of allergic
 CC diseases and in the screening of drug candidates for the treatment of
 CC such diseases. The present sequence represents a PCR primer
 CC used in the isolation of human pollinosis-associated gene 513 cDNA.
 XX
 XX Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 other;
 SQ
 Query Match 1.4%; Score 15; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 4e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1084 AAAAAAAAAAAAAA 1098
 Db |||||||
 16 AAAAAAAAAAAAAA 2
 RESULT 791
 AAC64173/C
 ID AAC64173 standard; DNA; 17 BP.
 XX
 AC AAC64173;
 XX
 XX 21-FEB-2001 (first entry)
 DT
 XX PCR anchor primer, SEQ ID NO:4, used in human gene 513 isolation.
 DE
 XX Human; pollinosis-associated gene 513; IgE; immunoglobulin E;
 KW cedar pollen allergy; T-cell; reduced expression; detection;
 KW diagnosis; drug screening; allergic disease; PCR primer; ss.
 XX Synthetic.
 OS
 XX WO200065049-A1.
 PN

XX 02-NOV-2000.
 PD
 XX
 XX 26-APR-2000; 2000WO-JP02733.
 PF
 XX
 XX 27-APR-1999; 99JP-0120491.
 PR
 XX
 XX (GENO-) GENOX RES INC.
 PA
 XX
 XX Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
 PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
 PI
 XX WPI; 2000-687342/67.
 DR
 XX
 XX Pollinosis-associated gene 513 undergoing significantly low expression
 PT in subjects with high cedar pollen-specific IgE levels, useful in
 PT diagnosis of allergic diseases and screening drug candidates -
 PT
 XX Example 6; Page 39; 46pp; Japanese.
 PS
 XX The invention relates to the human pollinosis-associated gene 513 which
 CC exhibits significantly reduced expression in the T-cells of individuals
 CC with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene
 CC was isolated from T-cells from individuals allergic to cedar pollen
 CC using the differential display method. The invention also relates
 CC to methods of detection of pollinosis-associated gene 513 nucleic acids;
 CC a method of diagnosis of allergic diseases via the detection of
 CC pollinosis-associated gene 513 nucleic acids; and methods of screening
 CC drug candidates for the treatment of allergic disease by measuring the
 CC expression of pollinosis-associated gene 513 in pollen antigen-stimulated
 CC T-cells in the presence of a test compound relative to a control.
 CC Pollinosis-associated gene 513 is useful in the diagnosis of allergic
 CC diseases and in the screening of drug candidates for the treatment of
 CC such diseases. The present sequence represents a PCR primer
 CC used in the isolation of human pollinosis-associated gene 513 cDNA.
 XX
 XX Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 other;
 SQ
 Query Match 1.4%; Score 15; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 4e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1084 AAAAAAAAAAAAAA 1098
 Db |||||||
 16 AAAAAAAAAAAAAA 2
 RESULT 792
 AAC64182/C
 ID AAC64182 standard; DNA; 17 BP.
 XX
 AC AAC64182;
 XX
 XX 21-FEB-2001 (first entry)
 DT
 XX PCR anchor primer, SEQ ID NO:3, used in human gene 419 isolation.
 DE
 XX Human; pollinosis-associated gene 419; FAF-1 homologue;
 KW Fas-associated factor-1; IgE; immunoglobulin E;
 KW cedar pollen allergy; T-cell; reduced expression; detection;
 KW diagnosis; drug screening; allergic disease; PCR primer; ss.
 XX Synthetic.
 OS
 XX WO200065045-A1.
 PN
 XX
 XX 02-NOV-2000.
 PD
 XX
 XX 26-APR-2000; 2000WO-JP02729.
 PF
 XX
 XX 27-APR-1999; 99JP-0120490.
 PR
 XX
 XX (GENO-) GENOX RES INC.
 PA

XX Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
 PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
 XX WPI; 2000-687338/67.
 DR
 XX Pollinosis-associated gene 419 undergoing significantly low expression
 PT in subjects with high cedar pollen-specific IgE levels, useful in
 PT diagnosis of allergic diseases and screening drug candidates -
 XX
 PS Example 6; Page 49; 77pp; Japanese.
 XX
 CC The invention relates to the human pollinosis-associated gene 419 which
 CC exhibits reduced expression in the T-cells of individuals with high cedar
 CC pollen-specific IgE (immunoglobulin E) levels. The gene was isolated
 CC from T-cells from individuals allergic to cedar pollen using the
 CC differential display method. Pollinosis-associated gene 419 has
 CC homology with the gene encoding human Fas-associated factor-1 (FAF-1).
 CC The invention also relates to the protein encoded by pollinosis gene
 CC 419; expression constructs and host cells comprising pollinosis-
 CC associated gene 419 nucleic acids; pollinosis-associated gene 419 primers
 CC and probes; antibodies against the protein encoded by the gene; methods
 CC of detection of pollinosis-associated gene 419 nucleic acids; and a
 CC method of diagnosis of allergic diseases via the detection of pollinosis-
 CC associated gene 419 nucleic acids. The invention additionally encompasses
 CC methods of screening drug candidates for the treatment of allergic
 CC disease by measuring the expression of pollinosis-associated gene 419 in
 CC pollen antigen-stimulated T-cells in the presence of a test compound
 CC relative to a control. Pollinosis-associated gene 419 is useful in the
 CC diagnosis of allergic diseases and in the screening of drug candidates
 CC for the treatment of such diseases. The present sequence represents
 CC a PCR primer used in the isolation of human pollinosis-associated gene
 CC 419 cDNA.
 XX
 SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 other;
 Query Match 1.4%; Score 15; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 4e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1084 AAAAAAAAAAAAAA 1098
 Db |||||
 16 AAAAAAAAAAAAAA 2
 RESULT 793
 AAC64183/c
 ID AAC64183 standard; DNA; 17 BP.
 AC AAC64183;
 XX
 DT 21-FEB-2001 (first entry)
 DE PCR anchor primer, SEQ ID NO:4, used in human gene 419 isolation.
 XX Human; pollinosis-associated gene 419; FAF-1 homologue;
 KW Fas-associated factor-1; IgE; immunoglobulin E;
 KW cedar pollen allergy; T-cell; reduced expression; detection;
 KW diagnosis; drug screening; allergic disease; PCR primer; ss.
 XX
 OS Synthetic.
 XX
 PN WO200065045-A1.
 XX
 PD 02-NOV-2000.
 XX
 PF 26-APR-2000; 2000WO-JP02729.
 XX
 PR 27-APR-1999; 99JP-0120490.
 XX
 PA (GENO-) GENOX RES INC.
 XX
 PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
 XX WPI; 2000-687338/67.

PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
 XX WPI; 2000-687338/67.
 XX Pollinosis-associated gene 419 undergoing significantly low expression
 PT in subjects with high cedar pollen-specific IgE levels, useful in
 PT diagnosis of allergic diseases and screening drug candidates -
 XX
 PS Example 6; Page 50; 77pp; Japanese.
 XX
 CC The invention relates to the human pollinosis-associated gene 419 which
 CC exhibits reduced expression in the T-cells of individuals with high cedar
 CC pollen-specific IgE (immunoglobulin E) levels. The gene was isolated
 CC from T-cells from individuals allergic to cedar pollen using the
 CC differential display method. Pollinosis-associated gene 419 has
 CC homology with the gene encoding human Fas-associated factor-1 (FAF-1).
 CC The invention also relates to the protein encoded by pollinosis gene
 CC 419; expression constructs and host cells comprising pollinosis-
 CC associated gene 419 nucleic acids; pollinosis-associated gene 419 primers
 CC and probes; antibodies against the protein encoded by the gene; methods
 CC of detection of pollinosis-associated gene 419 nucleic acids; and a
 CC method of diagnosis of allergic diseases via the detection of pollinosis-
 CC associated gene 419 nucleic acids. The invention additionally encompasses
 CC methods of screening drug candidates for the treatment of allergic
 CC disease by measuring the expression of pollinosis-associated gene 419 in
 CC pollen antigen-stimulated T-cells in the presence of a test compound
 CC relative to a control. Pollinosis-associated gene 419 is useful in the
 CC diagnosis of allergic diseases and in the screening of drug candidates
 CC for the treatment of such diseases. The present sequence represents
 CC a PCR primer used in the isolation of human pollinosis-associated gene
 CC 419 cDNA.
 XX
 SQ Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 other;
 Query Match 1.4%; Score 15; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 4e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1084 AAAAAAAAAAAAAA 1098
 Db |||||
 16 AAAAAAAAAAAAAA 2
 RESULT 794
 AAC64203/c
 ID AAC64203 standard; DNA; 17 BP.
 AC AAC64203;
 XX
 DT 21-FEB-2001 (first entry)
 DE PCR anchor primer, SEQ ID NO:4, used in human gene 373 isolation.
 XX Human; pollinosis-associated gene 373; IgE; immunoglobulin E;
 KW cedar pollen allergy; T-cell; reduced expression; detection;
 KW diagnosis; drug screening; allergic disease; PCR primer; ss.
 XX
 OS Synthetic.
 XX
 PN WO200065046-A1.
 XX
 PD 02-NOV-2000.
 XX
 PF 26-APR-2000; 2000WO-JP02730.
 XX
 PR 27-APR-1999; 99JP-0120489.
 XX
 PA (GENO-) GENOX RES INC.
 XX
 PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
 PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
 XX WPI; 2000-687339/67.

XX Pollinosis-associated gene 373 undergoing significantly low expression
PT in subjects with high cedar pollen-specific immunoglobulin-E levels,
PT useful in diagnosis of allergic diseases and screening drug candidates
XX
XX Example 6; Page 70; 80pp; Japanese.
XX
CC The invention relates to the human pollinosis-associated gene 373 which
CC exhibits significantly reduced expression in the T-cells of individuals
CC with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene
CC was isolated from T-cells from individuals allergic to cedar pollen
CC using the differential display method. The invention also relates also
CC relates to the protein encoded by pollinosis gene 373; expression
CC constructs and host cells comprising pollinosis-associated gene 373
CC nucleic acids; pollinosis-associated gene 373 primers and probes;
CC antibodies against the protein encoded by the gene; methods of detection
CC of pollinosis-associated gene 373 nucleic acids; and a method of
CC diagnosis of allergic diseases via the detection of pollinosis-associated
CC gene 373 nucleic acids. The invention additionally encompasses methods of
CC screening drug candidates for the treatment of allergic disease by
CC measuring the expression of pollinosis-associated gene 373 in pollen
CC antigen-stimulated T-cells in the presence of a test compound relative to
CC a control. Pollinosis-associated gene 373 is useful in the diagnosis of
CC allergic diseases and in the screening of drug candidates for the
CC treatment of such diseases. The present sequence represents a PCR primer
CC used in the isolation of human pollinosis-associated gene 373 cDNA.
XX
SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 other;

Query Match 1.4%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1098
Db |||||
16 AAAAAAAAAAAAAA 2

RESULT 795
AAC64204/c
ID AAC64204 standard; DNA; 17 BP.
XX AAC64204;
AC
XX 21-FEB-2001 (first entry)
DT
DE PCR anchor primer, SEQ ID NO:5, used in human gene 373 isolation.
XX Human; pollinosis-associated gene 373; IgE; immunoglobulin E;
KW cedar pollen allergy; T-cell; reduced expression; detection;
KW diagnosis; drug screening; allergic disease; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO200065046-A1.
XX
XX 02-NOV-2000.
XX
XX 26-APR-2000; 2000WO-JF02730.
XX
XX 27-APR-1999; 99JP-0120489.
XX
XX (GENO-) GENOX RES INC.
XX
XX Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
XX
XX WPI; 2000-687339/67.
XX
XX Pollinosis-associated gene 373 undergoing significantly low expression
PT in subjects with high cedar pollen-specific immunoglobulin-E levels,
PT useful in diagnosis of allergic diseases and screening drug candidates
XX

PT
XX
PS Example 6; Page 70; 80pp; Japanese.
XX
CC The invention relates to the human pollinosis-associated gene 373 which
CC exhibits significantly reduced expression in the T-cells of individuals
CC with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene
CC was isolated from T-cells from individuals allergic to cedar pollen
CC using the differential display method. The invention also relates also
CC relates to the protein encoded by pollinosis gene 373; expression
CC constructs and host cells comprising pollinosis-associated gene 373
CC nucleic acids; pollinosis-associated gene 373 primers and probes;
CC antibodies against the protein encoded by the gene; methods of detection
CC of pollinosis-associated gene 373 nucleic acids; and a method of
CC diagnosis of allergic diseases via the detection of pollinosis-associated
CC gene 373 nucleic acids. The invention additionally encompasses methods of
CC screening drug candidates for the treatment of allergic disease by
CC measuring the expression of pollinosis-associated gene 373 in pollen
CC antigen-stimulated T-cells in the presence of a test compound relative to
CC a control. Pollinosis-associated gene 373 is useful in the diagnosis of
CC allergic diseases and in the screening of drug candidates for the
CC treatment of such diseases. The present sequence represents a PCR primer
CC used in the isolation of human pollinosis-associated gene 373 cDNA.
XX
SQ Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 other;

Query Match 1.4%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1098
Db |||||
16 AAAAAAAAAAAAAA 2

RESULT 796
AAC64214/c
ID AAC64214 standard; DNA; 17 BP.
XX AAC64214;
AC
XX 21-FEB-2001 (first entry)
DT
DE PCR anchor primer, SEQ ID NO:3, used in human gene 627 isolation.
XX Human; pollinosis-associated gene 627; IgE; immunoglobulin E;
KW cedar pollen allergy; T-cell; reduced expression; detection;
KW diagnosis; drug screening; allergic disease; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO200065051-A1.
XX
XX 02-NOV-2000.
XX
XX 26-APR-2000; 2000WO-JP02735.
XX
XX 27-APR-1999; 99JP-0120493.
XX
XX (GENO-) GENOX RES INC.
XX
XX Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
XX
XX WPI; 2000-687344/67.
XX
XX Pollinosis-associated gene 627 undergoing significantly low expression
PT in subjects with high cedar pollen-specific IgE levels, useful in
PT diagnosis of allergic diseases and screening drug candidates -
XX
XX Example 6; Page 42; 51pp; Japanese.
XX
CC The invention relates to the human pollinosis-associated gene 627 which

CC exhibits significantly reduced expression in the T-cells of individuals
 CC with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene
 CC was isolated from T-cells from individuals allergic to cedar pollen using
 CC the differential display method. The invention also relates to methods of
 CC detection of pollinosis-associated gene 627 nucleic acids; a method of
 CC diagnosis of allergic diseases via the detection of pollinosis-associated
 CC gene 627 nucleic acids; and a method of screening drug candidates for the
 CC treatment of allergic disease by measuring the expression of pollinosis-
 CC associated gene 627 in pollen antigen-stimulated T-cells in the presence
 CC of a test compound relative to a control. Pollinosis-associated gene 627
 CC is useful in the diagnosis of allergic diseases and in the screening of
 CC drug candidates for the treatment of such diseases. The present sequence
 CC represents a PCR primer used in the isolation of human pollinosis-
 CC associated gene 627 cDNA.

CC Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 other;

Query Match 1.4%; Score 15; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 4e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1098
 |||||
 DB 16 AAAAAAAAAAAAAA 2

RESULT 797
 AAC64215/c
 ID AAC64215 standard; DNA; 17 BP.
 AC AAC64215;
 XX
 XX 21-FEB-2001 (first entry)
 XX PCR anchor primer, SEQ ID NO:4, used in human gene 627 isolation.

XX Human; pollinosis-associated gene 627; IgE; immunoglobulin E;
 KW cedar pollen allergy; T-cell; reduced expression; detection;
 KW diagnosis; drug screening; allergic disease; PCR primer; ss.
 XX Synthetic.
 OS
 XX WO200065051-A1.
 XX 02-NOV-2000.
 XX 26-APR-2000; 2000WO-JP02735.
 XX 27-APR-1999; 99JP-0120493.
 XX (GENO-) GENOX RES INC.
 XX Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
 PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
 PI Yokoi A;
 DR WPI; 2000-687344/67.
 XX Pollinosis-associated gene 627 undergoing significantly low expression
 PT in subjects with high cedar pollen-specific IgE levels, useful in
 PT diagnosis of allergic diseases and screening drug candidates -
 XX Example 6; Page 42; 51pp; Japanese.

XX The invention relates to the human pollinosis-associated gene 627 which
 CC exhibits significantly reduced expression in the T-cells of individuals
 CC with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene
 CC was isolated from T-cells from individuals allergic to cedar pollen using
 CC the differential display method. The invention also relates to methods of
 CC detection of pollinosis-associated gene 627 nucleic acids; a method of
 CC diagnosis of allergic diseases via the detection of pollinosis-associated
 CC gene 627 nucleic acids; and a method of screening drug candidates for the
 CC treatment of allergic disease by measuring the expression of pollinosis-
 CC associated gene 627 in pollen antigen-stimulated T-cells in the presence

CC of a test compound relative to a control. Pollinosis-associated gene 627
 CC is useful in the diagnosis of allergic diseases and in the screening of
 CC drug candidates for the treatment of such diseases. The present sequence
 CC represents a PCR primer used in the isolation of human pollinosis-
 CC associated gene 627 cDNA.

CC Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 other;
 Query Match 1.4%; Score 15; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 4e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1098
 |||||
 DB 16 AAAAAAAAAAAAAA 2

RESULT 798
 AAC64231/c
 ID AAC64231 standard; DNA; 17 BP.

XX AAC64231;
 XX 21-FEB-2001 (first entry)

XX PCR anchor primer, SEQ ID NO:3, used in human gene 795 isolation.

XX Human; pollinosis-associated gene 795; vimentin homologue;
 KW IgE; immunoglobulin E; cedar pollen allergy; T-cell; reduced expression;
 KW detection; diagnosis; drug screening; allergic disease; PCR primer; ss.
 XX Synthetic.

XX WO200065050-A1.
 XX 02-NOV-2000.
 XX 26-APR-2000; 2000WO-JP02734.
 XX 27-APR-1999; 99JP-0120494.

XX (GENO-) GENOX RES INC.
 XX (EISA) EISAI CO LTD.

XX Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
 PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K, Takahashi E;
 PI Yokoi A;

XX WPI; 2000-687343/67.

XX Pollinosis-associated gene 795 undergoing significantly low expression
 PT in subjects with high cedar pollen-specific IgE levels, useful in
 PT diagnosis of allergic diseases and screening drug candidates -
 XX Page 45; Example 6; 73pp; Japanese.

XX The invention relates to the human pollinosis-associated gene 795 which
 CC exhibits significantly reduced expression in the T-cells of individuals
 CC with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene
 CC was isolated from T-cells from individuals allergic to cedar pollen using
 CC the differential display method. Pollinosis-associated gene 795 has
 CC homology with the human vimentin gene. The invention also relates also
 CC relates to the protein encoded by pollinosis gene 795; to expression
 CC constructs and host cells comprising pollinosis-associated gene 795
 CC nucleic acids; pollinosis-associated gene 795 primers and probes;
 CC antibodies against the protein encoded by the gene; methods of detection
 CC of pollinosis-associated gene 795 nucleic acids; and a method of
 CC diagnosis of allergic diseases via the detection of pollinosis-associated
 CC gene 795 nucleic acids. The invention additionally encompasses methods of
 CC screening drug candidates for the treatment of allergic disease by
 CC measuring the expression of pollinosis-associated gene 795 in pollen
 CC antigen-stimulated T-cells in the presence of a test compound relative to
 CC a control. Pollinosis-associated gene 795 is useful in the diagnosis of

CC allergic diseases and in the screening of drug candidates for the
 CC treatment of such diseases. The present sequence represents a PCR primer
 CC used in the isolation of human pollinosis-associated gene 795 cDNA.
 XX
 SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 other;
 Query Match 1.4%; Score 15; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 4e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1084 AAAAAAAAAAAAAA 1098
 Db 16 AAAAAAAAAAAAAA 2

RESULT 799
 AAC64232/c
 ID AAC64232 standard; DNA; 17 BP.
 XX
 AC AAC64232;
 XX
 DT 21-FEB-2001 (first entry)
 XX
 DE PCR anchor primer, SEQ ID NO:4, used in human gene 795 isolation.
 XX
 KW Human; pollinosis-associated gene 795; vimentin homologue;
 KW IGE; immunoglobulin E; cedar pollen allergy; T-cell; reduced expression;
 KW detection; diagnosis; drug screening; allergic disease; PCR primer; ss.
 OS Synthetic.
 XX
 PN WO20006050-A1.
 XX
 PD 02-NOV-2000.
 XX
 PF 26-APR-2000; 2000WO-JP02734.
 XX
 PR 27-APR-1999; 99JP-0120494.
 XX
 PA (GENO-) GENOX RES INC.
 PA (EISA) EISAI CO LTD.
 XX
 PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
 PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K, Takahashi E;
 PI Yokoi A;
 XX
 WPI; 2000-687343/67.
 XX
 PT Pollinosis-associated gene 795 undergoing significantly low expression
 PT in subjects with high cedar pollen-specific IgE levels; useful in
 PT diagnosis of allergic diseases and screening drug candidates -
 XX
 PS Page 46; Example 6; 73pp; Japanese.
 XX
 CC The invention relates to the human pollinosis-associated gene 795 which
 CC exhibits significantly reduced expression in the T-cells of individuals
 CC with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene
 CC was isolated from T-cells from individuals allergic to cedar pollen using
 CC the differential display method. Pollinosis-associated gene 795 has
 CC homology with the human vimentin gene. The invention also relates also
 CC relates to the protein encoded by pollinosis gene 795; to expression
 CC constructs and host cells comprising pollinosis-associated gene 795
 CC nucleic acids; pollinosis-associated gene 795 primers and probes;
 CC antibodies against the protein encoded by the gene; methods of detection
 CC of pollinosis-associated gene 795 nucleic acids; and a method of
 CC diagnosis of allergic diseases via the detection of pollinosis-associated
 CC gene 795 nucleic acids. The invention additionally encompasses methods of
 CC screening drug candidates for the treatment of allergic disease by
 CC measuring the expression of pollinosis-associated gene 795 in pollen
 CC antigen-stimulated T-cells in the presence of a test compound relative to
 CC a control. Pollinosis-associated gene 795 is useful in the diagnosis of
 CC allergic diseases and in the screening of drug candidates for the
 CC treatment of such diseases. The present sequence represents a PCR primer

CC used in the isolation of human pollinosis-associated gene 795 cDNA.
 XX
 SQ Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 other;
 Query Match 1.4%; Score 15; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 4e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1084 AAAAAAAAAAAAAA 1098
 Db 16 AAAAAAAAAAAAAA 2

RESULT 800
 AAX82721/c
 ID AAX82721 standard; DNA; 17 BP.
 XX
 AC AAX82721;
 XX
 DT 10-NOV-2000 (first entry)
 XX
 DE Human IGA nephropathy-associated cDNA primer #62.
 XX
 KW IGA nephropathy-associated protein; diagnosis; treatment; antisense;
 KW human; primer; ss.
 OS Homo sapiens.
 XX
 PN WO9963085-A1.
 XX
 PD 09-DEC-1999.
 XX
 PF 28-MAY-1999; 99WO-JP02855.
 XX
 PR 02-JUN-1998; 98JP-0152603.
 XX
 PA (KYOW) KYOWA HAKKO KOGYO KK.
 XX
 PI Ishiwata T, Sakurada M, Kawabata A, Nakagawa S, Nishi T, Kuga T;
 PI Sawada S, Takei M, Shibata K, Furuya A;
 XX
 WPI; 2000-097328/08.
 XX
 PT DNA sequences preferentially expressed in IGA nephropathy patients,
 PT proteins encoded by them, and antibodies to those proteins -
 XX
 PS Claim 3; Page 170; 180pp; Japanese.
 XX
 CC This invention describes novel DNA sequences preferentially expressed in
 CC IGA nephropathy patients, and DNA sequences stringently hybridizing to
 CC them. Independent claims cover diagnostic reagents for IGA nephropathy
 CC incorporating the antisense sequences; the treatment of IGA nephropathy
 CC using the antisense sequences for mRNA inhibition; proteins associated
 CC with IGA nephropathy, containing sequences encoded by the DNA sequences;
 CC antibodies recognizing these proteins; the production of the proteins
 CC by culture of host cells transformed with DNA encoding them; diagnostic
 CC reagents for IGA nephropathy containing the antibodies; and compositions
 CC for the treatment of IGA nephropathy which contain the antibodies. The
 CC products of the invention can be used for the diagnosis and treatment of
 CC IGA nephropathy. This sequence represents a primer used in the isolation
 CC and identification of the human IGA nephropathy-associated proteins
 CC described in the method of the invention.
 XX
 SQ Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 other;
 Query Match 1.4%; Score 15; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 4e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1084 AAAAAAAAAAAAAA 1098
 Db 16 AAAAAAAAAAAAAA 2

```

RESULT 801
AA30180/c
ID AAX82722 standard; DNA; 17 BP.
XX
AC AAX82722;
XX
DT 10-NOV-2000 (first entry)
XX
DE Human IGA nephropathy-associated cDNA primer #63.
XX
KW IGA nephropathy-associated protein; diagnosis; treatment; antisense;
KW human; primer; ss.
XX
OS Homo sapiens.
XX
PN WO9963085-A1.
XX
PD 09-DEC-1999.
XX
PF 28-MAY-1999; 99WO-JP02855.
XX
PR 02-JUN-1998; 98JP-0152603.
XX
PA (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI Ihiwata T, Sakurada M, Kawabata A, Nakagawa S, Nishi T, Kuga T;
PI Sawada S, Takei M, Shibata K, Furuya A;
XX
DR WPI; 2000-097328/08.
XX
KW DNA sequences preferentially expressed in IGA nephropathy patients,
PT proteins encoded by them, and antibodies to those proteins
XX
PS Claim 3; Page 170; 180pp; Japanese.
XX
CC This invention describes novel DNA sequences preferentially expressed in
CC IGA nephropathy patients, and DNA sequences stringently hybridizing to
CC them. Independent claims cover diagnostic reagents for IGA nephropathy
CC incorporating the antisense sequences; the treatment of IGA nephropathy
CC using the antisense sequences for mRNA inhibition; proteins associated
CC with IGA nephropathy, containing sequences encoded by the DNA sequences;
CC antibodies recognizing these proteins; the production of the proteins
CC by culture of host cells transformed with DNA encoding them; diagnostic
CC reagents for IGA nephropathy containing the antibodies; and compositions
CC for the treatment of IGA nephropathy which contain the antibodies. The
CC products of the invention can be used for the diagnosis and treatment of
CC IGA nephropathy. This sequence represents a primer used in the isolation
CC and identification of the human IGA nephropathy-associated proteins
CC described in the method of the invention.
XX
SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 other;

Query Match 1-4%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1098
Db 16 AAAAAAAAAAAAAA 2

RESULT 802
AA30180/c
ID AAA30180 standard; DNA; 17 BP.
XX
AC AAA30180;
XX
DT 16-AUG-2000 (first entry)
XX
DE PCR primer GT15C used in pollenosis associated gene identification.
XX
KW Pollenosis-associated protein; high pollen-specific immunoglobulin E;
KW IGE; diagnose; cedar pollenosis; treatment; human; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO200020575-A1.
XX
PD 13-APR-2000.
XX
PF 06-OCT-1999; 99WO-JP05506.
XX
PR 06-OCT-1998; 98JP-0284610.
XX
PA (GENO-) GENOX RES INC.
XX
PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Lu N, Ogawa K;
XX
KW Pollenosis-associated protein; high pollen-specific immunoglobulin E;

```

```

KW IGE; diagnose; cedar pollenosis; treatment; human; PCR primer; ss.
XX Synthetic.
XX WO200020575-A1.
XX PN 13-APR-2000.
XX PD 06-OCT-1999; 99WO-JP05506.
XX PF 06-OCT-1998; 98JP-0284610.
XX PR (GENO-) GENOX RES INC.
XX PA Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
XX PI Obayashi I, Imai Y, Lu N, Ogawa K;
XX DR WPI; 2000-317712/27.
XX KW Gene highly expressed in patients with high cedar pollen-specific IGE
XX levels, useful for diagnosing pollenosis, and screening candidate
XX compounds for pollenosis treatment
XX Example 6; Page 38; 44pp; Japanese.
XX CC This sequence represents a PCR primer used in the identification of a
XX human pollenosis associated gene. The gene is highly expressed in
XX individuals with high pollen-specific immunoglobulin E (IGE) levels. The
XX invention relates to the nucleotide sequence encoding the pollenosis
XX associated protein, diagnosing pollenosis and screening candidate
XX compounds for treating pollenosis. The gene can be used in diagnosing
XX pollenosis, particularly cedar pollenosis, and screening candidate
XX compounds for pollenosis treatment.
XX SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 other;

Query Match 1-4%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1098
Db 16 AAAAAAAAAAAAAA 2

RESULT 803
AA30181/c
ID AAA30181 standard; DNA; 17 BP.
XX
AC AAA30181;
XX
DT 16-AUG-2000 (first entry)
XX
DE PCR primer GT15G used in pollenosis associated gene identification.
XX
KW Pollenosis-associated protein; high pollen-specific immunoglobulin E;
KW IGE; diagnose; cedar pollenosis; treatment; human; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO200020575-A1.
XX
PD 13-APR-2000.
XX
PF 06-OCT-1999; 99WO-JP05506.
XX
PR 06-OCT-1998; 98JP-0284610.
XX
PA (GENO-) GENOX RES INC.
XX
PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Lu N, Ogawa K;
XX
KW Pollenosis-associated protein; high pollen-specific immunoglobulin E;

```

```

DR WPI; 2000-317712/27.
XX Gene highly expressed in patients with high cedar pollen-specific IgE
PT levels, useful for diagnosing pollenosis, and screening candidate
PT compounds for pollenosis treatment -
XX Example 6; Page 38; 44pp; Japanese.
XX This sequence represents a PCR primer used in the identification of a
CC human pollenosis associated gene. The gene is highly expressed in
CC individuals with high pollen-specific immunoglobulin E (IgE) levels. The
CC invention relates to the nucleotide sequence encoding the pollenosis
CC associated protein, diagnosing pollenosis and screening candidate
CC compounds for treating pollenosis. The gene can be used in diagnosing
CC pollenosis, particularly cedar pollenosis, and screening candidate
CC compounds for pollenosis treatment.
XX Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 other;
SQ
Query Match 1.4%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1084 AAAAAAAAAAAAAA 1098
Db 16 AAAAAAAAAAAAAA 2
RESULT 804
AA25448/c
ID AAA25448 standard; DNA; 17 BP.
XX
AC AAA25448;
XX
DT 19-JUL-2000 (first entry)
XX
DE Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1946.
XX
KW Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage;
KW hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
KW gene expression modification; cancer; phosphorothioate; endonuclease;
KW anticancer; breast cancer; endometrium cancer; ss.
XX
OS Homo sapiens.
XX
PN WO9954459-A2.
XX
PD 28-OCT-1999.
XX
PF 19-APR-1999; 99WO-US08547.
XX
PR 20-APR-1998; 98US-0082404.
PR 23-JUN-1998; 98US-0103636.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Thompson JD, Beigelman L, McSwiggen JA, Karpeisky A, Bellon L;
PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haerberli P;
PI Matulic-Adamic J;
XX
DR WPI; 2000-013248/01.
XX
XX New nucleic acids that interact, and optionally cleave, target
PT sequences, used to treat cancer -
XX
PS Claim 77; Page 79; 148pp; English.
XX
CC The present invention describes nucleic acids (A) that interact stably
CC with a target sequence and contain at least one phosphorodithioate
CC link, having endonuclease activity. (A), and more generally any
CC catalytic nucleic acid (A') that modulates expression of the oestrogen
CC receptor gene, are used to treat cancer (particularly of breast or
CC endometrium), in vivo or by transforming cells ex vivo and implanting

```

```

CC treated cells, or for other conditions associated with levels of
CC oestrogen receptor. Because of the high selectivity for targeted RNA, (A)
CC can also be used to correlate inhibition of gene expression with
CC alterations in phenotype, particularly for identification of therapeutic
CC targets, and as research reagents (for RNA, in the same way that
CC restriction endonucleases are used with DNA). The combination of
CC modifications in (A) improves resistance to nucleases, binding affinity
CC and/or activity. AAA23503 to AAA24747 represent oestrogen receptor
CC hammerhead ribozyme sequences, and AAA24748 to AAA25992 represent their
CC corresponding target sequences. AAA25993 to AAA26105 represent oestrogen
CC receptor hairpin ribozyme sequences, and AAA26107 to AAA26218 represent
CC their corresponding target sequences. AAA26219 to AAA26271 represent
CC other ribozyme sequences and antisense oligonucleotides used in the
CC exemplification of the present invention.
XX Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 other;
SQ
Query Match 1.4%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1084 AAAAAAAAAAAAAA 1098
Db 17 AAAAAAAAAAAAAA 3
RESULT 805
AAZ36740/c
ID AAZ36740 standard; DNA; 17 BP.
XX
AC AAZ36740;
XX
DT 13-MAR-2000 (first entry)
XX
DE Anchored oligo(dT) primer GT15G used for modified differential display.
XX
KW Stimulus-regulated nucleic acid; sequence profile; nucleic acid level;
KW differentially expressed nucleic acid; disease state; cancer;
KW autoimmune disease; infectious disease; aging; developmental disorder;
KW proliferative disorder; neurological disorder; toxicity; primer;
KW treatment resistance; differential expression; drug discovery;
KW growth factor; epidermal growth factor; radiation; stress; pathogen; ss.
XX
OS Synthetic.
XX
PN WO9955913-A2.
XX
PD 04-NOV-1999.
XX
PF 27-APR-1999; 99WO-US09119.
XX
PR 27-APR-1998; 98US-0083331.
PR 27-AUG-1998; 98US-0098070.
PR 04-FEB-1999; 99US-0118624.
XX
PA (KIMM-) KIMMEL CANCER CENT SIDNEY.
XX
PI McClelland M, Welsh J, Trenkle T;
XX
DR WPI; 2000-086388/07.
XX
XX Measuring expression of low abundance reduced complexity target nucleic
PT acid molecules -
XX
PS Example 3; Page 91; 187pp; English.
XX
CC AAZ36739-41 represent oligo(dT) primers used for modified differential
CC display, in the method of the invention. The specification describes a
CC method for measuring the level of two or more nucleic acid molecules in
CC a target. The method comprises contacting a probe with an arbitrarily or
CC statistically sampled target and detecting the amount of specific
CC binding of the target to the probe. The methods can be used to identify
CC differentially expressed nucleic acid molecules associated with disease

```


CC states, such as cancer, autoimmune disease, infectious disease, aging,
CC developmental disorder, proliferative disorder or neurological disorder.
CC Alternatively the methods can be used to assess the efficacy or toxicity
CC of or a resistance to a treatment. Also the methods can be used to
CC determine differential expression of nucleic acid molecules in response
CC to a stimulus, e.g. a chemical, drug or growth factor (especially
CC epidermal growth factor), radiation, stress or a pathogen. The methods
CC can also be used to determine co-regulated genes that can be potential
CC targets for drug discovery.

XX Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 other;

Query Match 1.4%; Score 15; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 4e+02; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0;

QY 1084 AAAAAAAAAAAAAA 1098

Db |||||
16 AAAAAAAAAAAAAA 2

RESULT 806

AAZ35714/c

ID AAZ35714 standard; DNA; 17 BP.

XX AAZ35714;

DT 31-JAN-2000 (first entry)

DE Murine gene anchor PCR primer SEQ ID NO:3.

XX Rare expressed gene; analysis; expression; nucleic acid sample;
KW PCR primer; ss.

XX Synthetic.

OS Mus sp.

XX EP959141-A2.

XX 24-NOV-1999.

PF 18-MAY-1999; 99EP-0109795.

PR 20-MAY-1998; 98JP-0153651.

XX (HITA) HITACHI LTD.

XX Muramatsu T, Fujita T, Kiyama M, Irie T, Okano K;

XX WPI; 2000-001284/01.

XX Preparation of nucleic acid sample, useful for analysis of rare
PT expressed genes -

PS Disclosure; Page 11; 22pp; English.

XX The present invention describes a process for the preparation of a
CC nucleic acid sample comprising: (a) providing a nucleic acid sample
CC having a plurality of species of sequences, and providing one or a
CC plurality of kinds of probes having a known sequence substantially
CC complementary to a portion of sequence of the nucleic acid sample; (b)
CC mixing and hybridizing the nucleic acid sample with probes; (c)
CC subsequently recovering nucleic acid molecules; or (i) providing a
CC nucleic acid sample having a plurality of species of sequences, and
CC providing one or a plurality of kinds of probes having a known sequence
CC substantially complementary to a portion of sequence of the nucleic acid
CC sample; (ii) mixing and hybridizing the nucleic acid sample with the
CC probes; (iii) treating the product of (ii) with nuclease activity of an
CC enzyme or the probe itself; and (iv) subsequently recovering the nucleic
CC acid molecules not digested by the nuclease activity in (iii); or (I)
CC providing a nucleic acid sample having a plurality of species of
CC sequences and oligonucleotides primer having predetermined sequences for
CC synthesizing DNA strands; (II) providing one or a plurality of kinds of

CC probes having a known sequence substantially complementary to a portion
CC of a sequence of the nucleic acid sample having such a structure to
CC prevent a polymerase reaction from its 3' end and a nuclease reaction
CC from its 5' end; (iii) mixing and hybridizing the nucleic acid sample
CC with the primers and probes; (iv) executing polymerase chain reaction
CC for the samples prepared in (iii); and (v) subsequently recovering
CC nucleic acid molecules synthesized in (iv). The method is useful for the
CC preparation of a nucleic acid sample for the analysis of rare expressed
CC genes. The present sequence represents a PCR primer used in the
CC exemplification of the present invention.

SQ Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 other;

Query Match 1.4%; Score 15; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 4e+02; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0;

QY 1084 AAAAAAAAAAAAAA 1098

Db |||||
16 AAAAAAAAAAAAAA 2

RESULT 807

AAC82875/c

ID AAC82875 standard; DNA; 17 BP.

XX AAC82875;

DT 20-MAR-2001 (first entry)

DE Human pollinosis-associated gene 441 primer #2.

XX Pollinosis; pollinosis-associated gene 441; allergy; T cell;

KW pollen scattering; antigen; primer; ss.

XX Homo sapiens.

XX WO200073435-A1.

XX 07-DEC-2000.

PF 18-MAY-2000; 2000WO-JP03190.

PR 27-MAY-1999; 99JP-0148783.

XX (GENO-) GENOX RES INC.

XX Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;

XX WPI; 2001-061526/07.

XX Pollinosis-associated gene 441 which undergoes lower expression in
PT subjects after pollen scattering, useful in diagnosis of allergic
PT diseases and screening candidate compounds to regulate response of T
PT cells to antigen stimulus -

PS Example 6; Page 35; 42pp; Japanese.

XX This invention describes a novel nucleic acid molecule comprising a
CC sequence (I) which undergoes significantly low expression in subjects
CC after pollen scattering, and is useful in diagnosis of allergic diseases
CC and screening candidate compounds for remedies capable of regulating the
CC response of T cells to the stimulus by an antigen.

XX Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 other;

Query Match 1.4%; Score 15; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 4e+02; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0;

QY 1084 AAAAAAAAAAAAAA 1098

Db |||||

Db 16 AAAAAAAAAAAAAA 2

RESULT 808
AAC82876/c
ID AAC82876 standard; DNA; 17 BP.
XX
XX AC AAC82876;
XX
XX DT 20-MAR-2001 (first entry)
XX
XX DE Human pollinosis-associated gene 441 primer #3.
XX
XX KW Pollinosis; pollinosis-associated gene 441; allergy; T cell;
XX
XX KW pollen scattering; antigen; primer; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO200073435-A1.
XX
XX PD 07-DEC-2000.
XX
XX PF 18-MAY-2000; 2000WO-JP03190.
XX
XX PR 27-MAY-1999; 99JP-0148783.
XX
XX PA (GENO-) GENOX RES INC.
XX
XX PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
XX
XX PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
XX
XX DR WPI; 2001-061526/07.
XX
XX PT Pollinosis-associated gene 441 which undergoes lower expression in
XX
XX PT subjects after pollen scattering, useful in diagnosis of allergic
XX
XX PT diseases and screening candidate compounds to regulate response of T
XX
XX PT cells to antigen stimulus -
XX
XX PS Example 6; Page 36; 42pp; Japanese.
XX
XX CC This invention describes a novel nucleic acid molecule comprising a
XX
XX CC sequence (I) which undergoes significantly low expression in subjects
XX
XX CC after pollen scattering, and is useful in diagnosis of allergic diseases
XX
XX CC and screening candidate compounds for remedies capable of regulating the
XX
XX CC response of T cells to the stimulus by an antigen.
XX
XX SQ Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 other;
XX
XX Query Match 1.4%; Score 15; DB 1; Length 17;
XX
XX Best Local Similarity 100.0%; Pred. No. 4e+02; 0; Indels 0; Gaps 0;
XX
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1084 AAAAAAAAAAAAAA 1098
XX
XX Db |||||
XX 16 AAAAAAAAAAAAAA 2

RESULT 809
AAC91720/c
ID AAC91720 standard; DNA; 17 BP.
XX
XX AC AAC91720;
XX
XX DT 27-MAR-2001 (first entry)
XX
XX DE PCR anchor primer, SEQ ID NO:3, used in human gene 787 isolation.
XX
XX DE PCR anchor primer, SEQ ID NO:4, used in human gene 787 isolation.
XX
XX KW Human; pollinosis-associated gene 787; pollen allergy; T-cell;
XX
XX KW reduced expression; detection; diagnosis; drug screening;
XX
XX KW allergic disease; PCR primer; ss.
XX
XX OS Synthetic.
XX
XX PN WO200073440-A1.
XX
XX PD 07-DEC-2000.

PN WO200073440-A1.
XX
XX PD 07-DEC-2000.
XX
XX PF 18-MAY-2000; 2000WO-JP03192.
XX
XX PR 27-MAY-1999; 99JP-0148785.
XX
XX PA (GENO-) GENOX RES INC.
XX
XX PA (EISA) EISAI CO LTD.
XX
XX PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
XX
XX PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K, Takahashi E;
XX
XX PI Yokoi A;
XX
XX DR WPI; 2001-032159/04.
XX
XX PT Pollinosis-associated gene 787 undergoing significantly low expression
XX
XX PT in subjects after pollen scattering, useful in diagnosis of allergic
XX
XX PT diseases and screening candidate compounds to regulate response of T
XX
XX PT cells to antigen stimulus -
XX
XX PS Example 6; Page 40; 54pp; Japanese.
XX
XX CC The invention relates to the human pollinosis-associated gene 787 which
XX
XX CC exhibits significantly reduced expression in the T-cells of individuals
XX
XX CC after the pollen-scattering season, relative to expression levels in
XX
XX CC T-cells before the pollen-scattering season. The gene was isolated from
XX
XX CC T-cells from individuals allergic to pollen using the differential
XX
XX CC display method. The invention also relates to pollinosis-associated gene
XX
XX CC 787 primers and probes; methods of detection of pollinosis-associated gene
XX
XX CC 787 nucleic acids; and a method of diagnosis of allergic diseases
XX
XX CC via the detection of pollinosis-associated gene 787 nucleic acids. The
XX
XX CC invention additionally encompasses a method of screening drug candidates
XX
XX CC for the treatment of allergic disease by measuring the expression of
XX
XX CC pollinosis-associated gene 787 in pollen antigen-stimulated T-cells in
XX
XX CC the presence of a test compound relative to a control. Pollinosis-
XX
XX CC associated gene 787 is useful in the diagnosis of allergic diseases and
XX
XX CC in the screening of drug candidates for the treatment of such diseases.
XX
XX CC The present sequence represents a PCR primer used in the isolation of
XX
XX CC human pollinosis-associated gene 787 cDNA.
XX
XX SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 other;
XX
XX Query Match 1.4%; Score 15; DB 1; Length 17;
XX
XX Best Local Similarity 100.0%; Pred. No. 4e+02; 0; Indels 0; Gaps 0;
XX
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1084 AAAAAAAAAAAAAA 1098
XX
XX Db |||||
XX 16 AAAAAAAAAAAAAA 2

RESULT 810
AAC91721/c
ID AAC91721 standard; DNA; 17 BP.
XX
XX AC AAC91721;
XX
XX DT 27-MAR-2001 (first entry)
XX
XX DE PCR anchor primer, SEQ ID NO:4, used in human gene 787 isolation.
XX
XX KW Human; pollinosis-associated gene 787; pollen allergy; T-cell;
XX
XX KW reduced expression; detection; diagnosis; drug screening;
XX
XX KW allergic disease; PCR primer; ss.
XX
XX OS Synthetic.
XX
XX PN WO200073440-A1.
XX
XX PD 07-DEC-2000.

```
PF 18-MAY-2000; 2000WO-JP03192.
XX
XX
XX 27-MAY-1999; 99JP-0148785.
XX
XX (GENO-) GENOX RES INC.
XX (EISA ) EISAI CO LTD.
XX
XX Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
XX PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K, Takahashi E;
XX PI Yokoi A;
XX
XX WPI; 2001-032159/04.
XX
XX Pollinosis-associated gene 787 undergoing significantly low expression
XX in subjects after pollen scattering, useful in diagnosis of allergic
XX diseases and screening candidate compounds to regulate response of T
XX cells to antigen stimulus
XX
XX Example 6; Page 41; 54pp; Japanese.
XX
XX The invention relates to the human pollinosis-associated gene 787 which
XX exhibits significantly reduced expression in the T-cells of individuals
XX after the pollen-scattering season, relative to expression levels in
XX T-cells before the pollen-scattering season. The gene was isolated from
XX T-cells from individuals allergic to pollen using the differential
XX display method. The invention also relates to pollinosis-associated
XX 787 primers and probes; methods of detection of pollinosis-associated
XX gene 787 nucleic acids; and a method of diagnosis of allergic diseases
XX via the detection of pollinosis-associated gene 787 nucleic acids. The
XX invention additionally encompasses a method of screening drug candidates
XX for the treatment of allergic disease by measuring the expression of
XX pollinosis-associated gene 787 in pollen antigen-stimulated T-cells in
XX the presence of a test compound relative to a control. Pollinosis-
XX associated gene 787 is useful in the diagnosis of allergic diseases and
XX in the screening of drug candidates for the treatment of such diseases.
XX The present sequence represents a PCR primer used in the isolation of
XX human pollinosis-associated gene 787 cDNA.
XX
XX Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 other;
XX
XX Query Match 1.4%; Score 15; DB 1; Length 17;
XX Best Local Similarity 100.0%; Pred. No. 4e+02;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1084 AAAAAAAAAAAAAA 1098
XX Db 16 AAAAAAAAAAAAAA 2
XX
XX RESULT 811
XX AAC92293/c
XX ID AAC92293 standard; DNA; 17 BP.
XX
XX AC AAC92293;
XX
XX DT 22-MAR-2001 (first entry)
XX
XX DE Human pollinosis-associated gene 465 related PCR primer SEQ ID NO.3.
XX
XX KW Human; pollinosis-associated gene 465; pollen scattering; allergy;
XX KW allergic disease; PCR primer; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO200073439-A1.
XX
XX PD 07-DEC-2000.
XX
XX PF 18-MAY-2000; 2000WO-JP03191.
XX
XX 27-MAY-1999; 99JP-0148784.
XX
XX (GENO-) GENOX RES INC.
XX
XX PA
XX
XX PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
XX PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K, Takahashi E;
XX PI Yokoi A;
XX
XX WPI; 2001-061528/07.
XX
XX Pollinosis-associated gene 465 undergoing significantly low expression
XX in subjects after pollen scattering, useful in diagnosis of allergic
XX diseases and screening candidate compounds to regulate response of T
XX cells to antigen stimulus
XX
XX Example 6; Page 44; 61pp; Japanese.
XX
XX The present invention describes the human pollinosis-associated gene 465
XX which has a nucleic acid sequence of 3442 base pairs (bp), given in
XX (AAC92291), that undergoes significantly low expression in subjects
XX after pollen scattering, and is useful in the diagnosis of allergic
XX diseases and screening candidate compounds for remedies capable of
XX regulating the response of T cells to the stimulus by an antigen. The
XX gene is useful in the diagnosis of allergic diseases and screening
XX candidate compounds for remedies capable of regulating the response of T
XX cells to the stimulus by an antigen. The present sequence represents a
XX PCR primer which is used in an example from the present invention.
XX
XX Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 other;
XX
XX Query Match 1.4%; Score 15; DB 1; Length 17;
XX Best Local Similarity 100.0%; Pred. No. 4e+02;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1084 AAAAAAAAAAAAAA 1098
XX Db 16 AAAAAAAAAAAAAA 2
XX
XX RESULT 812
XX AAC92294/c
XX ID AAC92294 standard; DNA; 17 BP.
XX
XX AC AAC92294;
XX
XX DT 22-MAR-2001 (first entry)
XX
XX DE Human pollinosis-associated gene 465 related PCR primer SEQ ID NO.4.
XX
XX KW Human; pollinosis-associated gene 465; pollen scattering; allergy;
XX KW allergic disease; PCR primer; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO200073439-A1.
XX
XX PD 07-DEC-2000.
XX
XX PF 18-MAY-2000; 2000WO-JP03191.
XX
XX 27-MAY-1999; 99JP-0148784.
XX
XX (GENO-) GENOX RES INC.
XX
XX PA (EISA ) EISAI CO LTD.
XX
XX PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
XX PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K, Takahashi E;
XX PI Yokoi A;
XX
XX WPI; 2001-061528/07.
XX
XX Pollinosis-associated gene 465 undergoing significantly low expression
XX in subjects after pollen scattering, useful in diagnosis of allergic
XX diseases and screening candidate compounds to regulate response of T
XX cells to antigen stimulus
XX
```

```

XX Example 6; Page 44; 61pp; Japanese.
PS
CC The present invention describes the human pollinosis-associated gene 465
CC which has a nucleic acid sequence of 3442 base pairs (bp), given in
CC (AAC92291), that undergoes significantly low expression in subjects
CC after pollen scattering, and is useful in the diagnosis of allergic
CC diseases and screening candidate compounds for remedies capable of
CC regulating the response of T cells to the stimulus by an antigen. The
CC gene is useful in the diagnosis of allergic diseases and screening
CC candidate compounds for remedies capable of regulating the response of T
CC cells to the stimulus by an antigen. The present sequence represents a
CC PCR primer which is used in an example from the present invention.
XX
SQ Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 other;

Query Match 1.4%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1098
Db |||||
16 AAAAAAAAAAAAAA 2

RESULT 813
AAH47127/c
ID AAH47127 standard; DNA; 17 BP.
XX
AC AAH47127;
XX
DT 30-NOV-2001 (first entry)
XX
DE Nucleotide sequence of primer GT15C.
XX
KW B1001; B1466; B1072; B1151; T-cell; allergy; atopic dermatitis;
XX human; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200165259-A1.
XX
PD 07-SEP-2001.
XX
PF 23-FEB-2001; 2001WO-JP01372.
XX
PR 02-MAR-2000; 2000JP-0061832.
XX
PA (GENO-) GENOX RES INC.
XX (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
XX
PI Nagasu T, Oshida T, Obayashi I, Matsui K, Saito H;
XX WPI; 2001-557789/62.
XX
DR Diagnosis of allergies including atopic dermatitis -
XX
PT Example 6; Page 66; 83pp; Japanese.
XX
CC The invention provides a method of diagnosis of allergies that involves:
CC assaying the levels of expression of genes B1001, B1466, B1072 or B1151
CC in T-cells; and comparing them with the level of expression in healthy
CC T-cells. The method is useful for diagnosing allergies, particularly
CC atopic dermatitis. The present sequence represents a PCR primer used
CC for analysis of the expression of the above genes.
XX
SQ Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 other;

Query Match 1.4%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1098
Db |||||
16 AAAAAAAAAAAAAA 2

RESULT 815
AAL49949/c
ID AAL49949 standard; DNA; 17 BP.
XX
AC AAL49949;
XX
DT 10-DEC-2002 (first entry)
XX
DE Human B1153 expression in allergic disease related PCR primer GT15C.
XX
KW Human; allergy; B1153; differential expression; anti-allergic; asthma;
XX antischismatic; antiinflammatory; atopic skin inflammation; PCR;
XX primer; ss.
XX
OS Unidentified.
XX
PN WO200250269-A1.

```

XX 27-JUN-2002.
 XX 21-DEC-2001; 2001WO-JP11286.
 XX 21-DEC-2000; 2000JP-0389476.
 XX (GENO-) GENOX RES INC.
 XX (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
 XX Matsumoto Y, Imai Y, Oshida T, Sugita Y, Nagasu T, Tsujimoto G;
 XX WPI; 2002-713252/77.
 XX Examination of allergic diseases comprises detecting gene B1153
 XX over-expressed in T cells of allergy patients for diagnosis treatment
 XX and investigation of atopic skin inflammation and asthma -
 XX Example 6; Page 82; 102pp; Japanese.
 XX The present invention relates to a method of examining allergic diseases
 XX which comprises comparing the expression level of gene B1153 in allergy
 XX patients with the expression level in healthy subjects. The method is
 XX useful for the treatment, prevention, diagnosis and study of allergic
 XX diseases including atopic skin inflammation and asthma. The present
 XX sequence is a PCR primer described in the exemplification of the
 XX invention.
 XX SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 other;
 XX Query Match 1.4%; Score 15; DB 1; Length 17;
 XX Best Local Similarity 100.0%; Pred. No. 4e+02;
 XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1084 AAAAAAAAAAAAAA 1098
 DB 16 AAAAAAAAAAAAAA 2
 RESULT 816
 AAL49950/c
 ID AAL49950 standard; DNA; 17 BP.
 XX AC AAL49950;
 XX 10-DEC-2002 (first entry)
 XX Human B1153 expression in allergic disease related PCR primer GT15G.
 XX Human; allergy; B1153; differential expression; antiallergic; asthma;
 XX antiasthmatic; antiinflammatory; atopic skin inflammation; PCR;
 XX primer; ss.
 XX Unidentified.
 XX WO200250269-AL.
 XX 27-JUN-2002.
 XX 21-DEC-2001; 2001WO-JP11286.
 XX 21-DEC-2000; 2000JP-0389476.
 XX (GENO-) GENOX RES INC.
 XX (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
 XX Matsumoto Y, Imai Y, Oshida T, Sugita Y, Nagasu T, Tsujimoto G;
 XX WPI; 2002-713252/77.
 XX Examination of allergic diseases comprises detecting gene B1153
 XX over-expressed in T cells of allergy patients for diagnosis treatment
 XX and investigation of atopic skin inflammation and asthma -

XX Example 6; Page 82; 102pp; Japanese.
 XX The present invention relates to a method of examining allergic diseases
 XX which comprises comparing the expression level of gene B1153 in allergy
 XX patients with the expression level in healthy subjects. The method is
 XX useful for the treatment, prevention, diagnosis and study of allergic
 XX diseases including atopic skin inflammation and asthma. The present
 XX sequence is a PCR primer described in the exemplification of the
 XX invention.
 XX SQ Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 other;
 XX Query Match 1.4%; Score 15; DB 1; Length 17;
 XX Best Local Similarity 100.0%; Pred. No. 4e+02;
 XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1084 AAAAAAAAAAAAAA 1098
 DB 16 AAAAAAAAAAAAAA 2
 RESULT 817
 AAL47235/c
 ID AAL47235 standard; DNA; 17 BP.
 XX AC AAL47235;
 XX 22-AUG-2002 (first entry)
 XX Allergic disease examination method related anchor primer SEQ ID NO: 3.
 XX Allergic disease; allergy; antiallergic; intersectin 2; eosinophil;
 XX atopic dermatitis; human; PCR; primer; ss.
 XX Unidentified.
 XX WO200233122-AL.
 XX 25-APR-2002.
 XX 11-OCT-2001; 2001WO-JP08937.
 XX 13-OCT-2000; 2000JP-0314093.
 XX (GENO-) GENOX RES INC.
 XX (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
 XX (EISA) EISAI CO LTD.
 XX Sugita Y, Hashida R, Ogawa K, Obayashi M, Nagasu T, Saito H;
 XX Takahashi E;
 XX WPI; 2002-372313/40.
 XX Method for examining allergic diseases by differential display of
 XX intersectin 2 gene showing different expression particularly
 XX significant increase in eosinophils in patients -
 XX Example 1; Page 53; 90pp; Japanese.
 XX The present invention relates to a method for examining allergic diseases
 XX with intersectin 2 gene or a gene with equivalent function of intersectin
 XX 2 as an indicator gene, which comprises determining the expression level
 XX of the gene in the eosinophils in a patient, and comparing the expression
 XX level with that in the eosinophils of a healthy individual. The method is
 XX for examining allergic diseases, particularly atopic dermatitis, which is
 XX also applicable in screening candidate compounds for remedies. The
 XX present sequence is an anchor primer described in the exemplification
 XX of the invention.
 XX SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 other;
 XX Query Match 1.4%; Score 15; DB 1; Length 17;

```

Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1098
DB 16 AAAAAAAAAAAAAA 2

RESULT 818
AAL47236/c
ID AAL47236 standard; DNA; 17 BP.
XX AC AAL47236;
XX DT 22-AUG-2002 (first entry)
XX DE Allergic disease examination method related anchor primer SEQ ID NO: 4.
XX KW Allergic disease; allergy; antiallergic; intersectin 2; eosinophil;
XX KW atopic dermatitis; human; PCR; primer; ss.
XX OS Unidentified.
XX PN W0200233122-A1.
XX PD 25-APR-2002.
XX PF 11-OCT-2001; 2001WO-JP08937.
XX PR 13-OCT-2000; 2000JP-0314093.
XX PA (GENO-) GENOX RES INC.
XX PA (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
XX PA (SISA) EISAI CO LTD.
XX PI Sugita Y, Hashida R, Ogawa K, Obayashi M, Nagasu T, Saito H;
XX PI Takahashi E;
XX DR WPI; 2002-372313/40.
XX PT Method for examining allergic diseases by differential display of
XX PT intersectin 2 gene showing different expression particularly
XX PT significant increase in eosinophils in patients -
XX PS Example 1; Page 53; 90pp; Japanese.
XX CC The present invention relates to a method for examining allergic diseases
XX CC with intersectin 2 gene or a gene with equivalent function of intersectin
XX CC 2 as an indicator gene, which comprises determining the expression level
XX CC of the gene in the eosinophils in a patient, and comparing the expression
XX CC level with that in the eosinophils of a healthy individual. The method is
XX CC for examining allergic diseases, particularly atopic dermatitis, which is
XX CC also applicable in screening candidate compounds for remedies. The
XX CC present sequence is an anchor primer described in the exemplification
XX CC of the invention.
SQ Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 other;

Query Match 1.4%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1098
DB 16 AAAAAAAAAAAAAA 2

RESULT 819
ABL59039/c
ID ABL59039 standard; DNA; 17 BP.
XX AC ABL59039;
XX DR WPI; 2002-439993/47.
XX PT Examining allergic diseases, involves measuring the expression levels of a

```

```

DT 20-AUG-2002 (first entry)
XX DE Nucleotide sequence of PCR primer GT15C.
XX KW Human; allergosis; eosinophil; PCR; primer; ss.
XX OS Homo sapiens.
XX PN JP2002095500-A.
XX PD 02-APR-2002.
XX PF 25-SEP-2000; 2000JP-0291316.
XX PR 25-SEP-2000; 2000JP-0291316.
XX PA (GENO-) GENOX SOYAKU KENKYUSHO KK.
XX PA (KOKU-) KOKURITSU SHONI BYOIN INCHO.
XX DR WPI; 2002-439993/47.
XX CC Examining allergosis, involves measuring the expression levels of a
XX CC specific gene, and comparing it to the levels in the eosinophils of a
XX CC healthy control -
XX PS Example 1; Page 17; 20pp; Japanese.
XX CC The specification describes a method for examining allergosis. The
XX CC method comprises measuring the expression level of the gene given
XX CC in ABL59037, and comparing it with the expression level of the gene
XX CC in the eosinophils of a healthy person. The method is used for the
XX CC examination of allergosis. The present sequence represents a PCR
XX CC primer, which is used in the course of the invention.
SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 other;

Query Match 1.4%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1098
DB 16 AAAAAAAAAAAAAA 2

RESULT 820
ABL59040/c
ID ABL59040 standard; DNA; 17 BP.
XX AC ABL59040;
XX DT 20-AUG-2002 (first entry)
XX DE Nucleotide sequence of PCR primer GT15G.
XX KW Human; allergosis; eosinophil; PCR; primer; ss.
XX OS Homo sapiens.
XX PN JP2002095500-A.
XX PD 02-APR-2002.
XX PF 25-SEP-2000; 2000JP-0291316.
XX PR 25-SEP-2000; 2000JP-0291316.
XX PA (GENO-) GENOX SOYAKU KENKYUSHO KK.
XX PA (KOKU-) KOKURITSU SHONI BYOIN INCHO.
XX DR WPI; 2002-439993/47.
XX PT Examining allergosis, involves measuring the expression levels of a

```

PT specific gene, and comparing it to the levels in the eosinophils of a
 XX healthy control -
 PS Example 1; Page 17; 20pp; Japanese.

XX The specification describes a method for examining allergic diseases. The
 CC method comprises measuring the expression level of the gene given
 CC in ABL59037, and comparing it with the expression level of the gene
 CC in the eosinophils of a healthy person. The method is used for the
 CC examination of allergic diseases. The present sequence represents a PCR
 CC primer, which is used in the course of the invention.

XX Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 other;

Query Match 1.4%; Score 15; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 4e+02; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1098
 DB 16 AAAAAAAAAAAAAA 2

RESULT 821

ABN99830/C
 ID ABN99830 standard; DNA; 17 BP.

AC ABN99830;

DT 15-AUG-2002 (first entry)

DE Human allergic disease related PCR primer SEQ ID NO: 19.

XX Human; allergy; atopic dermatitis; eosinophil; anti-allergic; PCR;
 KW primer; ss.

OS Homo sapiens.

PN WO200233069-A1.

PD 25-APR-2002.

PF 28-SEP-2001; 2001WO-JP08574.

PR 13-OCT-2000; 2000JP-0314093.

XX (GENO-) GENOX RES INC.

PA (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.

PI Sugita Y, Hashida R, Ogawa K, Obayashi M, Nagasu T, Saito H;

DR WPI; 2002-372311/40.

XX Method for examining allergic diseases by differential display of
 PT seventeen genes showing different expression particularly significant
 PT increase in eosinophils in patients with mild atopic dermatitis, also
 PT applicable in screening compounds -

PS Example 1; Page 109; 165pp; Japanese.

XX The present invention relates to a method for examining allergic diseases
 CC which involves determining the expression level of a gene, having one of
 CC the 17 nucleotide sequences shown in ABN99812-ABN99828, in the
 CC eosinophils in a patient and comparing the expression level with that in
 CC the eosinophils of a healthy individual. The method can be used to
 CC examine allergic diseases, particularly atopic dermatitis, and its early
 CC diagnosis, which is also applicable in screening candidate compounds for
 CC remedies. The present sequence is a PCR primer described in the
 CC exemplification of the invention.

XX Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 other;

Query Match

1.4%; Score 15; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 4e+02; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1098
 DB 16 AAAAAAAAAAAAAA 2

RESULT 822

ABN99831/C

ID ABN99831 standard; DNA; 17 BP.

AC ABN99831;

DT 15-AUG-2002 (first entry)

DE Human allergic disease related PCR primer SEQ ID NO: 20.

XX Human; allergy; atopic dermatitis; eosinophil; anti-allergic; PCR;
 KW primer; ss.

OS Homo sapiens.

PN WO200233069-A1.

PD 25-APR-2002.

PF 28-SEP-2001; 2001WO-JP08574.

PR 13-OCT-2000; 2000JP-0314093.

XX (GENO-) GENOX RES INC.

PA (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.

PI Sugita Y, Hashida R, Ogawa K, Obayashi M, Nagasu T, Saito H;

DR WPI; 2002-372311/40.

XX Method for examining allergic diseases by differential display of
 PT seventeen genes showing different expression particularly significant
 PT increase in eosinophils in patients with mild atopic dermatitis, also
 PT applicable in screening compounds -

PS Example 1; Page 110; 165pp; Japanese.

XX The present invention relates to a method for examining allergic diseases
 CC which involves determining the expression level of a gene, having one of
 CC the 17 nucleotide sequences shown in ABN99812-ABN99828, in the
 CC eosinophils in a patient and comparing the expression level with that in
 CC the eosinophils of a healthy individual. The method can be used to
 CC examine allergic diseases, particularly atopic dermatitis, and its early
 CC diagnosis, which is also applicable in screening candidate compounds for
 CC remedies. The present sequence is a PCR primer described in the
 CC exemplification of the invention.

XX Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 other;

Query Match 1.4%; Score 15; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 4e+02; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1098
 DB 16 AAAAAAAAAAAAAA 2

RESULT 823

ABK49635/C

ID ABK49635 standard; DNA; 17 BP.

AC ABK49635;

DT 15-JUL-2002 (first entry)

XX DE Human Acetyltransferase-like protein 20-90-05 PCR primer GT15C.
XX KW Human; ss; PCR; acetyltransferase; 20-90-05; allergic disease; primer;
XX KW differential display; eosinophil; antiallergic; atopic dermatitis;
XX KW GT15C.
XX OS Homo sapiens.
XX PN WO200224903-A1.
XX PD 28-MAR-2002.
XX PF 21-SEP-2001; 2001WO-JP08246.
XX PP 25-SEP-2000; 2000JP-0291318.
XX PR (GENO-) GENOX RES INC.
XX PA (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
XX PA (EISA) EISAI CO LTD.
XX PI Sugita Y, Hashida R, Ogawa K, Fujishima T, Nagasu T, Tsujimoto G;
XX PI Takahashi E;
XX DR WPI; 2002-315738/35.
XX PT Examining allergic diseases by differential display of gene showing
XX PT different expression particularly increased expression in remission
XX PT stage in eosinophils of patients, also applicable in screening
XX PT candidate compounds for remedies -
XX PS Example 1; Page 56; 72pp; Japanese.
XX CC The invention relates to a method for examining allergic diseases
XX CC comprising determining the expression level of a gene containing,
XX CC the human cDNA appearing as ABK49633 which has homology with
XX CC acetyltransferases in the eosinophils of a patient and comparing the
XX CC expression level with that in the eosinophils of a healthy individual
XX CC (i.e. differential display). Also included are methods of screening
XX CC for candidate compounds which affect the expression level of the gene or
XX CC the activity of the protein encoded by the gene (including related
XX CC proteins and mutants), the use of probes based on the gene sequence
XX CC in the examination of allergic diseases, the use of reporter
XX CC constructs in the screening of candidate compounds, a vector containing a
XX CC the transcription-controlling region of the gene, cells transformed
XX CC with the vector, an antibody against the protein and a model animal for
XX CC allergic diseases which is a transgenic non-human vertebrate with
XX CC lowering of expression intensity of the gene in eosinophils.
XX CC The method is examining allergic diseases particularly atopic
XX CC dermatitis which is also applicable in screening candidate
XX CC compounds for remedies. Such method can be performed in high throughput,
XX CC at low cost. The present sequence is a differential display PCR primer
XX CC for the cDNA encoding the human acetyltransferase-like protein 20-90-05.
XX SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 other;

Query Match 1.4%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1098
Db 16 AAAAAAAAAAAAAA 2

RESULT 824
ABK49636/C
ID ABK49636 standard; DNA; 17 BP.
XX AC ABK49636;
XX DT 15-JUL-2002 (first entry)
XX DE Human atopic dermatitis cDNA related PCR primer GT15C.

DE XX Human Acetyltransferase-like protein 20-90-05 PCR primer GT15G.
XX KW Human; ss; PCR; acetyltransferase; 20-90-05; allergic disease; primer;
XX KW differential display; eosinophil; antiallergic; atopic dermatitis;
XX KW GT15G.
XX OS Homo sapiens.
XX PN WO200224903-A1.
XX PD 28-MAR-2002.
XX PF 21-SEP-2001; 2001WO-JP08246.
XX PP 25-SEP-2000; 2000JP-0291318.
XX PR (GENO-) GENOX RES INC.
XX PA (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
XX PA (EISA) EISAI CO LTD.
XX PI Sugita Y, Hashida R, Ogawa K, Fujishima T, Nagasu T, Tsujimoto G;
XX PI Takahashi E;
XX DR WPI; 2002-315738/35.
XX PT Examining allergic diseases by differential display of gene showing
XX PT different expression particularly increased expression in remission
XX PT stage in eosinophils of patients, also applicable in screening
XX PT candidate compounds for remedies -
XX PS Example 1; Page 57; 72pp; Japanese.
XX CC The invention relates to a method for examining allergic diseases
XX CC comprising determining the expression level of a gene containing,
XX CC the human cDNA appearing as ABK49633 which has homology with
XX CC acetyltransferases in the eosinophils of a patient and comparing the
XX CC expression level with that in the eosinophils of a healthy individual
XX CC (i.e. differential display). Also included are methods of screening
XX CC for candidate compounds which affect the expression level of the gene or
XX CC the activity of the protein encoded by the gene (including related
XX CC proteins and mutants), the use of probes based on the gene sequence
XX CC in the examination of allergic diseases, the use of reporter
XX CC constructs in the screening of candidate compounds, a vector containing a
XX CC the transcription-controlling region of the gene, cells transformed
XX CC with the vector, an antibody against the protein and a model animal for
XX CC allergic diseases which is a transgenic non-human vertebrate with
XX CC lowering of expression intensity of the gene in eosinophils.
XX CC The method is examining allergic diseases particularly atopic
XX CC dermatitis which is also applicable in screening candidate
XX CC compounds for remedies. Such method can be performed in high throughput,
XX CC at low cost. The present sequence is a differential display PCR primer
XX CC for the cDNA encoding the human acetyltransferase-like protein 20-90-05.
XX SQ Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 other;

Query Match 1.4%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1098
Db 16 AAAAAAAAAAAAAA 2

RESULT 825
ABK49757/C
ID ABK49757 standard; DNA; 17 BP.
XX AC ABK49757;
XX DT 15-JUL-2002 (first entry)
XX DE Human atopic dermatitis cDNA related PCR primer GT15C.


```

XX Atopic dermatitis; ss; differential display; primer; PCR;
KW eosinophil; allergic disease; antiallergic; dermatological; GT15c.
XX Synthetic.
OS
XX WO200226962-A1.
XX PD 04-APR-2002.
XX
XX 21-SEP-2001; 2001WO-JP08247.
XX PR 26-SEP-2000; 2000JP-0293021.
XX
XX (GENO-) GENOX RES INC.
XX (NICE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
XX
XX Sugita Y, Hashida R, Ogawa K, Fujishima T, Nagasu T, Saito H;
XX WPI; 2002-330097/36.
XX
XX Examining allergic diseases by differential display of genes showing
XX different expression particularly increase in remission stage in
XX eosinophils in patients -
XX
XX Example 1; Page 55; 74pp; Japanese.
XX
XX This invention relates to gene sequences that are differentially
XX expressed in eosinophils from patients with atopic dermatitis in the
XX increment stage as compared with those in the remission stage. These
XX sequences are used in a novel method for examining allergic diseases
XX comprising determining the expression levels of these genes and
XX comparing the expression level with that in the eosinophils of a
XX healthy individual. The method of the invention may have antiallergic
XX or dermatological activities. The method can be used to diagnose
XX allergic diseases particularly atopic dermatitis, and may also
XX be used to screen candidate compounds for remedies. The method of the
XX invention can be performed in high throughput, at low cost. The
XX present sequence represents the G15c PCR primer used to amplify
XX the differentially amplified atopic dermatitis related cDNA sequences
XX of the invention.
XX
XX Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 other;
XX
XX Query Match 1.4%; Score 15; DB 1; Length 17;
XX Best Local Similarity 100.0%; Pred. No. 4e+02;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1084 AAAAAAAAAAAAAA 1098
XX | | | | | | | | | |
XX Db 16 AAAAAAAAAAAAAA 2
XX
XX RESULT 826
XX ABK49758/c
XX ID ABK49758 standard; DNA; 17 BP.
XX AC
XX AC ABK49758;
XX
XX DT 15-JUL-2002 (first entry)
XX
XX DE Human atopic dermatitis cDNA related PCR primer GT15g.
XX
XX KW Atopic dermatitis; ss; differential display; primer; PCR;
XX KW eosinophil; allergic disease; antiallergic; dermatological; GT15g.
XX
XX OS Synthetic.
XX
XX WO200226962-A1.
XX
XX PD 04-APR-2002.
XX
XX 21-SEP-2001; 2001WO-JP08247.
XX
XX PR 26-SEP-2000; 2000JP-0293021.
XX
XX (GENO-) GENOX RES INC.
XX (NICE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
XX
XX Sugita Y, Hashida R, Ogawa K, Fujishima T, Nagasu T, Saito H;
XX WPI; 2002-330097/36.
XX
XX Examining allergic diseases by differential display of genes showing
XX different expression particularly increase in remission stage in
XX eosinophils in patients -
XX
XX Example 1; Page 55; 74pp; Japanese.
XX
XX This invention relates to gene sequences that are differentially
XX expressed in eosinophils from patients with atopic dermatitis in the
XX increment stage as compared with those in the remission stage. These
XX sequences are used in a novel method for examining allergic diseases
XX comprising determining the expression levels of these genes and
XX comparing the expression level with that in the eosinophils of a
XX healthy individual. The method of the invention may have antiallergic
XX or dermatological activities. The method can be used to diagnose
XX allergic diseases particularly atopic dermatitis, and may also
XX be used to screen candidate compounds for remedies. The method of the
XX invention can be performed in high throughput, at low cost. The
XX present sequence represents the G15c PCR primer used to amplify
XX the differentially amplified atopic dermatitis related cDNA sequences
XX of the invention.
XX
XX Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 other;
XX
XX Query Match 1.4%; Score 15; DB 1; Length 17;
XX Best Local Similarity 100.0%; Pred. No. 4e+02;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1084 AAAAAAAAAAAAAA 1098
XX | | | | | | | | | |
XX Db 16 AAAAAAAAAAAAAA 2
XX
XX RESULT 826
XX ABK49758/c
XX ID ABK49758 standard; DNA; 17 BP.
XX AC
XX AC ABK49758;
XX
XX DT 15-JUL-2002 (first entry)
XX
XX DE Human atopic dermatitis cDNA related PCR primer GT15g.
XX
XX KW Atopic dermatitis; ss; differential display; primer; PCR;
XX KW eosinophil; allergic disease; antiallergic; dermatological; GT15g.
XX
XX OS Synthetic.
XX
XX WO200226962-A1.
XX
XX PD 04-APR-2002.
XX
XX 21-SEP-2001; 2001WO-JP08247.

```

```

XX 26-SEP-2000; 2000JP-0293021.
XX (GENO-) GENOX RES INC.
XX (NICE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
XX
XX Sugita Y, Hashida R, Ogawa K, Fujishima T, Nagasu T, Saito H;
XX WPI; 2002-330097/36.
XX
XX Examining allergic diseases by differential display of genes showing
XX different expression particularly increase in remission stage in
XX eosinophils in patients -
XX
XX Example 1; Page 55; 74pp; Japanese.
XX
XX This invention relates to gene sequences that are differentially
XX expressed in eosinophils from patients with atopic dermatitis in the
XX increment stage as compared with those in the remission stage. These
XX sequences are used in a novel method for examining allergic diseases
XX comprising determining the expression levels of these genes and
XX comparing the expression level with that in the eosinophils of a
XX healthy individual. The method of the invention may have antiallergic
XX or dermatological activities. The method can be used to diagnose
XX allergic diseases particularly atopic dermatitis, and may also
XX be used to screen candidate compounds for remedies. The method of the
XX invention can be performed in high throughput, at low cost. The
XX present sequence represents the G15g PCR primer used to amplify
XX the differentially amplified atopic dermatitis related cDNA sequences
XX of the invention.
XX
XX Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 other;
XX
XX Query Match 1.4%; Score 15; DB 1; Length 17;
XX Best Local Similarity 100.0%; Pred. No. 4e+02;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1084 AAAAAAAAAAAAAA 1098
XX | | | | | | | | | |
XX Db 16 AAAAAAAAAAAAAA 2
XX
XX RESULT 827
XX ABX79793/c
XX ID ABX79793 standard; cDNA; 17 BP.
XX AC
XX AC ABX79793;
XX
XX DT 17-APR-2003 (first entry)
XX
XX DE EST polymorphic DNA repeat polynucleotide #118.
XX
XX KW EST; expressed sequence tag; ss; polymorphic repeat; tandem repeat;
XX KW polymorphic marker prediction of ubiquitous simple sequences; POMPOUS;
XX KW Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;
XX KW Haw River syndrome; Huntington's disease; fragile-X syndrome;
XX KW Fredreich's ataxia; myotonic dystrophy; hyperandrogenaemia;
XX KW spinal atrophy; bulbar atrophy; spinocerebellar ataxia.
XX
XX OS Homo sapiens.
XX
XX PN US6472154-B1.
XX
XX PD 29-OCT-2002.
XX
XX PF 31-DEC-1999; 99US-0475947.
XX
XX PR 31-DEC-1999; 99US-0475947.
XX
XX (TEXA ) UNIV TEXAS SYSTEM.
XX
XX Garner HR, Wren JD, Minna JD, Fondon JW;
XX

```

DR WPI; 2003-208818/20.

XX Identifying a candidate polymorphic repeat within a coding sequence,
PT for understanding or treating genetic disease, comprises detecting
PT tandem repeats in a target coding sequence and scoring the repeats for
PT polymorphic probability -

XX Examples; Column 483; 588pp; English.

XX The invention discloses a method for identifying a candidate polymorphic
CC repeat within a coding sequence (expressed sequence tag, EST), which
CC comprises detecting tandem repeats in a target coding sequence, scoring
CC the repeats for polymorphic probability and generating a dataset
CC correlating the repeats with polymorphic probability to identify a
CC candidate polymorphic repeat. The computational methods (polymorphic
CC marker prediction of ubiquitous simple sequences, POMPOUS, and Rep-X) are
CC useful for identifying and detecting candidate polymorphic repeats in
CC human genes, which can be used to understand, treat or eliminate genetic
CC diseases, predispositions or adverse drug-treatment reactions. Examples
CC of diseases linked to nucleotide repeats are Machado-Joseph, Haw River
CC syndrome, Huntington's disease, fragile-X syndrome, Friedreich's ataxia,
CC myotonic dystrophy, hyperandrogenaemia, spinal and bulbar atrophy and
CC spinocerebellar ataxia. The sequences presented in ABX79676-ABX80022 are
CC the polymorphic repeats identified for a search of human ESTs.

XX Sequence 17 BP; 0 A; 2 C; 0 G; 15 T; 0 other;

Query Match 1.4%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1098
|||
Db 15 AAAAAAAAAAAAAA 1

RESULT 828

AAV54171/c
ID AAV54171 standard; cDNA; 18 BP.

AC AAV54171;

XX 21-DEC-1998 (first entry)

XX Nucleotide sequence PCR primer 8.

XX PCR; primer; amplification; apoptosis; antibody; inhibition; ss;
KW immunohistological staining.

XX Synthetic.

PN WO9839437-A1.

XX 11-SEP-1998.

XX 05-MAR-1998; 98WO-JP00905.

XX 05-MAR-1997; 97JP-0050302.

XX (KYOW) KYOWA HAKKO KOGYO KK.

XX Sakaki Y;

XX WPI; 1998-495844/42.

XX Novel apoptosis-related DNAs and proteins - for diagnosis,
PT preventing or treating diseases associated with apoptosis

XX Example 1; Page 49; 70pp; Japanese.

XX This is the nucleotide sequence of a PCR primer used in the method
CC of the invention, involving the use of novel apoptosis-related DNAs
CC and proteins. The inventions can be used as diagnostic reagents for

CC apoptosis e.g. (monoclonal) antibodies for the protein, as a reagent
CC in immunohistological staining, as apoptosis inhibitors. It can also
CC be used for treatment of apoptosis-related diseases.

XX Sequence 18 BP; 0 A; 0 C; 3 G; 15 T; 0 other;

Query Match 1.4%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1098
|||
Db 16 AAAAAAAAAAAAAA 2

RESULT 829

AAV54172/c
ID AAV54172 standard; cDNA; 18 BP.

XX AAV54172;

XX 21-DEC-1998 (first entry)

XX Nucleotide sequence PCR primer 9.

XX PCR; primer; amplification; apoptosis; antibody; inhibition; ss;
KW immunohistological staining.

XX Synthetic.

PN WO9839437-A1.

XX 11-SEP-1998.

XX 05-MAR-1998; 98WO-JP00905.

XX 05-MAR-1997; 97JP-0050302.

XX (KYOW) KYOWA HAKKO KOGYO KK.

XX Sakaki Y;

XX WPI; 1998-495844/42.

XX Novel apoptosis-related DNAs and proteins - for diagnosis,
PT preventing or treating diseases associated with apoptosis

XX Example 1; Page 50; 70pp; Japanese.

XX This is the nucleotide sequence of a PCR primer used in the method
CC of the invention, involving the use of novel apoptosis-related DNAs
CC and proteins. The inventions can be used as diagnostic reagents for
CC apoptosis e.g. (monoclonal) antibodies for the protein, as a reagent
CC in immunohistological staining, as apoptosis inhibitors. It can also
CC be used for treatment of apoptosis-related diseases.

XX Sequence 18 BP; 0 A; 1 C; 2 G; 15 T; 0 other;

Query Match 1.4%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1098
|||
Db 16 AAAAAAAAAAAAAA 2

RESULT 830

AAV54174/c
ID AAV54174 standard; cDNA; 18 BP.

XX AAV54174;

XX

DT 21-DEC-1998 (first entry)
 XX Nucleotide sequence PCR primer 11.
 DE PCR; primer; amplification; apoptosis; antibody; inhibition; ss;
 XX immunohistological staining.
 KW Synthetic.
 XX
 OS WO9839437-A1.
 XX
 PN 11-SEP-1998.
 PD
 XX 05-MAR-1998; 98WO-JP00905.
 XX
 PF 05-MAR-1997; 97JP-0050302.
 XX
 PR (KYOW) KYOWA HAKKO KOGYO KK.
 XX
 PI Sakaki Y;
 XX
 DR WPI; 1998-495844/42.
 XX
 CC Novel apoptosis-related DNAs and proteins - for diagnosis,
 CC preventing or treating diseases associated with apoptosis
 CC
 CC Example 1; Page 50; 70pp; Japanese.
 CC
 CC This is the nucleotide sequence of a PCR primer used in the method
 CC of the invention, involving the use of novel apoptosis-related DNAs
 CC and proteins. The inventions can be used as diagnostic reagents for
 CC apoptosis e.g. (monoclonal) antibodies for the protein, as a reagent
 CC in immunohistological staining, as apoptosis inhibitors. It can also
 CC be used for treatment of apoptosis-related diseases.
 CC
 CC Sequence 18 BP; 0 A; 1 C; 2 G; 15 T; 0 other;
 SQ
 Query Match 1.4%; Score 15; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 QY 1084 AAAAAAAAAAAAAA 1098
 DB ||||||||||||
 16 AAAAAAAAAAAAAA 2
 RESULT 831
 ID AAV54175/c
 XX
 AC AAV54175 standard; cDNA; 18 BP.
 XX
 XX AAV54175;
 XX
 XX 21-DEC-1998 (first entry)
 XX
 DE Nucleotide sequence PCR primer 12.
 XX
 XX PCR; primer; amplification; apoptosis; antibody; inhibition; ss;
 KW immunohistological staining.
 XX
 OS Synthetic.
 XX
 PN WO9839437-A1.
 XX
 PD 11-SEP-1998.
 XX
 PF 05-MAR-1998; 98WO-JP00905.
 XX
 PR 05-MAR-1997; 97JP-0050302.
 XX
 PA (KYOW) KYOWA HAKKO KOGYO KK.
 XX
 PI Sakaki Y;
 XX

DR WPI; 1998-495844/42.
 XX
 CC Novel apoptosis-related DNAs and proteins - for diagnosis,
 CC preventing or treating diseases associated with apoptosis
 CC
 CC Example 1; Page 51; 70pp; Japanese.
 CC
 CC This is the nucleotide sequence of a PCR primer used in the method
 CC of the invention, involving the use of novel apoptosis-related DNAs
 CC and proteins. The inventions can be used as diagnostic reagents for
 CC apoptosis e.g. (monoclonal) antibodies for the protein, as a reagent
 CC in immunohistological staining, as apoptosis inhibitors. It can also
 CC be used for treatment of apoptosis-related diseases.
 CC
 CC Sequence 18 BP; 0 A; 2 C; 1 G; 15 T; 0 other;
 SQ
 Query Match 1.4%; Score 15; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1084 AAAAAAAAAAAAAA 1098
 DB ||||||||||||
 16 AAAAAAAAAAAAAA 2
 RESULT 832
 ID AAV35391/c
 XX
 AC AAV35391 standard; DNA; 18 BP.
 XX
 XX AAV35391;
 XX
 DT 13-OCT-1998 (first entry)
 XX
 DE HIV-1 gag protein DNA primer #4.
 XX
 XX Hypervariable region; ENV protein; vaccinia virus; gag gene; retrovirus;
 KW vaccines; infection; protection; primer; ss.
 XX
 OS Synthetic.
 XX
 PN WO9822596-A1.
 XX
 PD 28-MAY-1998.
 XX
 PF 19-NOV-1997; 97WO-JP04216.
 XX
 PR 19-NOV-1996; 96JP-0323412.
 XX
 PA (NINA-) JAPAN NAT INST INFECTIOUS DISEASES.
 PA (JAPG) NIPPON ZEON KK.
 XX
 PI Kojima A, Kurata T, Yasuda A;
 XX
 DR WPI; 1998-312481/27.
 XX
 CC Recombinant vaccinia virus containing fusion H1B gag gene - for
 CC production in host cells of gag protein for use as vaccine
 CC
 CC Example 1; Page 64; 84pp; Japanese.
 CC
 CC AAV35388-V35414 are primers used in a method which results in a
 CC recombinant vaccinia virus comprising of a gag gene from a retrovirus
 CC such as HIV-1 or HIV-2, fused to a DNA fragment containing an epitope
 CC region (30-300 bases in length) of a retroviral gene other than the gag
 CC gene. The gag gene may be altered so as to produce a gag protein modified
 CC from the natural sequence by the addition, deletion or substitution of at
 CC least 1 amino acid residue. The fusion gene is inserted into a region of
 CC a vaccinia virus not essential to its propagation, to give a recombinant
 CC vaccinia virus vector which is used to transform a host cell (such as
 CC HeLa, Vero, VEF, rabbit kidney RK13 or human myeloma TK-143 cells). Upon
 CC culturing the host cell produces particulate structures containing the
 CC fusion gag protein. The recombinant vaccinia virus or the fusion gag
 CC protein particles may be used in the production of vaccines for

CC protecting against infection with retroviruses such as HIV.
 XX Sequence 18 BP; 1 A; 1 C; 1 G; 15 T; 0 other;
 SQ

Query Match 1.4%; Score 15; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1098
 |||||
 Db 18 AAAAAAAAAAAAAA 4

RESULT 833

AA58385
 ID AAA58385 standard; DNA; 18 BP.

XX
 AC AAA58385;

XX 01-NOV-2000 (first entry)

XX Polynucleotide # 1 used in a biomolecule detection system.

XX Nanocrystal; biomolecule detection; nonisotopic detection system; ss.
 XX Synthetic.

XX WO200028088-A1.

XX 18-MAY-2000.

XX 10-NOV-1999; 99WO-US26612.

XX 10-NOV-1998; 98US-0107828.

XX 09-NOV-1999; 99US-0437076.

XX (BIOC-) BIOCRYSTAL LTD.

XX Barbera-Guillem E, Nelson MB, Castro S;

XX WPI; 2000-376593/32.

XX Functionalized nanocrystal carrying polynucleotide, used for detecting target analyte, forms dendrimers with complementary nanocrystals to amplify the fluorescent signal -

XX Example 3; Page 68; 72pp; English.

XX The present invention relates to functionalised nanocrystals for use in nonisotopic detection systems for biomolecules e.g. nucleic acids, proteins, lipids or drugs. The nanocrystals have polynucleotide strands attached to their surfaces with one end of the polynucleotide extending outwardly from the nanocrystal. The present sequence is one such polynucleotide. These nanocrystals are used with a second series of nanocrystals, which have polynucleotides complementary to the first polynucleotides, so that the respective complementary strands hybridise to each other and form a dendrimer. This dendrimer produces a signal which can then be detected e.g. fluorescence. The present sequence is composed mainly of Adenine bases. This sequence may therefore be used with a polynucleotide composed mainly of Thymine bases (AAA58386).

XX Sequence 18 BP; 15 A; 0 C; 3 G; 0 T; 0 other;

Query Match 1.4%; Score 15; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1098
 |||||
 Db 4 AAAAAAAAAAAAAA 18

RESULT 834

AA58386/c

ID AAA58386 standard; DNA; 18 BP.

XX
 AC AAA58386;

XX 01-NOV-2000 (first entry)

XX Polynucleotide # 2 used in a biomolecule detection system.

XX Nanocrystal; biomolecule detection; nonisotopic detection system; ss.

XX Synthetic.

XX WO200028088-A1.

XX 18-MAY-2000.

XX 10-NOV-1999; 99WO-US26612.

XX 10-NOV-1998; 98US-0107828.

XX 09-NOV-1999; 99US-0437076.

XX (BIOC-) BIOCRYSTAL LTD.

XX Barbera-Guillem E, Nelson MB, Castro S;

XX WPI; 2000-376593/32.

XX Functionalized nanocrystal carrying polynucleotide, used for detecting target analyte, forms dendrimers with complementary nanocrystals to amplify the fluorescent signal -

XX Example 3; Page 69; 72pp; English.

XX The present invention relates to functionalised nanocrystals for use in nonisotopic detection systems for biomolecules e.g. nucleic acids, proteins, lipids or drugs. The nanocrystals have polynucleotide strands attached to their surfaces with one end of the polynucleotide extending outwardly from the nanocrystal. The present sequence is one such polynucleotide. These nanocrystals are used with a second series of nanocrystals, which have polynucleotides complementary to the first polynucleotides, so that the respective complementary strands hybridise to each other and form a dendrimer. This dendrimer produces a signal which can then be detected e.g. fluorescence. The present sequence is composed mainly of Thymine bases. This sequence may therefore be used with a polynucleotide composed mainly of Adenine bases (AAA58385).

XX Sequence 18 BP; 0 A; 0 C; 3 G; 15 T; 0 other;

Query Match 1.4%; Score 15; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1098
 |||||
 Db 18 AAAAAAAAAAAAAA 4

RESULT 835

AAZ90641/c

ID AAZ90641 standard; DNA; 18 BP.

XX
 AC AAZ90641;

XX 13-JUN-2000 (first entry)

XX Human adipose tissue gene amplifying primer #2.

XX Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;
 XX arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.
 XX Homo sapiens.

```
PN JP2000037190-A.
XX
PD 08-FEB-2000.
XX
PF 23-JUL-1998; 98JP-0225228.
XX
PR 23-JUL-1998; 98JP-0225228.
XX
PA (NISH ) JAPAN TOBACCO INC.
XX
DR WPI; 2000-306578/27.
XX
PT A physiologically active protein specifically derived from mammal
PT tissue -
XX
PS Example 2; Page 18; 50pp; Japanese.
XX
CC The invention relates to identification of genes and proteins of adipose
CC tissue relating to obesity, particularly complications of visceral
CC obesity including diabetes, hyperlipemia, hypertension,
CC arteriosclerosis, hyperuricemia and sleep apnea syndrome. The genes
CC (AAZ90631-633) and the proteins (AAZ90631-633) are used in the genetic
CC diagnosis, prevention and treatment of adipose tissue related diseases.
CC Sequences AAZ90640-51 represent PCR primers amplifying the human adipose
CC tissue genes.
XX
SQ Sequence 18 BP; 0 A; 0 C; 3 G; 15 T; 0 other;
Query Match 1.4%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred.No. 4.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1084 AAAAAAAAAAAAAA 1098
DB |||||
16 AAAAAAAAAAAAAA 2
RESULT 836
ID AAZ90642/c
XX AAZ90642 standard; DNA; 18 BP.
XX
AC AAZ90642;
XX
DT 13-JUN-2000 (first entry)
XX
DE Human adipose tissue gene amplifying primer #3.
XX
KW Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;
KW arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.
XX
OS Homo sapiens.
XX
WPI; 2000-306578/27.
XX
PT A physiologically active protein specifically derived from mammal
PT tissue -
XX
PS Example 2; Page 18; 50pp; Japanese.
XX
CC The invention relates to identification of genes and proteins of adipose
CC tissue relating to obesity, particularly complications of visceral
CC obesity including diabetes, hyperlipemia, hypertension,
CC arteriosclerosis, hyperuricemia and sleep apnea syndrome. The genes
CC (AAZ90631-633) and the proteins (AAZ90631-633) are used in the genetic
CC diagnosis, prevention and treatment of adipose tissue related diseases.
CC Sequences AAZ90640-51 represent PCR primers amplifying the human adipose
CC tissue genes.
XX
SQ Sequence 18 BP; 0 A; 1 C; 2 G; 15 T; 0 other;
Query Match 1.4%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred.No. 4.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1084 AAAAAAAAAAAAAA 1098
DB |||||
16 AAAAAAAAAAAAAA 2
RESULT 837
ID AAZ90650/c
XX AAZ90650 standard; DNA; 18 BP.
XX
AC AAZ90650;
XX
DT 13-JUN-2000 (first entry)
XX
DE Human adipose tissue gene amplifying primer #11.
XX
KW Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;
KW arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.
XX
OS Homo sapiens.
XX
WPI; 2000-306578/27.
XX
PT A physiologically active protein specifically derived from mammal
PT tissue -
XX
PS Example 2; Page 18; 50pp; Japanese.
XX
CC The invention relates to identification of genes and proteins of adipose
CC tissue relating to obesity, particularly complications of visceral
CC obesity including diabetes, hyperlipemia, hypertension,
CC arteriosclerosis, hyperuricemia and sleep apnea syndrome. The genes
CC (AAZ90631-633) and the proteins (AAZ90631-633) are used in the genetic
CC diagnosis, prevention and treatment of adipose tissue related diseases.
CC Sequences AAZ90640-51 represent PCR primers amplifying the human adipose
CC tissue genes.
XX
SQ Sequence 18 BP; 0 A; 1 C; 2 G; 15 T; 0 other;
Query Match 1.4%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred.No. 4.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1084 AAAAAAAAAAAAAA 1098
DB |||||
16 AAAAAAAAAAAAAA 2
RESULT 838
ID AAZ90651/c
XX AAZ90651 standard; DNA; 18 BP.
XX
AC AAZ90651;
XX
```


CC The methods can also be employed for diseases where allelic and genetic
 CC heterogeneity exist, such as breast cancer, neurofibromatosis, and
 CC hereditary non-polyposis colorectal cancer. Identification of functional
 CC alleles is necessary for identification of mutations which may be
 CC implicated in the disease. Sequences AAX32001-172 represent primers for
 CC determining the functional allele profiles of various genes. The
 CC primers are specific for genes such as MSH2 gene, MLH1 gene, BRCA1 gene,
 CC BRCA2 gene and BAP1 gene.

XX SQ Sequence 20 BP; 2 A; 2 C; 1 G; 15 T; 0 other;

Query Match 1.4%; Score 15; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 4.7e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1083 TAAAAAATAAAAAA 1097
 Db 15 TAAAAAATAAAAAA 1

RESULT 843
 AAC82908/c
 ID AAC82908 standard; DNA; 20 BP.

XX AC AAC82908;

XX DT 21-MAR-2001 (first entry)

XX DE Human beta-actin derived oligonucleotide #1.

XX KW Recognition system; screening; identification; pharmaceutical; toxin;
 KW plant protection agent; toxin; venom; carcinogen; venom; teratogen;
 KW herbicide; fungicide; pesticide; beta-actin; human; ss.

XX OS Homo sapiens.

XX FN DE19923966-Al.

XX PD 30-NOV-2000.

XX PF 25-MAY-1999; 99DE-1023966.

XX PR 25-MAY-1999; 99DE-1023966.

XX PA (AVET) AVENTIS RES & TECHNOLOGIES GMBH & CO KG.

XX PI Boekenkamp D, Hoppe H, Burgstaller P;

XX DR WPI; 2001-050938/07.

XX PT Recognition system, e.g. for identifying nucleic acids, comprises at
 PT least one recognition unit comprising a region with a defined structure
 PT adjacent to a region with a randomized structure -

XX PS Examples; Fig 1; 8pp; German.

XX CC This invention describes a novel recognition system comprising at least
 CC 1 recognition unit bound to a support, each recognition unit comprising a
 CC region A with a defined structure adjacent to a region B with a
 CC randomized structure. The recognition system is useful for screening,
 CC identifying, or characterizing at least 1 component of a sample,
 CC especially nucleic acids and/or proteins, and for screening for and/or
 CC identifying cellular or synthetic binding partners, preferably proteins,
 CC peptides, nucleic acids, chemical agents, preferably organic compounds,
 CC pharmaceuticals, plant protection agents, toxins, venoms, carcinogens,
 CC teratogens, herbicides, fungicides or pesticides.

XX SQ Sequence 20 BP; 2 A; 0 C; 3 G; 15 T; 0 other;

Query Match 1.4%; Score 15; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 4.7e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1082 TAAAAAATAAAAAA 1096
 Db 15 TAAAAAATAAAAAA 1

RESULT 844
 AAC82909/c
 ID AAC82909 standard; DNA; 20 BP.

XX AC AAC82909;

XX DT 21-MAR-2001 (first entry)

XX DE Human beta-actin derived oligonucleotide #2.

XX KW Recognition system; screening; identification; pharmaceutical; toxin;
 KW plant protection agent; toxin; venom; carcinogen; venom; teratogen;
 KW herbicide; fungicide; pesticide; beta-actin; human; ss.

XX OS Homo sapiens.

XX FN DE19923966-Al.

XX PD 30-NOV-2000.

XX PF 25-MAY-1999; 99DE-1023966.

XX PR 25-MAY-1999; 99DE-1023966.

XX PA (AVET) AVENTIS RES & TECHNOLOGIES GMBH & CO KG.

XX PI Boekenkamp D, Hoppe H, Burgstaller P;

XX DR WPI; 2001-050938/07.

XX PT Recognition system, e.g. for identifying nucleic acids, comprises at
 PT least one recognition unit comprising a region with a defined structure
 PT adjacent to a region with a randomized structure -

XX PS Examples; Fig 1; 8pp; German.

XX CC This invention describes a novel recognition system comprising at least
 CC 1 recognition unit bound to a support, each recognition unit comprising a
 CC region A with a defined structure adjacent to a region B with a
 CC randomized structure. The recognition system is useful for screening,
 CC identifying, or characterizing at least 1 component of a sample,
 CC especially nucleic acids and/or proteins, and for screening for and/or
 CC identifying cellular or synthetic binding partners, preferably proteins,
 CC peptides, nucleic acids, chemical agents, preferably organic compounds,
 CC pharmaceuticals, plant protection agents, toxins, venoms, carcinogens,
 CC teratogens, herbicides, fungicides or pesticides.

XX SQ Sequence 20 BP; 2 A; 0 C; 4 G; 14 T; 0 other;

Query Match 1.4%; Score 15; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 4.7e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1082 TAAAAAATAAAAAA 1096
 Db 15 TAAAAAATAAAAAA 1

RESULT 845
 AAC82910/c
 ID AAC82910 standard; DNA; 20 BP.

XX AC AAC82910;

XX DT 21-MAR-2001 (first entry)

XX DE Human beta-actin derived oligonucleotide #3.

Recognition system; screening; identification; pharmaceutical; toxin;
plant protection agent; toxin; venom; carcinogen; venom; teratogen;
herbicide; fungicide; pesticide; beta-actin; human; ss.
Homo sapiens.
DE19923966-A1.
30-NOV-2000.
25-MAY-1999; 99DE-1023966.
25-MAY-1999; 99DE-1023966.
(AVET) AVENTIS RES & TECHNOLOGIES GMBH & CO KG.
Boekenkamp D, Hoppe H, Bургstaller P;
WPI; 2001-050938/07.
Recognition system, e.g. for identifying nucleic acids, comprises at
least one recognition unit comprising a region with a defined structure
adjacent to a region with a randomized structure -
Examples; Fig 1; 8pp; German.
This invention describes a novel recognition system comprising at least
1 recognition unit bound to a support, each recognition unit comprising a
region A with a defined structure adjacent to a region B with a
randomized structure. The recognition system is useful for screening,
identifying, or characterizing at least 1 component of a sample,
especially nucleic acids and/or proteins, and for screening for and/or
identifying cellular or synthetic binding partners, preferably proteins,
peptides, nucleic acids, chemical agents, preferably organic compounds,
pharmaceuticals, plant protection agents, toxins, venoms, carcinogens,
teratogens, herbicides, fungicides or pesticides.
Sequence 20 BP; 3 A; 0 C; 3 G; 14 T; 0 other;
Query Match 1.4%; Score 15; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1082 TTAAAAAATAAAAAA 1096
DB 15 TTAAAAAATAAAAAA 1
RESULT 846
AAC82911/C
ID AAC82911 standard; DNA; 20 BP.
AC AAC82911;
AC AAC82911;
21-MAR-2001 (first entry)
Human beta-actin derived oligonucleotide #4.
Recognition system; screening; identification; pharmaceutical; toxin;
plant protection agent; toxin; venom; carcinogen; venom; teratogen;
herbicide; fungicide; pesticide; beta-actin; human; ss.
Homo sapiens.
DE19923966-A1.
30-NOV-2000.
25-MAY-1999; 99DE-1023966.
25-MAY-1999; 99DE-1023966.
(AVET) AVENTIS RES & TECHNOLOGIES GMBH & CO KG.

XX Boekenkamp D, Hoppe H, Bургstaller P;
XX WPI; 2001-050938/07.
XX Recognition system, e.g. for identifying nucleic acids, comprises at
XX least one recognition unit comprising a region with a defined structure
XX adjacent to a region with a randomized structure -
XX Examples; Fig 1; 8pp; German.
XX This invention describes a novel recognition system comprising at least
XX 1 recognition unit bound to a support, each recognition unit comprising a
XX region A with a defined structure adjacent to a region B with a
XX randomized structure. The recognition system is useful for screening,
XX identifying, or characterizing at least 1 component of a sample,
XX especially nucleic acids and/or proteins, and for screening for and/or
XX identifying cellular or synthetic binding partners, preferably proteins,
XX peptides, nucleic acids, chemical agents, preferably organic compounds,
XX pharmaceuticals, plant protection agents, toxins, venoms, carcinogens,
XX teratogens, herbicides, fungicides or pesticides.
XX Sequence 20 BP; 2 A; 1 C; 3 G; 14 T; 0 other;
Query Match 1.4%; Score 15; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1082 TTAAAAAATAAAAAA 1096
DB 15 TTAAAAAATAAAAAA 1
RESULT 847
AAC82914/C
ID AAC82914 standard; DNA; 20 BP.
AC AAC82914;
AC AAC82914;
21-MAR-2001 (first entry)
Human beta-actin derived oligonucleotide #7.
Recognition system; screening; identification; pharmaceutical; toxin;
plant protection agent; toxin; venom; carcinogen; venom; teratogen;
herbicide; fungicide; pesticide; beta-actin; human; ss.
Homo sapiens.
DE19923966-A1.
30-NOV-2000.
25-MAY-1999; 99DE-1023966.
25-MAY-1999; 99DE-1023966.
(AVET) AVENTIS RES & TECHNOLOGIES GMBH & CO KG.
Boekenkamp D, Hoppe H, Bургstaller P;
WPI; 2001-050938/07.
XX Recognition system, e.g. for identifying nucleic acids, comprises at
XX least one recognition unit comprising a region with a defined structure
XX adjacent to a region with a randomized structure -
XX Examples; Fig 1; 8pp; German.
XX This invention describes a novel recognition system comprising at least
XX 1 recognition unit bound to a support, each recognition unit comprising a
XX region A with a defined structure adjacent to a region B with a
XX randomized structure. The recognition system is useful for screening,
XX identifying, or characterizing at least 1 component of a sample,
XX especially nucleic acids and/or proteins, and for screening for and/or
XX identifying cellular or synthetic binding partners, preferably proteins,
XX peptides, nucleic acids, chemical agents, preferably organic compounds,
XX pharmaceuticals, plant protection agents, toxins, venoms, carcinogens,
XX teratogens, herbicides, fungicides or pesticides.

CC identifying, or characterizing at least 1 component of a sample,
CC especially nucleic acids and/or proteins, and for screening for and/or
CC identifying cellular or synthetic binding partners, preferably proteins,
CC peptides, nucleic acids, chemical agents, preferably organic compounds,
CC pharmaceuticals, plant protection agents, toxins, venoms, carcinogens,
CC teratogens, herbicides, fungicides or pesticides.
XX Sequence 20 BP; 2 A; 1 C; 2 G; 15 T; 0 other;
SQ Query Match 1.4%; Score 15; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1082 TTAAAAA 1096
DB 15 TTAAAAA 1

RESULT 848
AAC82917/c
ID AAC82917 standard; DNA; 20 BP.
XX AC AAC82917;
XX DT 21-MAR-2001 (first entry)
XX DE Human S-9 derived oligonucleotide #1.
XX KW Recognition system; screening; identification; pharmaceutical; toxin;
XX plant protection agent; toxin; venom; carcinogen; venom; teratogen;
XX herbicide; fungicide; pesticide; beta-actin; human; ss.
XX OS Homo sapiens.
XX PN DE19923966-A1.
XX PD 30-NOV-2000.
XX PF 25-MAY-1999; 99DE-1023966.
XX PR 25-MAY-1999; 99DE-1023966.
XX PA (AVET) AVENTIS RES & TECHNOLOGIES GMBH & CO KG.
XX PI Boekenkamp D, Hoppe H, Burgstaller P;
XX WPI; 2001-050938/07.
XX PT Recognition system, e.g. for identifying nucleic acids, comprises at
XX least one recognition unit comprising a region with a defined structure
XX adjacent to a region with a randomized structure -
XX Examples; Fig 1; 8pp; German.
XX CC This invention describes a novel recognition system comprising at least
XX 1 recognition unit bound to a support, each recognition unit comprising a
XX region A with a defined structure adjacent to a region B with a
XX randomized structure. The recognition system is useful for screening,
XX identifying, or characterizing at least 1 component of a sample,
XX especially nucleic acids and/or proteins, and for screening for and/or
XX identifying cellular or synthetic binding partners, preferably proteins,
XX peptides, nucleic acids, chemical agents, preferably organic compounds,
XX pharmaceuticals, plant protection agents, toxins, venoms, carcinogens,
XX teratogens, herbicides, fungicides or pesticides.
XX SQ Sequence 20 BP; 3 A; 2 C; 2 G; 13 T; 0 other;
Query Match 1.4%; Score 15; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1082 TTAAAAA 1096
DB 15 TTAAAAA 1

RESULT 848
AAC82917/c
ID AAC82917 standard; DNA; 20 BP.
XX AC AAC82917;
XX DT 21-MAR-2001 (first entry)
XX DE Human S-9 derived oligonucleotide #1.
XX KW Recognition system; screening; identification; pharmaceutical; toxin;
XX plant protection agent; toxin; venom; carcinogen; venom; teratogen;
XX herbicide; fungicide; pesticide; beta-actin; human; ss.
XX OS Homo sapiens.
XX PN DE19923966-A1.
XX PD 30-NOV-2000.
XX PF 25-MAY-1999; 99DE-1023966.
XX PR 25-MAY-1999; 99DE-1023966.
XX PA (AVET) AVENTIS RES & TECHNOLOGIES GMBH & CO KG.
XX PI Boekenkamp D, Hoppe H, Burgstaller P;
XX WPI; 2001-050938/07.
XX PT Recognition system, e.g. for identifying nucleic acids, comprises at
XX least one recognition unit comprising a region with a defined structure
XX adjacent to a region with a randomized structure -
XX Examples; Fig 1; 8pp; German.
XX CC This invention describes a novel recognition system comprising at least
XX 1 recognition unit bound to a support, each recognition unit comprising a
XX region A with a defined structure adjacent to a region B with a
XX randomized structure. The recognition system is useful for screening,
XX identifying, or characterizing at least 1 component of a sample,
XX especially nucleic acids and/or proteins, and for screening for and/or
XX identifying cellular or synthetic binding partners, preferably proteins,
XX peptides, nucleic acids, chemical agents, preferably organic compounds,
XX pharmaceuticals, plant protection agents, toxins, venoms, carcinogens,
XX teratogens, herbicides, fungicides or pesticides.
XX SQ Sequence 20 BP; 3 A; 2 C; 2 G; 13 T; 0 other;
Query Match 1.4%; Score 15; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1082 TTAAAAA 1096
DB 15 TTAAAAA 1

RESULT 850
AAC82920/c
ID AAC82920 standard; DNA; 20 BP.
XX AC AAC82920;
XX DT 21-MAR-2001 (first entry)
XX DE Human S-9 derived oligonucleotide #4.
XX KW Recognition system; screening; identification; pharmaceutical; toxin;
XX plant protection agent; toxin; venom; carcinogen; venom; teratogen;
XX herbicide; fungicide; pesticide; beta-actin; human; ss.

DB 15 TTAAAAA 1

RESULT 849
AAC82919/c
ID AAC82919 standard; DNA; 20 BP.
XX AC AAC82919;
XX DT 21-MAR-2001 (first entry)
XX DE Human S-9 derived oligonucleotide #3.
XX KW Recognition system; screening; identification; pharmaceutical; toxin;
XX plant protection agent; toxin; venom; carcinogen; venom; teratogen;
XX herbicide; fungicide; pesticide; beta-actin; human; ss.
XX OS Homo sapiens.
XX PN DE19923966-A1.
XX PD 30-NOV-2000.
XX PF 25-MAY-1999; 99DE-1023966.
XX PR 25-MAY-1999; 99DE-1023966.
XX PA (AVET) AVENTIS RES & TECHNOLOGIES GMBH & CO KG.
XX PI Boekenkamp D, Hoppe H, Burgstaller P;
XX WPI; 2001-050938/07.
XX PT Recognition system, e.g. for identifying nucleic acids, comprises at
XX least one recognition unit comprising a region with a defined structure
XX adjacent to a region with a randomized structure -
XX Examples; Fig 1; 8pp; German.
XX CC This invention describes a novel recognition system comprising at least
XX 1 recognition unit bound to a support, each recognition unit comprising a
XX region A with a defined structure adjacent to a region B with a
XX randomized structure. The recognition system is useful for screening,
XX identifying, or characterizing at least 1 component of a sample,
XX especially nucleic acids and/or proteins, and for screening for and/or
XX identifying cellular or synthetic binding partners, preferably proteins,
XX peptides, nucleic acids, chemical agents, preferably organic compounds,
XX pharmaceuticals, plant protection agents, toxins, venoms, carcinogens,
XX teratogens, herbicides, fungicides or pesticides.
XX SQ Sequence 20 BP; 4 A; 1 C; 2 G; 13 T; 0 other;
Query Match 1.4%; Score 15; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1082 TTAAAAA 1096
DB 15 TTAAAAA 1

RESULT 850
AAC82920/c
ID AAC82920 standard; DNA; 20 BP.
XX AC AAC82920;
XX DT 21-MAR-2001 (first entry)
XX DE Human S-9 derived oligonucleotide #4.
XX KW Recognition system; screening; identification; pharmaceutical; toxin;
XX plant protection agent; toxin; venom; carcinogen; venom; teratogen;
XX herbicide; fungicide; pesticide; beta-actin; human; ss.

KW herbicide; fungicide; pesticide; beta-actin; human; ss.
 XX Homo sapiens.
 XX DE19923966-A1.
 XX 30-NOV-2000.
 XX 25-MAY-1999; 99DE-1023966.
 XX 25-MAY-1999; 99DE-1023966.
 XX (AVET) AVENTIS RES & TECHNOLOGIES GMBH & CO KG.
 XX Boekenkamp D, Hoppe H, Burgstaller P;
 XX WPI; 2001-050938/07.
 XX Recognition system, e.g. for identifying nucleic acids, comprises at
 PT least one recognition unit comprising a region with a defined structure
 PT adjacent to a region with a randomized structure -
 XX Examples; Fig 1; 8pp; German.
 XX This invention describes a novel recognition system comprising at least
 CC 1 recognition unit bound to a support, each recognition unit comprising a
 CC region A with a defined structure adjacent to a region B with a
 CC randomized structure. The recognition system is useful for screening,
 CC identifying, or characterizing at least 1 component of a sample,
 CC especially nucleic acids and/or proteins, and for screening for and/or
 CC identifying cellular or synthetic binding partners, preferably proteins,
 CC peptides, nucleic acids, chemical agents, preferably organic compounds,
 CC pharmaceuticals, plant protection agents, toxins, venoms, carcinogens,
 CC teratogens, herbicides, fungicides or pesticides.
 XX Sequence 20 BP; 3 A; 1 C; 3 G; 13 T; 0 other;
 XX Query Match 1.4%; Score 15; DB 1; Length 20;
 XX Best Local Similarity 100.0%; Pred. No. 4.7e+02;
 XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1082 TTAAAAAATAAAAA 1096
 DB 15 TTAAAAAATAAAAA 1
 RESULT 851
 AAC82921/c
 ID AAC82921 standard; DNA; 20 BP.
 XX AC AAC82921;
 XX 21-MAR-2001 (first entry)
 XX Human S-9 derived oligonucleotide #5.
 XX Recognition system; screening; identification; pharmaceutical; toxin;
 KW plant protection agent; toxin; venom; carcinogen; venom; teratogen;
 KW herbicide; fungicide; pesticide; beta-actin; human; ss.
 XX Homo sapiens.
 XX DE19923966-A1.
 XX 30-NOV-2000.
 XX 25-MAY-1999; 99DE-1023966.
 XX 25-MAY-1999; 99DE-1023966.
 XX (AVET) AVENTIS RES & TECHNOLOGIES GMBH & CO KG.
 XX Boekenkamp D, Hoppe H, Burgstaller P;
 XX WPI; 2001-050938/07.
 XX Recognition system, e.g. for identifying nucleic acids, comprises at
 PT least one recognition unit comprising a region with a defined structure
 PT adjacent to a region with a randomized structure -
 XX Examples; Fig 1; 8pp; German.
 XX This invention describes a novel recognition system comprising at least
 CC 1 recognition unit bound to a support, each recognition unit comprising a
 CC region A with a defined structure adjacent to a region B with a
 CC randomized structure. The recognition system is useful for screening,
 CC identifying, or characterizing at least 1 component of a sample,
 CC especially nucleic acids and/or proteins, and for screening for and/or
 CC identifying cellular or synthetic binding partners, preferably proteins,
 CC peptides, nucleic acids, chemical agents, preferably organic compounds,
 CC pharmaceuticals, plant protection agents, toxins, venoms, carcinogens,
 CC teratogens, herbicides, fungicides or pesticides.
 XX Sequence 20 BP; 3 A; 1 C; 3 G; 13 T; 0 other;
 XX Query Match 1.4%; Score 15; DB 1; Length 20;
 XX Best Local Similarity 100.0%; Pred. No. 4.7e+02;
 XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1082 TTAAAAAATAAAAA 1096
 DB 15 TTAAAAAATAAAAA 1
 RESULT 851
 AAC82921/c
 ID AAC82921 standard; DNA; 20 BP.
 XX AC AAC82921;
 XX 21-MAR-2001 (first entry)
 XX Human S-9 derived oligonucleotide #5.
 XX Recognition system; screening; identification; pharmaceutical; toxin;
 KW plant protection agent; toxin; venom; carcinogen; venom; teratogen;
 KW herbicide; fungicide; pesticide; beta-actin; human; ss.
 XX Homo sapiens.
 XX DE19923966-A1.
 XX 30-NOV-2000.
 XX 25-MAY-1999; 99DE-1023966.
 XX 25-MAY-1999; 99DE-1023966.
 XX (AVET) AVENTIS RES & TECHNOLOGIES GMBH & CO KG.
 XX Boekenkamp D, Hoppe H, Burgstaller P;
 XX WPI; 2001-050938/07.
 XX Recognition system, e.g. for identifying nucleic acids, comprises at
 PT least one recognition unit comprising a region with a defined structure
 PT adjacent to a region with a randomized structure -
 XX Examples; Fig 1; 8pp; German.
 XX This invention describes a novel recognition system comprising at least
 CC 1 recognition unit bound to a support, each recognition unit comprising a
 CC region A with a defined structure adjacent to a region B with a
 CC randomized structure. The recognition system is useful for screening,
 CC identifying, or characterizing at least 1 component of a sample,
 CC especially nucleic acids and/or proteins, and for screening for and/or
 CC identifying cellular or synthetic binding partners, preferably proteins,
 CC peptides, nucleic acids, chemical agents, preferably organic compounds,
 CC pharmaceuticals, plant protection agents, toxins, venoms, carcinogens,
 CC teratogens, herbicides, fungicides or pesticides.

XX WPI; 2001-050938/07.
 XX Recognition system, e.g. for identifying nucleic acids, comprises at
 PT least one recognition unit comprising a region with a defined structure
 PT adjacent to a region with a randomized structure -
 XX Examples; Fig 1; 8pp; German.
 XX This invention describes a novel recognition system comprising at least
 CC 1 recognition unit bound to a support, each recognition unit comprising a
 CC region A with a defined structure adjacent to a region B with a
 CC randomized structure. The recognition system is useful for screening,
 CC identifying, or characterizing at least 1 component of a sample,
 CC especially nucleic acids and/or proteins, and for screening for and/or
 CC identifying cellular or synthetic binding partners, preferably proteins,
 CC peptides, nucleic acids, chemical agents, preferably organic compounds,
 CC pharmaceuticals, plant protection agents, toxins, venoms, carcinogens,
 CC teratogens, herbicides, fungicides or pesticides.
 XX Sequence 20 BP; 2 A; 2 C; 3 G; 13 T; 0 other;
 XX Query Match 1.4%; Score 15; DB 1; Length 20;
 XX Best Local Similarity 100.0%; Pred. No. 4.7e+02;
 XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1082 TTAAAAAATAAAAA 1096
 DB 15 TTAAAAAATAAAAA 1
 RESULT 852
 AAC82922/c
 ID AAC82922 standard; DNA; 20 BP.
 XX AC AAC82922;
 XX 21-MAR-2001 (first entry)
 XX Human S-9 derived oligonucleotide #6.
 XX Recognition system; screening; identification; pharmaceutical; toxin;
 KW plant protection agent; toxin; venom; carcinogen; venom; teratogen;
 KW herbicide; fungicide; pesticide; beta-actin; human; ss.
 XX Homo sapiens.
 XX DE19923966-A1.
 XX 30-NOV-2000.
 XX 25-MAY-1999; 99DE-1023966.
 XX 25-MAY-1999; 99DE-1023966.
 XX (AVET) AVENTIS RES & TECHNOLOGIES GMBH & CO KG.
 XX Boekenkamp D, Hoppe H, Burgstaller P;
 XX WPI; 2001-050938/07.
 XX Recognition system, e.g. for identifying nucleic acids, comprises at
 PT least one recognition unit comprising a region with a defined structure
 PT adjacent to a region with a randomized structure -
 XX Examples; Fig 1; 8pp; German.
 XX This invention describes a novel recognition system comprising at least
 CC 1 recognition unit bound to a support, each recognition unit comprising a
 CC region A with a defined structure adjacent to a region B with a
 CC randomized structure. The recognition system is useful for screening,
 CC identifying, or characterizing at least 1 component of a sample,
 CC especially nucleic acids and/or proteins, and for screening for and/or
 CC identifying cellular or synthetic binding partners, preferably proteins,
 CC peptides, nucleic acids, chemical agents, preferably organic compounds,
 CC pharmaceuticals, plant protection agents, toxins, venoms, carcinogens,
 CC teratogens, herbicides, fungicides or pesticides.

CC identifying cellular or synthetic binding partners, preferably proteins,
 CC peptides, nucleic acids, chemical agents, preferably organic compounds,
 CC pharmaceuticals, plant protection agents, toxins, venoms, carcinogens,
 CC teratogens, herbicides, fungicides or pesticides.
 XX

SQ Sequence 20 BP; 2 A; 3 C; 2 G; 13 T; 0 other;
 Query Match 1.4%; Score 15; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 4.7e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1082 TTTAAAAA 1096
 DB 15 TTTAAAAA

RESULT 853
 AAF87713/C
 ID AAF87713 standard; DNA; 20 BP.

XX AAF87713;
 DT 06-JUL-2001 (first entry)
 DE Human glutathione S-transferase pi promoter (GSTP1) PCR primer N-F1.
 KW Human; glutathione S-transferase pi; GSTP1; CpG island; diagnosis;
 KW hepatic cell proliferative disorder; liver cancer; anticancer;
 KW tumorigenesis; detection; PCR primer; ss.
 XX Homo sapiens.

OS WO200126536-A2.
 PN 19-APR-2001.
 PD 12-OCT-2000; 2000WO-US28427.
 PF 13-OCT-1999; 99US-0159168.

XX (UJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
 XX Nelson WG, Lin X, Tchou JC, Bakker J;
 XX WPI; 2001-290647/30.

XX Detecting hepatic cell proliferative disorder useful for detecting
 PT hepatocellular carcinoma comprises detecting a methylated
 FT CpG-containing glutathione-S-transferase nucleic acid -
 XX Claim 83; Page 42; 64pp; English.

CC The present invention describes a method for detecting hepatic cell
 CC proliferative disorders. The method comprises detecting a methylated
 CC CpG-containing glutathione-S-transferase (GST) nucleic acid (I) in a
 CC hepatic specimen or a biological fluid, where a methylated GST nucleic
 CC acid is indicative of a hepatic cell proliferative disorder. The method
 CC can be used to diagnose hepatocellular carcinoma, and to monitor
 CC progress of its treatment. Increasing the level of GST is useful in the
 CC treatment of liver cancer, in humans or animals. The method can detect
 CC the early stages of tumorigenesis in liver cells simply. The present
 CC sequence represents a PCR primer which is used in the amplification
 CC of the human glutathione S-transferase pi gene (GSTP1) promoter in an
 CC example from the present invention for mapping somatic GSTP1 CpG island
 CC DNA hypermethylation changes by genomic sequencing after bisulfite
 CC treatment.

SQ Sequence 20 BP; 4 A; 0 C; 2 G; 14 T; 0 other;
 Query Match 1.4%; Score 15; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 4.7e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1082 TTTAAAAA 1096
 DB 19 TTTAAAAA

RESULT 854
 AAD35095/C
 ID AAD35095 standard; DNA; 20 BP.

XX AAD35095;
 DT 25-JUL-2002 (first entry)
 DE HT15-C downstream PCR primer used for identification of genes.

XX Mouse; X-chromosome; germ cell less gene; gcl gene; gene diagnosis;
 KW sex discrimination; infertility treatment; chromosomal manipulation;
 KW sperm separation; gene therapy; PCR; primer; ss.
 XX Unidentified.

XX EF1195382-A2.
 PN 10-APR-2002.
 PD 02-OCT-2001; 2001BP-0123259.
 PF 03-OCT-2000; 2000JP-0303994.

XX (LIVE-) LIVESTOCK IMPROVEMENT ASSOC JAPAN INC.
 XX (UYGU-) UNIV GUNMA.
 XX Aizawa A, Kawakami A, Kondo T;
 XX WPI; 2002-354153/39.

XX New X-chromosome gene expressed in haploid cells of the testis, useful
 PT for gene diagnosis, discrimination of sex, separation of sperm,
 PT infertility treatment and chromosomal manipulation -
 XX Example 1; Page 4; 28pp; English.

XX The present invention relates to genes located on the X-chromosome of
 CC mammals. These genes are specifically expressed in haploid cells of the
 CC testis and encode amino acid sequences having homology with the amino
 CC acid sequence encoded by drosophila germ cell less (gcl) gene. Sequences
 CC of the invention are used for gene diagnosis, discrimination of sex,
 CC separation of sperm, infertility treatment and chromosomal manipulation,
 CC especially in livestock. They are also used in gene therapy. The present
 CC DNA sequence is a PCR primer which is used for the identification of
 CC genes by differential display method.

XX Sequence 20 BP; 2 A; 2 C; 1 G; 15 T; 0 other;
 SQ Query Match 1.4%; Score 15; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 4.7e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAA 1098
 DB 19 AAAAAA

RESULT 855
 ABL57070
 ID ABL57070 standard; DNA; 20 BP.

XX ABL57070;
 DT 22-JUL-2002 (first entry)
 XX Molecular beacon target sequence.

```
KW Molecular beacon; fluorophore; nanoparticle; nucleic acid detection;
KW ss.
XX Synthetic.
XX Key Location/Qualifiers
FH misc_binding 1..20
FT /*tag= a
FT /bound moiety= "Molecular beacon"
FT /note= "forms double-stranded region with bases
FT 1-20 of sequence in ABL57069"
XX
XX PN WO200218951-A2.
XX PD 07-MAR-2002.
XX PF 29-AUG-2001; 2001WO-US41941.
XX PR 29-AUG-2000; 2000US-228728P.
XX PR 30-MAR-2001; 2001US-280350P.
XX PA (UYRQ ) UNIV ROCKEFELLER.
XX PI Dubertret B, Calame M, Libchaber A;
XX WPI; 2002-401727/43.
XX
XX Sensitively detecting proximity changes in a system that utilizes an
XX interacting fluorophore and quencher, for high sensitivity
XX applications, involves utilizing a metal surface as quencher -
XX
XX Example 2; Page 26; 62pp; English.
XX
XX The present sequence is that of a perfectly matched target
XX sequence for a molecular beacon comprising an oligonucleotide probe
XX (see ABL57069) covalently attached at the 3' end to fluorescent
XX dye and at the 5' end to a nanoparticle. In the native state, the
XX probe forms a hairpin conformation with hybridised termini. The
XX proximity of the fluorophore and quencher (gold nanoparticle) in
XX the molecular beacon results in little or no detectable
XX fluorescence. Upon hybridisation of the central complementary
XX stretch of the probe to a target sequence, such as the present
XX sequence, the hairpin undergoes a conformational change resulting
XX in an increase in fluorescence, the extent of which is proportional
XX to the amount of target sequence present. Single mismatches can
XX be detected. The invention relates generally to the use of metal
XX surface quenchers such as particles or films for high sensitivity
XX applications in, for example, detection and diagnostic systems.
XX
XX Sequence 20 BP; 15 A; 3 C; 1 G; 1 T; 0 other;
Query Match 1.4%; Score 15; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1084 AAAAAAAAAAAAAA 1098
Db 1 AAAAAAAAAAAAAA 15
RESULT 856
ABL58300
ID ABL58300 standard; DNA; 20 BP.
XX AC ABL58300;
XX
XX 15-JUL-2002 (first entry)
XX
XX Human GLUT 10 SSCP analysis primer GLUT10 ex2cF.
XX
XX Glucose transporter; GLUT10; insulin; chromosome 20Q12-13.3; human;
KW glucose metabolism; single strand conformational polymorphism; PCR;
KW type 2 diabetes; SSCP; primer; ss.
```

```
XX Homo sapiens.
XX WO200218621-A2.
XX PN 07-MAR-2002.
XX PD
XX PF 22-AUG-2001; 2001WO-US26184.
XX PR 31-AUG-2000; 2000US-0652292.
XX PA (UYWA-) UNIV WAKE FOREST.
XX
XX Bowden DM, Dawson PA, Fossey SC;
XX WPI; 2002-371828/40.
XX
XX New glucose transporter gene and protein, designated GLUT10, useful for
XX studying and analyzing biological processes of glucose metabolism and
XX Type 2 diabetes, as well as for screening modulators of glucose
XX transporter activity -
XX
XX Example 4; Page 52; 85pp; English.
XX
XX The invention relates to a novel glucose transporter gene and protein,
XX designated GLUT10. GLUT 10 is an insulin-responsive glucose transporter
XX gene located in the type 2 diabetes linked region of chromosome
XX 20Q12-13.3. The GLUT 10 polypeptide can be expressed by standard
XX recombinant methodology. The GLUT 10 glucose transporter gene and protein
XX are useful for studying and analysing biological processes of both
XX glucose metabolism and type 2 diabetes. These are also useful in drug
XX screening techniques, especially for screening modulators of glucose
XX transporter activity or compounds having the ability to be transported
XX across the cell membranes. Sequences ABL58290-315 represent primers
XX specific for the various regions of the human GLUT 10 glucose transporter
XX gene, used in single strand conformational polymorphism (SSCP) analysis
XX of the gene.
XX
XX Sequence 20 BP; 3 A; 4 C; 8 G; 5 T; 0 other;
Query Match 1.4%; Score 15; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 335 GGAGCAACTTGGTGC 349
Db 1 GGAGCAACTTGGTGC 15
RESULT 857
ABI96929/c
ID ABI96929 standard; DNA; 20 BP.
XX AC ABI96929;
XX
XX 16-FEB-2002 (first entry)
XX
XX Capture oligonucleotide Zip ID#4016 oligo #9.
XX
XX Human; K-ras; PCR primer; probe; capture probe; mutation detection;
KW ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
KW infection; 21 hydroxylase deficiency; Turner Syndrome; obesity;
KW cancer; oncogene; tumour suppressor; human papillomavirus; forensic;
KW environmental monitoring; food industry; feed industry; ss.
XX
XX Synthetic.
XX
XX WO200179548-A2.
XX
XX 25-OCT-2001.
XX
XX 04-APR-2001; 2001WO-US10958.
XX
```

```

PR 14-APR-2000; 2000US-197271P.
XX (CORR ) CORNELL RES FOUND INC.
XX Barany F, Zirvi M, Gerry NP, Favis R, Kliman R;
PI WPI; 2002-034366/04.
XX Designing capture oligonucleotide probes for use on a support to which
XX complementary oligonucleotides hybridize with little mismatch -
XX Example 5; Fig 29; 300pp; English.
XX The present invention describes a method (M1) for designing capture
XX oligonucleotide probes (II) for use on a support to which complementary
XX oligonucleotide probes (II) will hybridize with little mismatch, where
XX (I) have melting temperatures within a narrow range. The method is useful
XX for detecting infectious diseases caused by bacterial infectious agents
XX e.g. Salmonella, Listeria monocytogenes and Haemophilus influenza, fungal
XX infectious agents e.g. Cryptococcus neoformans, Candida albicans and
XX Aspergillus fumigatus, viruses e.g. T-cell lymphocyctotropic virus,
XX Epstein-Barr virus and polio virus, and parasitic infectious agents
XX selected from Onchoverva volvulus, Entamoeba histolytica and Dracunculus
XX medineis. The method is also useful for detecting genetic diseases such
XX as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
XX Detecting cancer involving oncogenes, tumour suppressor genes, or genes
XX involved in DNA amplification, replication, recombination or repair, the
XX cancer is specifically associated with a gene selected from BRCA1 gene,
XX p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
XX method is also used for environmental monitoring, forensics and the food
XX and feed industry, detecting comprises scanning (using e.g. a scanning
XX electron microscope and infrared microscope) the support at the
XX particular sites and identifying if ligation of the oligonucleotide probe
XX sets occurred and correlating (using a computer) identified ligation to a
XX presence or absence of the target nucleotide sequences. ABI82074 to a
XX ABI97546 represent oligonucleotide sequences used in the exemplification
XX of the present invention.
XX Sequence 20 BP; 6 A; 6 C; 5 G; 3 T; 0 other;
SQ Query Match 1.4%; Score 15; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 23 GCGGCTAGGTCCTC 37
Db 18 GCGGCTAGGTCCTC 4
RESULT 858
AAF96192
ID AAF96192 standard; DNA; 21 BP.
XX AAF96192;
AC AAF96192;
XX 06-JUN-2001 (first entry)
DE Human gene single nucleotide polymorphism #953.
XX Human; variant thrombospondin 1; variant thrombospondin 4; SNP;
XX polymorphism; vascular disease; coronary artery disease; forensics;
XX myocardial infarction; atherosclerosis; stroke; venous thromboembolism;
XX pulmonary embolism; paternity test; ds.
XX Homo sapiens.
XX Key Location/Qualifiers
XX Variation replace(11,A)
XX /*tag= a
XX /standard_name= "single nucleotide polymorphism"
XX WO200118250-A2.

```

```

PD 15-MAR-2001.
XX 07-SEP-2000; 2000WO-US24503.
XX 10-SEP-1999; 99US-0153357.
XX 26-JUL-2000; 2000US-0220947.
XX 16-AUG-2000; 2000US-0225724.
XX (WHEED ) WHITEHEAD INST BIOMEDICAL RES.
XX (MILL-) MILLENNIUM PHARM INC.
XX Lander ES, Gargill M, Ireland JS, Bolk S, Daley GQ, McCarthy JJ;
XX WPI; 2001-226749/23.
XX Nucleic acids comprising single nucleotide polymorphisms, useful in
XX applications such as forensics, paternity testing, medicine, genetic
XX analysis and phenotype correlations to diseases such as diabetes and
XX atherosclerosis -
XX Examples; Page 116; 242pp; English.
XX The present invention provides a method of diagnosing a vascular disease
XX in an individual, involving determining the sequence at various
XX polymorphic sites within the human thrombospondin 1 and thrombospondin 4
XX genes. The sequences at a number of polymorphic sites are also provided
XX in the specification. In particular, the method can be used in the
XX diagnosis of atherosclerosis, myocardial infarction, coronary heart
XX disease, stroke, peripheral vascular diseases, venous thromboembolism
XX and pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also
XX useful in forensics, paternity testing, genetic analysis and phenotype
XX correlations to diseases. The present sequence is an example of one of
XX the human gene SNPs shown in the specification.
XX Sequence 21 BP; 3 A; 9 C; 6 G; 3 T; 0 other;
SQ Query Match 1.4%; Score 15; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 348 GCCAGCGCCACCTG 362
Db 7 GCCAGCGCCACCTG 21
RESULT 859
ABS97669
ID ABS97669 standard; DNA; 21 BP.
XX ABS97669;
AC ABS97669;
XX 23-DEC-2002 (first entry)
DE Histamine N-methyl transferase (HNMT) PCR Primer #4.
XX Human; ss; primer; cytochrome P450 A1; CYP450A1; UGT2B4; MDR1; PCR;
XX cytochrome P450 A2; CYP450A2; cytochrome P450 02B; CYP45002E1; LTF;
XX adrenergic receptor beta1; ADRB1; aryl hydrocarbon; AHR; MRP3; NR12;
XX aryl hydrocarbon receptor nuclear translocator; ARNT; cathepsin S; CTSS;
XX cyclooxygenase 2; COX2; diazepam binding inhibitor; DBI; haematological;
XX epoxide hydroxylase 2; EPHX2; 5-lipoxygenase activating protein; FLAP;
XX glutathione-S-transferase 12; GST12; histamine-N-methyl transferase;
XX HNMT; kallikrein 2; KLK2; nicotinamide-N-methyl transferase; NNMT;
XX NADPH quinone oxidoreductase 2; NQO2; sulfoltransferase thermolabile;
XX STM; UDP-glucuronosyl transferase 2B4; UDP-glucuronosyl transferase 2B7;
XX UGT2B7; UDP-glucuronosyl transferase; UGT2B15; urokinase receptor; uPA;
XX multidrug resistance 1; lactotransferrin; orphan nuclear receptor;
XX acetylcholine muscarinic receptor; CHMR1; CHMR2; CHMR3; CHMR4; CHMR5;
XX altered drug metabolism; cardiovascular function; colorectal tumour;
XX central nervous system; pulmonary; immunological.
XX Homo sapiens.

```



```
CC treatment.
CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297
CC and 3367, are not actually given a sequence in the Sequence Listing
CC from the present invention.
XX
SQ Sequence 18 BP; 9 A; 1 C; 7 G; 1 T; 0 other;
    Query Match          1.3%; Score 14.8; DB 1; Length 18;
    Best Local Similarity 88.9%; Pred. No. 4.6e+02;
    Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
QY 117 AAACGGGAAGAAAGGATG 134
    ||||| ||||| |||||
DB 1 AAACGAGAAGGAAGGATG 18

RESULT 863
AAQ20030/c
ID AAQ20030 standard; DNA; 19 BP.
XX
AC AAQ20030;
XX
DT 01-APR-1992 (first entry)
XX
DE Cross-linking oligomer 116 for targeting HUM11B.
XX
KW deoxyribonucleic acid; major groove; ethanoino group; IL-1;
KW aziridinylcytosine; cross-linking group; o-xylose linking group;
KW human interleukin-1 beta; inverted polarity region; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1 /tag= a
FT /mod_base= OTHER
FT /note= "N4M4-ethanocytosine"
FT modified_base 4
FT /tag= b
FT /mod_base= OTHER
FT /note= "N-methyl-8-oxo-2'-deoxyadenine"
FT misc_feature 14..19
FT /tag= c
FT /label= inverted_polarity_region
FT /note= "see comments"
FT modified_base 14
FT /tag= d
FT /mod_base= OTHER
FT /note= "N-methyl-8-oxo-2'-deoxyadenine"
FT modified_base 18
FT /tag= e
FT /mod_base= OTHER
FT /note= "N-methyl-8-oxo-2'-deoxyadenine"
FT modified_base 19
FT /tag= f
FT /mod_base= OTHER
FT /note= "N-methyl-8-oxo-2'-deoxyadenine"
XX
PN WO9118997-A.
XX
PD 12-DEC-1991.
XX
PF 24-MAY-1991; 91WO-1003680.
XX
PR 14-JAN-1991; 91US-0640654.
PR 25-MAY-1990; 90US-0529346.
XX
XX (GILE-) GILEAD SCIE INC.
XX
XX Matteucci MD, Krawczyk S;
XX
XX WPI; 1992-007480/01.
XX
```

```
PT New sequence-specific non-photo-activated crosslinking agents -
PT bind to the major groove of duplex DNA and are esp. useful for
PT treating latent infections e.g. HIV
XX
PS Example 4; Page 25; 42pp; English.
XX
CC This oligomer contains an inverted polarity region formed from an
CC o-xylose dimer synthon. Residues 13 and 14 are linked via an
CC o-xylose group (i.e. nucleotides that have xylose sugar linked via
CC the o-xyline ring). The sequence is designed to target the Human
CC interleukin-1 beta gene beginning at nucleotide 7378 and will
CC covalently cross-link to it via the N4M4-ethanocytosine group.
CC See also AAQ20026-Q20029.
XX
SQ Sequence 19 BP; 4 A; 1 C; 0 G; 14 T; 0 other;
    Query Match          1.3%; Score 14.8; DB 1; Length 19;
    Best Local Similarity 88.9%; Pred. No. 4.9e+02;
    Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
QY 1082 TTAAAAAATAAAAAA 1099
    ||||| ||||| |||||
DB 19 TTAATAAAAAAATAA 2

RESULT 864
AAQ30373/c
ID AAQ30373 standard; DNA; 19 BP.
XX
AC AAQ30373;
XX
DT 25-MAR-2003 (updated)
DT 07-DEC-1992 (first entry)
XX
DE Oligomer HUM beta 113 for forming triplex with IL-1 target duplex.
KW Human interleukin - 1 beta gene; herpes simplex; AIDS; modified;
KW HIV; RSV; HPV; malignancy; hepatitis; inflammation; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1 /tag= a
FT /mod_base= OTHER
FT /note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"
FT modified_base 4
FT /tag= b
FT /mod_base= OTHER
FT /note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"
FT modified_base 14
FT /tag= c
FT /mod_base= OTHER
FT /note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"
FT modified_base 18
FT /tag= d
FT /mod_base= OTHER
FT /note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"
FT modified_base 19
FT /tag= e
FT /mod_base= OTHER
FT /note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"
FT misc_feature 14..19
FT /tag= f
FT /label= inverted_polarity_region
FT /note= "see comments"
FT misc_feature 13..14
FT /tag= g
FT /note= "o-xylose dimer synthon linkage"
XX
XX WO9209705-A1.
XX
PD 11-JUN-1992.
```

```

XX 25-NOV-1991; 91WO-US08811.
XX 23-NOV-1990; 90US-0617907.
XX 18-JAN-1991; 91US-0643382.
XX 08-APR-1991; 91US-0683420.
XX 17-APR-1991; 91US-0686544.
XX 17-APR-1991; 91US-0686546.
XX 17-APR-1991; 91US-0686547.
XX 27-SEP-1991; 91US-0766733.
XX (GILE-) GILEAD SCI INC.
XX
XX Froehler B, Krawczyk S, Matteucci MD, Milligan J;
XX WPI; 1992-217083/26.
XX
XX New oligomers contg. modified bases - which form a triplex with
XX G-C doublet in a DNA duplex, for treating and diagnosing HIV,
XX hepatitis, herpes, malignancy and inflammation
XX
XX Claim 12; Page 70; 77pp; English.
XX
XX The synthetic oligomer is capable of forming a triplex at
XX physiological pH with a purine rich target sequence by coupling
XX into the major groove of the duplex. The specific target sequence
XX of this oligomer is the human interleukin -1 beta gene beginning at
XX nucleotide 7378 contg. a purine rich sequence concd. on one strand
XX of the duplex. The oligomer, and others like it are useful in
XX diagnosis and therapy of diseases characterised by specific DNA
XX duplex targets, e.g. HPV; HER; HIV, hepatitis B, herpes, malignant
XX tumours and inflammation. The triple helices form under mild conditions
XX thus assays may be carried out without subjecting the test specimen to
XX harsh conditions. The oligomer contains an inverted polarity region
XX formed from an o-xylosa dimer synthon. The linking gp. is o-xylosa
XX (nucleotides have the 3' positions of xylose sugars linked via the
XX o-xylosa ring). Two nucleotides are coupled through a xylose residue
XX to form the dimer synthon. This additional modifications may render
XX the oligomer stable to nuclease activity. The oligomer is able to
XX inhibit gene expression, as verified by in vitro systems.
XX See also AAQ25452-25501 and AAQ30226-448.
XX (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 19 BP; 5 A; 0 C; 0 G; 14 T; 0 other;
XX
XX Query Match 1.3%; Score 14.8; DB 1; Length 19;
XX Best Local Similarity 88.9%; Pred. No. 4.9e+02;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 1082 TTAATAAAAAAAAAAAAAA 1099
XX ||||| ||||| ||||| |||||
XX 19 TTAATAAAAAAAAAAAAAATA 2
XX
XX RESULT 865
XX AAQ30376/c
XX ID AAQ30376 standard; DNA; 19 BP.
XX AC AAQ30376;
XX AC
XX DT 25-MAR-2003 (updated)
XX DT 07-DEC-1992 (first entry)
XX
XX Oligomer HUM beta 116 for forming triplex with IL-1 target duplex.
XX
XX Human interleukin - 1 beta gene; herpes simplex; AIDS; modified;
XX HIV; RSV; HPV; malignancy; hepatitis; inflammation; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX modified_base 1 /*tag= a
XX

```

```

FT /mod_base= OTHER
FT /note= "OTHER= N4 N4 ethanocytosine"
FT 4
FT /*tag= b
FT /mod_base= OTHER
FT /note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"
FT 14
FT /*tag= c
FT /mod_base= OTHER
FT /note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"
FT 18
FT /*tag= d
FT /mod_base= OTHER
FT /note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"
FT 19
FT /*tag= e
FT /mod_base= OTHER
FT /note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"
FT 14..19
FT /*tag= f
FT /label= inverted_polarity_region
FT /note= "see comments"
FT 13..14
FT /*tag= g
FT /note= "o-xylosa dimer synthon linkage"
FT
FT W09209705-A1.
FT
FT 11-JUN-1992.
FT
FT 25-NOV-1991; 91WO-US08811.
FT
FT 23-NOV-1990; 90US-0617907.
FT 18-JAN-1991; 91US-0643382.
FT 08-APR-1991; 91US-0683420.
FT 17-APR-1991; 91US-0686544.
FT 17-APR-1991; 91US-0686546.
FT 17-APR-1991; 91US-0686547.
FT 27-SEP-1991; 91US-0766733.
FT
FT (GILE-) GILEAD SCI INC.
FT
FT Froehler B, Krawczyk S, Matteucci MD, Milligan J;
FT WPI; 1992-217083/26.
FT
FT New oligomers contg. modified bases - which form a triplex with
FT G-C doublet in a DNA duplex, for treating and diagnosing HIV,
FT hepatitis, herpes, malignancy and inflammation
FT
FT Claim 12; Page 70; 77pp; English.
FT
FT The synthetic oligomer is capable of forming a triplex at
FT physiological pH with a purine rich target sequence by coupling
FT into the major groove of the duplex. The specific target sequence
FT of this oligomer is the human interleukin -1 beta gene beginning at
FT nucleotide 7378 contg. a purine rich sequence concd. on one strand
FT of the duplex. The oligomer, and others like it are useful in
FT diagnosis and therapy of diseases characterised by specific DNA
FT duplex targets, e.g. HPV; HER; HIV, hepatitis B, herpes, malignant
FT tumours and inflammation. The triple helices form under mild conditions
FT thus assays may be carried out without subjecting the test specimen to
FT harsh conditions. The oligomer contains an inverted polarity region
FT formed from an o-xylosa dimer synthon. The linking gp. is o-xylosa
FT (nucleotides have the 3' positions of xylose sugars linked via the
FT o-xylosa ring). Two nucleotides are coupled through a xylose residue
FT to form the dimer synthon. This additional modifications may render
FT the oligomer stable to nuclease activity. The oligomer is able to
FT inhibit gene expression, as verified by in vitro systems.
FT See also AAQ25452-25501 and AAQ30226-448.
FT (Updated on 25-MAR-2003 to correct PN field.)
FT
FT Sequence 19 BP; 4 A; 1 C; 0 G; 14 T; 0 other;
FT
FT Query Match 1.3%; Score 14.8; DB 1; Length 19;
FT Best Local Similarity 88.9%; Pred. No. 4.9e+02;
FT Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
FT
FT QY 1082 TTAATAAAAAAAAAAAAAA 1099
FT ||||| ||||| ||||| |||||
FT 19 TTAATAAAAAAAAAAAAAATA 2
FT
FT RESULT 865
FT AAQ30376/c
FT ID AAQ30376 standard; DNA; 19 BP.
FT AC AAQ30376;
FT AC
FT DT 25-MAR-2003 (updated)
FT DT 07-DEC-1992 (first entry)
FT
FT Oligomer HUM beta 116 for forming triplex with IL-1 target duplex.
FT
FT Human interleukin - 1 beta gene; herpes simplex; AIDS; modified;
FT HIV; RSV; HPV; malignancy; hepatitis; inflammation; ss.
FT
FT Synthetic.
FT
FT Key Location/Qualifiers
FT modified_base 1 /*tag= a
FT

```

```

CC See also AAQ33501-34437.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 other;

Query Match      1.5%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1084 AAAAAAAAAAAAAAAAAA 1100
Db 20 AAAAAAAAAAAAAAAAAA 4

RESULT 331
AAQ58578
ID AAQ58578 standard; RNA; 20 BP.
XX
AC AAQ58578;
XX
DT 25-MAR-2003 (updated)
DT 21-AUG-1994 (first entry)
XX
DE Sequence of synthetic RNA oligo which is a target nucleotide for
DE a novel receptor.
XX
KW Novel receptor; nucleic acid; transport; oligo; ss.
XX
OS Synthetic.
XX
PN W09404194-A1.
XX
PD 03-MAR-1994.
XX
PF 13-AUG-1993; 93WO-US07603.
XX
PR 14-AUG-1992; 92US-0930087.
XX
PA (MASI ) MASSACHUSETTS INST TECHNOLOGY.
XX
PI De MENDOZA J, Rebek J, Usman N;
XX
DR WFI; 1994-082846/10.
XX
PT Transport of nucleic acid derivs. across membranes - using new
PT receptors which use salt bridging, aromatic stacking, hydrogen
PT bonding and chelation.
XX
PS Example; Table 1, page 38; 103pp; English.
XX
CC The inventors claim a method of transporting a nucleic acid deriv.
CC across a membrane which comprises using a receptor that uses salt
CC bridging, aromatic stacking, H bonding and chelation to recognise
CC the nucleic acid deriv. AAQ56305, AAQ58577-86 are nucleic acid derivs
CC used in the examples.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 other;

Query Match      1.5%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1084 AAAAAAAAAAAAAAAAAA 1100
Db 1 AAAAAAAAAAAAAAAAAA 17

RESULT 332
AAQ4917/c
ID AAQ4917 standard; cDNA; 20 BP.
XX
AC AAQ4917;
XX
DT 25-MAR-2003 (updated)
DT 15-MAY-1996 (first entry)

```

```

XX
DT 25-MAR-2003 (updated)
DT 15-MAY-1996 (first entry)
XX
DE Mammalian stem cell factor (SCF) cDNA oligonucleotide primer 220-3.
XX
KW Stem cell factor; progenitor; haematopoiesis; SCF; anaemia;
KW thrombocytopenia; leucopenia; AIDS; immunodeficiency; bone graft;
KW transplant; neoplasia; myelosuppression; bone marrow; ss.
XX
OS Synthetic.
XX
PN EP676470-A1.
XX
PD 11-OCT-1995.
XX
PF 04-OCT-1990; 95EP-0105391.
XX
PR 01-OCT-1990; 90US-0589701.
PR 16-OCT-1989; 89US-0422383.
PR 11-JUN-1990; 90US-0537198.
PR 24-AUG-1990; 90US-0573616.
PR 28-SEP-1990; 90WO-US05548.
XX
PA (AMGE-) AMGEN INC.
XX
XX
PI Bosselman RA, Martin FH, Suggs SV, Zsebo KM;
XX
DR WFI; 1995-346090/45.
XX
PT New stem cell factor polypeptide(s) - for stimulating the growth of
PT primitive progenitor cells, esp. for treating disorders involving
PT blood cells
XX
PS Example 3; Fig 12C; 127pp; English.
XX
CC AAQ4915-T04922 are oligonucleotide primers and probes used for the
CC amplification and sequencing of mammalian stem cell factor (SCF).
CC Non-naturally occurring SCF and C-terminally truncated polypeptides,
CC having amino acid sequences sufficiently duplicative of naturally
CC occurring SCF, stimulate growth of primitive progenitors such as
CC haematopoietic progenitor cells, neural stem cells and primordial
CC germ stem cells. The peptides can be used in a composition for
CC treating leucopenia, anaemia or thrombocytopenia, for enhancing
CC engraftment of bone marrow during transplantation or for bone marrow
CC recovery after chemotherapy or radiation-induced bone marrow aplasia
CC or myelosuppression. They can also be used for treating neoplasia,
CC nerve damage, infertility, intestinal damage or myeloproliferative
CC disorders. Antibodies may be raised against the peptides for use in
CC detection or neutralisation of SCF in serum. SCF may be useful for
CC the treatment of AIDS and severe combined immunodeficiency (SCID)
CC states alone or in combination with other factors such as IL-7.
CC (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 other;

Query Match      1.5%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1084 AAAAAAAAAAAAAAAAAA 1100
Db 18 AAAAAAAAAAAAAAAAAA 2

RESULT 333
AAQ4918/c
ID AAQ4918 standard; cDNA; 20 BP.
XX
AC AAQ4918;
XX
DT 25-MAR-2003 (updated)
DT 15-MAY-1996 (first entry)

```

XX DE Mammalian stem cell factor (SCF) cDNA oligonucleotide primer 220-11.
 XX KW Stem cell factor; progenitor; haematopoiesis; SCF; anaemia;
 XX KW thrombocytopenia; leucopenia; AIDS; immunodeficiency; bone graft;
 XX KW transplant; neoplasia; myelosuppression; bone marrow; ss.
 XX OS Synthetic.
 XX PN EP676470-A1.
 XX PD 11-OCT-1995.
 XX PF 04-OCT-1990; 95EP-0105391.
 XX PR 01-OCT-1990; 90US-0589701.
 XX PR 16-OCT-1989; 89US-0423283.
 XX PR 11-JUN-1990; 90US-0537198.
 XX PR 24-AUG-1990; 90US-0573616.
 XX PR 28-SEP-1990; 90WO-US05548.
 XX PA (AMGE-) AMGEN INC.
 XX PI Bosselman RA, Martin FH, Suggs SV, Zsebo KM;
 XX WPI; 1995-346090/45.
 XX DR New stem cell factor polypeptide(s) - for stimulating the growth of
 XX PT primitive progenitor cells, esp. for treating disorders involving
 XX PT blood cells
 XX Example 3; Fig 12C; 127pp; English.
 XX AA04915-T04922 are oligonucleotide primers and probes used for the
 CC amplification and sequencing of mammalian stem cell factor (SCF).
 CC Non-naturally occurring SCF and C-terminally truncated polypeptides,
 CC having amino acid sequences sufficiently duplicative of naturally
 CC occurring SCF, stimulate growth of primitive progenitors such as
 CC haematopoietic progenitor cells, neural stem cells and primordial
 CC germ stem cells. The peptides can be used in a composition for
 CC treating leucopenia, anaemia or thrombocytopenia, for enhancing
 CC engraftment of bone marrow during transplantation or for bone marrow
 CC recovery after chemotherapy or radiation-induced bone marrow aplasia
 CC or myelosuppression. They can also be used for treating neoplasia,
 CC nerve damage, infertility, intestinal damage or myeloproliferative
 CC disorders. Antibodies may be raised against the peptides for use in
 CC detection or neutralisation of SCF in serum. SCF may be useful for
 CC the treatment of AIDS and severe combined immunodeficiency (SCID).
 CC states alone or in combination with other factors such as IL-7.
 CC (Updated on 25-MAR-2003 to correct PF field.)
 XX SQ Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 other;
 Query Match 1.5%; Score 17; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02; Indels 0; Gaps 0;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1084 AAAAAAAAAAAAAAAAAA 1100
 Db 18 AAAAAAAAAAAAAAAAAA 2
 RESULT 334
 AAQ90405/c
 ID AAQ90405 standard; DNA; 20 BP.
 AC AAQ90405;
 XX 08-JAN-1996 (first entry)
 DT T2 (synthetic DNA probe with 5' amino terminal #4).
 DE T2; HLA; dQa; self-addressable electronic device; SAED; hybridisation;
 XX KW

XX KW ss.
 XX OS Synthetic.
 XX FH Key Location/Qualifiers
 FT misc_feature 1
 FT /*tag= a
 FT /note= "3' aminolink2 Thymine; allows binding to any
 FT amine"
 XX PN WO9512808-A1.
 XX PD 11-MAY-1995.
 XX PF 26-OCT-1994; 94WO-US12270.
 XX PR 01-NOV-1993; 93US-0146504.
 XX PA (NANO-) NANOGEN INC.
 XX PI Heller MJ, Tu E;
 XX WPI; 1995-185870/24.
 XX DR New self-addressable electronic devices - used for multi-step and
 XX PT multiplex reactions such as DNA hybridisation(s), clinical
 XX PT diagnostics and bio:polymer synthesis
 XX Example 1; Page 41; 86pp; English.
 XX CC The sequences represented by, AAQ90402-15 are synthetic DNA probes
 CC containing 5' amino termini. The sequences shown in AAQ90390-401 are
 CC synthetic DNA probes with 3' ribonucleoside termini. These sequences
 CC were specific for the polymorphisms of HLA gene dQa. The sequences
 CC used in the device of the invention. This is a self-addressable
 CC electronic device (SAED) that can be used to carry out multi-step and
 CC multiplex reactions, such as nucleic acid hybridisations. The
 CC advantages of this method are that these reactions can be carried out
 CC with complete and precise electronic control, and that the rate,
 CC specificity and sensitivity of these reactions are greatly improved at
 CC micro-locations.
 XX SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 other;
 Query Match 1.5%; Score 17; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02; Indels 0; Gaps 0;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1084 AAAAAAAAAAAAAAAAAA 1100
 Db 20 AAAAAAAAAAAAAAAAAA 4
 RESULT 335
 AAQ94205/c
 ID AAQ94205 standard; DNA; 20 BP.
 XX AC AAQ94205;
 XX 25-MAR-2003 (updated)
 DT 24-AUG-1995 (first entry)
 DE Alpha-anomeric oligonucleotide ligand 1803 for oestradiol hapten.
 XX KW Oligonucleotide ligand; steroid hormone; hapten; immobilisation;
 XX KW immunodetection; estradiol; alpha-anomer; ss.
 XX OS Synthetic.
 XX FH Key Location/Qualifiers
 FT modified_base 20
 FT /*tag= a
 FT /mod_base= OTHER

CC separate lanes. The method can be used to analyse gene expression
 XX rapidly and easily.

SQ Sequence 20 BP; 1 A; 1 C; 0 G; 18 T; 0 other;
 Query Match 1.5%; Score 17; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1084 AAAAAAAAAAAAAAAAAA 1100
 |||||
 Db 17 AAAAAAAAAAAAAAAAAA 1

RESULT 338

AAQ75601/C
 ID AAQ75601 standard; DNA; 20 BP.

XX AC AAQ75601;

XX DT 04-AUG-1995 (first entry)

DE Reverse transcription primer used in cDNA analysis technique.

XX Analysis; gene expression; reverse transcription; primer; cDNA;
 KW aggregate; restriction enzyme; ss.

XX OS Synthetic.

XX PN JP06303997-A.

XX PD 01-NOV-1994.

XX PF 16-APR-1993; 93JP-0112515.

XX PR 16-APR-1993; 93JP-0112515.

XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

XX WPI; 1995-018287/03.

XX Analysis of cDNA and gene expression - by amplification of mRNA
 PT followed by digestion with restriction enzymes

XX Disclosure; Page 5; 11pp; Japanese.

XX A method for the analysis of cDNA comprises (a) preparing an
 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
 CC and a plural type of labelled reverse transcription primers
 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
 CC template for each reverse transcription primer; (b) digesting each of
 CC the prepared aggregates of the double-stranded cDNAs with restriction
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
 CC separate lanes. The method can be used to analyse gene expression
 CC rapidly and easily.

XX Sequence 20 BP; 0 A; 1 C; 0 G; 19 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1084 AAAAAAAAAAAAAAAAAA 1100
 |||||
 Db 17 AAAAAAAAAAAAAAAAAA 1

RESULT 339

AAQ75602/C
 ID AAQ75602 standard; DNA; 20 BP.

XX AC AAQ75602;

DT 04-AUG-1995 (first entry)
 XX Reverse transcription primer used in cDNA analysis technique.

XX Analysis; gene expression; reverse transcription; primer; cDNA;
 KW aggregate; restriction enzyme; ss.

XX OS Synthetic.

XX PN JP06303997-A.

XX PD 01-NOV-1994.

XX PF 16-APR-1993; 93JP-0112515.

XX PR 16-APR-1993; 93JP-0112515.

XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

XX WPI; 1995-018287/03.

XX Analysis of cDNA and gene expression - by amplification of mRNA
 PT followed by digestion with restriction enzymes

XX Disclosure; Page 5; 11pp; Japanese.

XX A method for the analysis of cDNA comprises (a) preparing an
 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
 CC and a plural type of labelled reverse transcription primers
 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
 CC template for each reverse transcription primer; (b) digesting each of
 CC the prepared aggregates of the double-stranded cDNAs with restriction
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
 CC separate lanes. The method can be used to analyse gene expression
 CC rapidly and easily.

XX Sequence 20 BP; 0 A; 2 C; 0 G; 18 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1084 AAAAAAAAAAAAAAAAAA 1100
 |||||
 Db 17 AAAAAAAAAAAAAAAAAA 1

RESULT 340

AAQ75603/C
 ID AAQ75603 standard; DNA; 20 BP.

XX AC AAQ75603;

XX DT 04-AUG-1995 (first entry)

DE Reverse transcription primer used in cDNA analysis technique.

XX Analysis; gene expression; reverse transcription; primer; cDNA;
 KW aggregate; restriction enzyme; ss.

XX OS Synthetic.

XX PN JP06303997-A.

XX PD 01-NOV-1994.

XX PF 16-APR-1993; 93JP-0112515.

XX PR 16-APR-1993; 93JP-0112515.

XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

XX WPI; 1995-018287/03.

| | | | | |
|----|---|---|---------------|--|
| XX | PR | 16-APR-1993; | 93JP-0112515. | |
| XX | XX | (NITE) NIPPON TELEGRAPH & TELEPHONE CORP. | | |
| PA | AC | WFI; 1995-018287/03. | | |
| XX | XX | | | |
| DR | XX | | | |
| XX | XX | | | |
| PT | PT | Analysis of cDNA and gene expression - by amplification of mRNA | | |
| PT | PT | followed by digestion with restriction enzymes | | |
| XX | XX | | | |
| PS | PS | Disclosure; Page 5; 11pp; Japanese. | | |
| XX | XX | | | |
| CC | CC | A method for the analysis of cDNA comprises (a) preparing an | | |
| CC | CC | aggregate of double-stranded cDNAs by using an aggregate of mRNAs | | |
| CC | CC | and a plural type of labelled reverse transcription primers | | |
| CC | CC | (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the | | |
| CC | CC | template for each reverse transcription primer; (b) digesting each of | | |
| CC | CC | the prepared aggregates of the double-stranded cDNAs with restriction | | |
| CC | CC | enzyme and; (c) electrophoresing the digested aggregate of cDNAs in | | |
| CC | CC | separate lanes. The method can be used to analyse gene expression | | |
| CC | CC | rapidly and easily. | | |
| XX | XX | | | |
| SQ | SQ | Sequence 20 BP; 0 A; 2 C; 1 G; 17 T; 0 other; | | |
| | | Query Match 1.5%; Score 17; DB 1; Length 20; | | |
| | | Best Local Similarity 100.0%; Pred. No. 2.1e+02; | | |
| | | Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | |
| QY | 1084 | AAAAAAAAAAAAAAAAAAAA 1100 | | |
| | | | | |
| Db | 17 | AAAAAAAAAAAAAAAAAAAA 1 | | |
| | | | | |
| | | RESULT 348 | | |
| | | AAQ75567/c | | |
| ID | AAQ75567 | standard; DNA; 20 BP. | | |
| XX | XX | | | |
| AC | AAQ75567; | | | |
| XX | XX | | | |
| DT | 04-AUG-1995 | (first entry) | | |
| XX | XX | | | |
| DE | Reverse transcription primer used in cDNA analysis technique. | | | |
| XX | XX | | | |
| KW | Analysis; gene expression; reverse transcription; primer; cDNA; | | | |
| XX | aggregate; restriction enzyme; ss. | | | |
| OS | Synthetic. | | | |
| XX | XX | | | |
| PN | JP06303997-A. | | | |
| XX | XX | | | |
| PD | 01-NOV-1994. | | | |
| XX | XX | | | |
| PF | 16-APR-1993; | 93JP-0112515. | | |
| XX | XX | | | |
| PR | 16-APR-1993; | 93JP-0112515. | | |
| XX | XX | | | |
| PA | (NITE) NIPPON TELEGRAPH & TELEPHONE CORP. | | | |
| XX | XX | | | |
| DR | WFI; 1995-018287/03. | | | |
| XX | XX | | | |
| PT | PT | Analysis of cDNA and gene expression - by amplification of mRNA | | |
| PT | PT | followed by digestion with restriction enzymes | | |
| XX | XX | | | |
| PS | PS | Disclosure; Page 5; 11pp; Japanese. | | |
| XX | XX | | | |
| CC | CC | A method for the analysis of cDNA comprises (a) preparing an | | |
| CC | CC | aggregate of double-stranded cDNAs by using an aggregate of mRNAs | | |
| CC | CC | and a plural type of labelled reverse transcription primers | | |
| CC | CC | (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the | | |
| CC | CC | template for each reverse transcription primer; (b) digesting each of | | |
| CC | CC | the prepared aggregates of the double-stranded cDNAs with restriction | | |
| CC | CC | enzyme and; (c) electrophoresing the digested aggregate of cDNAs in | | |
| CC | CC | separate lanes. The method can be used to analyse gene expression | | |
| CC | CC | rapidly and easily. | | |
| XX | XX | | | |
| SQ | SQ | Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 other; | | |
| | | Query Match 1.5%; Score 17; DB 1; Length 20; | | |
| | | Best Local Similarity 100.0%; Pred. No. 2.1e+02; | | |
| | | Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | |
| QY | 1084 | AAAAAAAAAAAAAAAAAAAA 1100 | | |
| | | | | |
| Db | 17 | AAAAAAAAAAAAAAAAAAAA 1 | | |
| | | | | |
| | | RESULT 347 | | |
| | | AAQ75594/c | | |
| ID | AAQ75594 | standard; DNA; 20 BP. | | |
| XX | XX | | | |
| AC | AAQ75594; | | | |
| XX | XX | | | |
| DT | 04-AUG-1995 | (first entry) | | |
| XX | XX | | | |
| DE | Reverse transcription primer used in cDNA analysis technique. | | | |
| XX | XX | | | |
| KW | Analysis; gene expression; reverse transcription; primer; cDNA; | | | |
| XX | aggregate; restriction enzyme; ss. | | | |
| OS | Synthetic. | | | |
| XX | XX | | | |
| PN | JP06303997-A. | | | |
| XX | XX | | | |
| PD | 01-NOV-1994. | | | |
| XX | XX | | | |
| PF | 16-APR-1993; | 93JP-0112515. | | |
| XX | XX | | | |

| | | | |
|----|----|---|---------------|
| XX | PR | 16-APR-1993; | 93JP-0112515. |
| XX | PA | (NITE) NIPPON TELEGRAPH & TELEPHONE CORP. | |
| XX | AC | WPI; 1995-018287/03. | |
| XX | DR | Analysis of cDNA and gene expression - by amplification of mRNA | |
| XX | DE | followed by digestion with restriction enzymes | |
| XX | PT | Disclosure; Page 5; 1lpp; Japanese. | |
| XX | PS | A method for the analysis of cDNA comprises (a) preparing an | |
| XX | OS | aggregate of double-stranded cDNAs by using an aggregate of mRNAs | |
| XX | KW | and a plural type of labelled reverse transcription primers | |
| XX | PV | (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the | |
| XX | PD | template for each reverse transcription primer; (b) digesting each of | |
| XX | PF | the prepared aggregates of the double-stranded cDNAs with restriction | |
| XX | PP | enzyme and; (c) electrophoresing the digested aggregate of cDNAs in | |
| XX | PR | separate lanes. The method can be used to analyse gene expression | |
| XX | PN | rapidly and easily. | |
| XX | PA | Sequence 20 BP; 0 A; 2 C; 1 G; 17 T; 0 other; | |
| XX | PT | Query Match 1.5%; Score 17; DB 1; Length 20; | |
| XX | PS | Best Local Similarity 100.0%; Pred. No. 2.1e+02; | |
| XX | OS | Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | |
| XX | KW | YQ 1084 AAAAAAAAAAAAAAAA 1100 | |
| XX | PV | | |
| XX | PD | Db 17 AAAAAAAAAAAAAAAA 1 | |
| XX | PF | RESULT 348 | |
| XX | PP | AAQ75567/c | |
| XX | PR | ID AAQ75567 standard; DNA; 20 BP. | |
| XX | PN | XX AAQ75567; | |
| XX | PA | DT 04-AUG-1995 (first entry) | |
| XX | PT | Reverse transcription primer used in cDNA analysis technique. | |
| XX | PS | Analysis; gene expression; reverse transcription; primer; cDNA; | |
| XX | OS | aggregate; restriction enzyme; ss. | |
| XX | KW | Synthetic. | |
| XX | PV | JF06303997-A. | |
| XX | PD | XX 01-NOV-1994. | |
| XX | PF | 16-APR-1993; 93JP-0112515. | |
| XX | PP | 16-APR-1993; 93JP-0112515. | |
| XX | PR | (NITE) NIPPON TELEGRAPH & TELEPHONE CORP. | |
| XX | PN | WPI; 1995-018287/03. | |
| XX | PA | Analysis of cDNA and gene expression - by amplification of mRNA | |
| XX | PT | followed by digestion with restriction enzymes | |
| XX | PS | Disclosure; Page 5; 1lpp; Japanese. | |
| XX | OS | A method for the analysis of cDNA comprises (a) preparing an | |
| XX | KW | aggregate of double-stranded cDNAs by using an aggregate of mRNAs | |
| XX | PV | and a plural type of labelled reverse transcription primers | |
| XX | PD | (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the | |
| XX | PF | template for each reverse transcription primer; (b) digesting each of | |
| XX | PP | the prepared aggregates of the double-stranded cDNAs with restriction | |
| XX | PR | enzyme and; (c) electrophoresing the digested aggregate of cDNAs in | |
| XX | PN | separate lanes. The method can be used to analyse gene expression | |
| XX | PA | rapidly and easily. | |
| XX | PT | Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 other; | |
| XX | PS | Query Match 1.5%; Score 17; DB 1; Length 20; | |
| XX | OS | Best Local Similarity 100.0%; Pred. No. 2.1e+02; | |
| XX | KW | Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | |
| XX | PV | YQ 1084 AAAAAAAAAAAAAAAA 1100 | |
| XX | PD | | |
| XX | PF | Db 17 AAAAAAAAAAAAAAAA 1 | |
| XX | PP | RESULT 347 | |
| XX | PR | AAQ75594/c | |
| XX | PN | ID AAQ75594 standard; DNA; 20 BP. | |
| XX | PA | XX AAQ75594; | |
| XX | PT | DT 04-AUG-1995 (first entry) | |
| XX | PS | Reverse transcription primer used in cDNA analysis technique. | |
| XX | OS | Analysis; gene expression; reverse transcription; primer; cDNA; | |
| XX | KW | aggregate; restriction enzyme; ss. | |
| XX | PV | Synthetic. | |
| XX | PD | JF06303997-A. | |
| XX | PF | XX 01-NOV-1994. | |
| XX | PP | 16-APR-1993; 93JP-0112515. | |

```

CC rapidly and easily.
SQ Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 other;

Query Match      1.5%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred.No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
DB 17 AAAAAAAAAAAAAAAAAA 1

RESULT 349
AAQ75568/c
ID AAQ75568 standard; DNA; 20 BP.
XX
AC AAQ75568;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-0112515.
XX
PR 16-APR-1993; 93JP-0112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA
followed by digestion with restriction enzymes
XX
PS Disclosure; Page 5; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an
aggregate of double-stranded cDNAs by using an aggregate of mRNAs
and a plural type of labelled reverse transcription primers
(GENESQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
template for each reverse transcription primer; (b) digesting each of
the prepared aggregates of the double-stranded cDNAs with restriction
enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
separate lanes. The method can be used to analyse gene expression
rapidly and easily.
SQ Sequence 20 BP; 0 A; 0 C; 1 G; 19 T; 0 other;

Query Match      1.5%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred.No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
DB 17 AAAAAAAAAAAAAAAAAA 1

RESULT 351
AAQ75570/c
ID AAQ75570 standard; DNA; 20 BP.
XX
AC AAQ75570;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-0112515.
XX
PR 16-APR-1993; 93JP-0112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX

```

PT Analysis of cDNA and gene expression - by amplification of mRNA
PT followed by digestion with restriction enzymes
PS Disclosure; Page 5; 11pp; Japanese.

XX A method for the analysis of cDNA comprises (a) preparing an
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC and a plural type of labelled reverse transcription primers
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
CC template for each reverse transcription primer; (b) digesting each of
CC the prepared aggregates of the double-stranded cDNAs with restriction
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC separate lanes. The method can be used to analyse gene expression
CC rapidly and easily.

XX Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
DB 17 AAAAAAAAAAAAAAAAAA 1

RESULT 352

AAQ75571/c
ID AAQ75571 standard; DNA; 20 BP.

AC AAQ75571;

DT 04-AUG-1995 (first entry)

DE Reverse transcription primer used in cDNA analysis technique.

KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.

OS Synthetic.

PN JP06303997-A.

PD 01-NOV-1994.

PF 16-APR-1993; 93JP-0112515.

PR 16-APR-1993; 93JP-0112515.

PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

DR WPI; 1995-018287/03.

PT Analysis of cDNA and gene expression - by amplification of mRNA
PT followed by digestion with restriction enzymes

PS Disclosure; Page 5; 11pp; Japanese.

XX A method for the analysis of cDNA comprises (a) preparing an
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC and a plural type of labelled reverse transcription primers
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
CC template for each reverse transcription primer; (b) digesting each of
CC the prepared aggregates of the double-stranded cDNAs with restriction
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC separate lanes. The method can be used to analyse gene expression
CC rapidly and easily.

XX Sequence 20 BP; 0 A; 1 C; 2 G; 17 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
DB 17 AAAAAAAAAAAAAAAAAA 1

RESULT 353

AAQ75572/c

ID AAQ75572 standard; DNA; 20 BP.

AC AAQ75572;

DT 04-AUG-1995 (first entry)

DE Reverse transcription primer used in cDNA analysis technique.

KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.

OS Synthetic.

PN JP06303997-A.

PD 01-NOV-1994.

PF 16-APR-1993; 93JP-0112515.

PR 16-APR-1993; 93JP-0112515.

PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

DR WPI; 1995-018287/03.

PT Analysis of cDNA and gene expression - by amplification of mRNA
PT followed by digestion with restriction enzymes

PS Disclosure; Page 5; 11pp; Japanese.

XX A method for the analysis of cDNA comprises (a) preparing an
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC and a plural type of labelled reverse transcription primers
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
CC template for each reverse transcription primer; (b) digesting each of
CC the prepared aggregates of the double-stranded cDNAs with restriction
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC separate lanes. The method can be used to analyse gene expression
CC rapidly and easily.

SQ Sequence 20 BP; 1 A; 1 C; 1 G; 17 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
DB 17 AAAAAAAAAAAAAAAAAA 1

RESULT 354

AAQ75573/c

ID AAQ75573 standard; DNA; 20 BP.

AC AAQ75573;

DT 04-AUG-1995 (first entry)

DE Reverse transcription primer used in cDNA analysis technique.

KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.

OS Synthetic.

```
XX JP06303997-A.
XX PN
XX CC
XX PD 01-NOV-1994.
XX XX
XX PF 16-APR-1993; 93JP-0112515.
XX XX
XX PR 16-APR-1993; 93JP-0112515.
XX XX
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX XX
XX DR WPI; 1995-018287/03.
XX XX
XX PT Analysis of cDNA and gene expression - by amplification of mRNA
XX followed by digestion with restriction enzymes
XX PS
XX FS Disclosure; Page 5; 11pp; Japanese.
XX XX
XX CC A method for the analysis of cDNA comprises (a) preparing an
XX aggregate of double-stranded cDNAs by using an aggregate of mRNAs
XX and a plural type of labelled reverse transcription primers
XX (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
XX template for each reverse transcription primer; (b) digesting each of
XX the prepared aggregates of the double-stranded cDNAs with restriction
XX enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
XX separate lanes. The method can be used to analyse gene expression
XX rapidly and easily.
XX CC
XX SQ Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 other;
XX
XX Query Match 1.5%; Score 17; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 2.1e+02;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1084 AAAAAAAAAAAAAAAAAA 1100
DB 17 AAAAAAAAAAAAAAAAAA 1
RESULT 355
AAQ75574/c
ID AAQ75574 standard; DNA; 20 BP.
XX AC AAQ75574;
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX XX
XX PF 16-APR-1993; 93JP-0112515.
XX XX
XX PR 16-APR-1993; 93JP-0112515.
XX XX
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX XX
XX DR WPI; 1995-018287/03.
XX XX
XX PT Analysis of cDNA and gene expression - by amplification of mRNA
XX followed by digestion with restriction enzymes
XX PS
XX FS Disclosure; Page 5; 11pp; Japanese.
XX XX
XX CC A method for the analysis of cDNA comprises (a) preparing an
XX aggregate of double-stranded cDNAs by using an aggregate of mRNAs
XX and a plural type of labelled reverse transcription primers
XX (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
XX template for each reverse transcription primer; (b) digesting each of
XX the prepared aggregates of the double-stranded cDNAs with restriction
XX enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
XX separate lanes. The method can be used to analyse gene expression
XX rapidly and easily.
XX CC
XX SQ Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 other;
XX
XX Query Match 1.5%; Score 17; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 2.1e+02;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1084 AAAAAAAAAAAAAAAAAA 1100
DB 17 AAAAAAAAAAAAAAAAAA 1
RESULT 355
AAQ75574/c
ID AAQ75574 standard; DNA; 20 BP.
XX AC AAQ75574;
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX XX
XX PF 16-APR-1993; 93JP-0112515.
XX XX
XX PR 16-APR-1993; 93JP-0112515.
XX XX
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX XX
XX DR WPI; 1995-018287/03.
XX XX
XX PT Analysis of cDNA and gene expression - by amplification of mRNA
XX followed by digestion with restriction enzymes
XX PS
XX FS Disclosure; Page 5; 11pp; Japanese.
XX XX
XX CC A method for the analysis of cDNA comprises (a) preparing an
XX aggregate of double-stranded cDNAs by using an aggregate of mRNAs
```

```
CC and a plural type of labelled reverse transcription primers
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
CC template for each reverse transcription primer; (b) digesting each of
CC the prepared aggregates of the double-stranded cDNAs with restriction
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC separate lanes. The method can be used to analyse gene expression
CC rapidly and easily.
XX XX
XX SQ Sequence 20 BP; 0 A; 2 C; 1 G; 17 T; 0 other;
XX
XX Query Match 1.5%; Score 17; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 2.1e+02;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1084 AAAAAAAAAAAAAAAAAA 1100
DB 17 AAAAAAAAAAAAAAAAAA 1
RESULT 356
AAQ75559/c
ID AAQ75559 standard; DNA; 20 BP.
XX AC AAQ75559;
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX XX
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX XX
XX PN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-0112515.
XX XX
XX PR 16-APR-1993; 93JP-0112515.
XX XX
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX XX
XX DR WPI; 1995-018287/03.
XX XX
XX PT Analysis of cDNA and gene expression - by amplification of mRNA
XX followed by digestion with restriction enzymes
XX PS
XX FS Disclosure; Page 5; 11pp; Japanese.
XX XX
XX CC A method for the analysis of cDNA comprises (a) preparing an
XX aggregate of double-stranded cDNAs by using an aggregate of mRNAs
XX and a plural type of labelled reverse transcription primers
XX (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
XX template for each reverse transcription primer; (b) digesting each of
XX the prepared aggregates of the double-stranded cDNAs with restriction
XX enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
XX separate lanes. The method can be used to analyse gene expression
XX rapidly and easily.
XX CC
XX SQ Sequence 20 BP; 0 A; 0 C; 3 G; 17 T; 0 other;
XX
XX Query Match 1.5%; Score 17; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 2.1e+02;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1084 AAAAAAAAAAAAAAAAAA 1100
DB 17 AAAAAAAAAAAAAAAAAA 1
RESULT 357
```

AAQ75560/c
ID AAQ75560 standard; DNA; 20 BP.
AC AAQ75560;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
OS Synthetic.
XX
FN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-0112515.
XX
PR 16-APR-1993; 93JP-0112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA
XX followed by digestion with restriction enzymes
XX
PS Disclosure; Page 5; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC and a plural type of labelled reverse transcription primers
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
CC template for each reverse transcription primer; (b) digesting each of
CC the prepared aggregates of the double-stranded cDNAs with restriction
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC separate lanes. The method can be used to analyse gene expression
CC rapidly and easily.
XX
SQ Sequence 20 BP; 1 A; 0 C; 2 G; 17 T; 0 other;
Query Match 1.5%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1084 AAAAAAAAAAAAAAAAAA 1100
DB 17 AAAAAAAAAAAAAAAAAA 1
RESULT 358
AAQ75561/c
ID AAQ75561 standard; DNA; 20 BP.
AC AAQ75561;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
OS Synthetic.
XX
FN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-0112515.
XX
PR 16-APR-1993; 93JP-0112515.
XX

PR 16-APR-1993; 93JP-0112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA
XX followed by digestion with restriction enzymes
XX
PS Disclosure; Page 5; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC and a plural type of labelled reverse transcription primers
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
CC template for each reverse transcription primer; (b) digesting each of
CC the prepared aggregates of the double-stranded cDNAs with restriction
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC separate lanes. The method can be used to analyse gene expression
CC rapidly and easily.
XX
SQ Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 other;
Query Match 1.5%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1084 AAAAAAAAAAAAAAAAAA 1100
DB 17 AAAAAAAAAAAAAAAAAA 1
RESULT 359
AAQ75562/c
ID AAQ75562 standard; DNA; 20 BP.
XX
AC AAQ75562;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
OS Synthetic.
XX
FN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-0112515.
XX
PR 16-APR-1993; 93JP-0112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA
XX followed by digestion with restriction enzymes
XX
PS Disclosure; Page 5; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC and a plural type of labelled reverse transcription primers
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
CC template for each reverse transcription primer; (b) digesting each of
CC the prepared aggregates of the double-stranded cDNAs with restriction
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC separate lanes. The method can be used to analyse gene expression
CC rapidly and easily.
XX

XX SQ Sequence 20 BP; 0 A; 1 C; 2 G; 17 T; 0 other;
 Query Match 1.5%; Score 17; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1084 AAAAAAAAAAAAAAAAAA 1100
 |||
 DB 17 AAAAAAAAAAAAAAAAAA 1
 RESULT 360
 AAT63649/c
 ID AAT63649 standard; DNA; 20 BP.
 XX
 AC AAT63649;
 XX
 DT 06-JUN-1997 (first entry)
 XX
 DE Anti-HTLV antisense reference oligonucleotide HT.
 XX
 KW antisense; complementary; tax gene; inhibit; HTLV-1;
 KW human T-cell lymphotropic virus type 1; viral antigen expression; ss.
 OS Synthetic.
 XX
 PN JP09052898-A.
 XX
 PD 25-FEB-1997.
 XX
 PF 09-AUG-1995; 95JP-0224606.
 XX
 PR 09-AUG-1995; 95JP-0224606.
 XX
 PA (SOYA-) SOYAKU GIUTSU KENKYUSHO KK.
 XX
 DR WPI; 1997-197252/18.
 XX
 PT Anti-HTLV-1 anti-sense oligo:nucleotide - is complementary to region
 PT of tax gene from human T-cell lymphotropic virus type 1 and inhibits
 PT viral antigen expression
 XX
 PS Example 1; Page 8; 10pp; Japanese.
 XX
 CC Oligonucleotides having a partial sequence consisting of at least 15
 CC bases of AAT63641 (an antisense oligo complementary to a region of the
 CC tax gene which can inhibit human T-cell lymphotropic virus type 1
 CC (HTLV-1) viral antigen expression) are claimed. In an example, six
 CC antisense oligos were designed, T1-T6 (AAT63650-55) and were compared to
 CC six oligos derived from other regions of HTLV-1, i.e. SJ1 (splice
 CC junction), P1 (p21), R1 (rex), RRI (rex response element), E1 (env) and
 CC G1 (gag), four reference oligonucleotides T1S (tax-sense), HC (dc20), HT
 CC (dt20) (AAT63647-49) and a random 20mer (RAN) in a HTLV-1 virus antigen
 CC expression inhibiting test. Oligonucleotide T1 gave the best results.
 XX
 SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 other;
 Query Match 1.5%; Score 17; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1084 AAAAAAAAAAAAAAAAAA 1100
 |||
 DB 20 AAAAAAAAAAAAAAAAAA 4
 RESULT 361
 AAV34591
 ID AAV34591 standard; DNA; 20 BP.
 XX
 AC AAV34591;
 XX

DT 25-AUG-1998 (first entry)
 DE M. vaccae antigenic sequence hybridising oligo AD12.
 XX
 KW Mycobacterium vaccae; antigen; therapy; prevention; cytokine production;
 KW M. avium; M. tuberculosis; immune response enhancer; cell proliferation;
 KW mycobacteria infection; vaccine; cancer; ss.
 XX
 OS Synthetic.
 OS Mycobacterium vaccae.
 XX
 PN WO9808542-A2.
 XX
 PD 05-MAR-1998.
 XX
 PF 28-AUG-1997; 97WO-NZ00105.
 XX
 PR 12-JUN-1997; 97US-0873970.
 PR 29-AUG-1996; 96US-0705347.
 XX
 PA (GENE-) GENESIS RES & DEV CORP.
 XX
 PI Hiyama J, Prestidge RL, Scott LM, Skinner MA, Tan P;
 PI Visser E;
 XX
 DR WPI; 1998-216926/19.
 XX
 XX Mycobacterium vaccae polypeptides - used to develop products for use
 PT in detection, therapy and prevention of mycobacteria infections or
 PT as immune response enhancers
 XX
 PS Example 8; Page 99; 153pp; English.
 XX
 CC This oligonucleotide is used in the DNA cloning strategies of the
 CC Mycobacterium vaccae antigens. The invention provides M. vaccae
 CC polypeptides that comprise an immunogenic portion of a soluble M. vaccae
 CC antigen, or a variant, where the antigen induces an immune response in
 CC patients previously exposed to a mycobacterium. Such M. vaccae
 CC polypeptides can be used in methods for enhancing non-specific immune
 CC response. The methods and products can be used for the detection,
 CC treatment and prevention of infectious diseases caused by mycobacteria
 CC such as M. vaccae, M. avium or M. tuberculosis. The products also have
 CC the ability to induce cell proliferation and cytokine production (e.g.
 CC interferon-gamma and interleukin-12 production) in T cells, NK cells,
 CC B cells, or macrophages. They can be used for enhancing immune
 CC responses for use in vaccines or immunotherapy of infectious diseases
 CC and cancers.
 XX
 SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 U; 0 other;
 Query Match 1.5%; Score 17; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1084 AAAAAAAAAAAAAAAAAA 1100
 |||
 DB 1 AAAAAAAAAAAAAAAAAA 17
 RESULT 362
 AAT86606/c
 ID AAT86606 standard; DNA; 20 BP.
 XX
 AC AAT86606;
 XX
 DT 04-JUN-1998 (first entry)
 XX
 DE Oligonucleotide separated by capillary affinity gel electrophoresis.
 XX
 KW Capillary affinity gel electrophoresis; separation; polymer-gel;
 KW polyacrylamide; ss.
 XX
 OS Synthetic.

XX WO9745721-A1.
 XX
 PD 04-DEC-1997.
 XX
 PF 23-MAY-1997; 97WO-EF02647.
 XX
 PR 24-MAY-1996; 96CH-0001320.
 XX
 PA (NOVS) NOVARTIS AG.
 XX
 PI Muscate A, Natt F, Paulus A;
 XX
 DR WPI; 1998-041763/04.
 XX
 PT Separation of electrically charged target molecules - by capillary
 PT affinity gel electrophoresis using polymer-gel to which receptors
 PT for target molecules are bound
 XX
 PS Example D3; Page 25; 41pp; English.
 XX
 CC A mixture of oligonucleotides (AAT96604-7) were separated by a new
 CC process using capillary affinity gel electrophoresis. The invention
 CC relates to selective separation of electrically charged target molecules
 CC in an analytical mixture. It comprises capillary affinity gel
 CC electrophoresis using a capillary tube which is at least partly filled
 CC with a polymer gel. Receptors for target molecules are covalently bound
 CC to the polymer. An electric field of at least 50 volts/cm is applied.
 CC The capillary tube is charged with the analytical mixture. In a first
 CC separation stage, the target molecules in the mixture are bound to the
 CC receptors and the remaining components are eluted, optionally whilst
 CC splitting open. In a second stage, the elution conditions are changed,
 CC optionally in stages, so that the affinity of the target molecules for
 CC the receptor is eliminated and the target molecules are eluted and
 CC detected, optionally whilst splitting open. The process is useful for
 CC selective separation and/or determination of charged organic compounds,
 CC such as oligonucleotides, peptides or carbohydrates. It may be used,
 CC e.g. for isolation of specific proteins and DNA molecules, purification
 CC of antibodies, analysis of antisense compounds or screening for enzyme
 CC inhibitors. The process achieves higher resolution and selectivity
 CC than prior art processes, especially in the case of complex biological
 CC analytical mixtures. It has high sensitivity, even with small amounts of
 CC samples. The derivatised polymers may be synthesised specifically using
 CC standard methods.
 XX
 SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 other;
 Query Match 1.5%; Score 17; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1084 AAAAAAAAAAAAAAAAAA 1100
 Db 20 AAAAAAAAAAAAAAAAAA 4
 RESULT 363
 AAZ11326
 ID AAZ11326 standard; DNA; 20 BP.
 XX
 AC AAZ11326;
 XX
 DT 25-OCT-1999 (first entry)
 XX
 DE Mycobacterial 16S rRNA specific oligo AD12.
 XX
 KW Mycobacterium vaccae protein; antigen; T cell activation; cytokine;
 KW dendritic cell maturation; infectious disease; immune disorder; cancer;
 KW respiratory system; mycobacterial infection; allergy; tuberculosis;
 KW leprosy; sarcoidosis; lung cancer; asthma; skin disorder; psoriasis;
 KW dermatitis; eczema; alopecia areata; skin cancer; basal carcinoma;
 KW squamous cell carcinoma; melanoma; PCR primer; ss.

OS Synthetic.
 OS Mycobacterium vaccae.
 XX
 PN WO9932634-A2.
 XX
 PD 01-JUL-1999.
 XX
 PF 23-DEC-1998; 98WO-NZ00189.
 XX
 PR 04-DEC-1998; 98US-0205426.
 PR 23-DEC-1997; 97US-0996624.
 PR 23-DEC-1997; 97US-0997080.
 PR 23-DEC-1997; 97US-0997362.
 PR 11-JUN-1998; 98US-0095855.
 PR 17-SEP-1998; 98US-0156181.
 XX
 PA (GENB-) GENESIS RES & DEV CORP LTD.
 XX
 PI Prestidge RL, Skinner MA, Tan P, Visser ES, Watson J;
 XX
 DR WPI; 1999-430163/36.
 XX
 XX Enhancing immune response to an antigen
 PT
 XX Example 15; Page 177; 243pp; English.
 XX
 CC The invention provides heat-killed Mycobacterium vaccae, or recombinant
 CC M. vaccae proteins. The M. vaccae proteins may be employed to activate
 CC T cells and natural killer cells, to stimulate the production of
 CC cytokines, to enhance the expression of co-stimulatory molecules on
 CC dendritic cells and monocytes, and to enhance dendritic cell maturation
 CC and function. The proteins can be expressed by standard recombinant
 CC methodology. Pharmaceutical compositions comprising the proteins or
 CC nucleic acid sequences encoding the proteins can be used for the
 CC treatment, prevention, and detection of disorders including infectious
 CC diseases, immune disorders and cancer. In particular, the compounds and
 CC methods are used for treatment of diseases of the respiratory system,
 CC such as mycobacterial infections, asthma, allergies, tuberculosis,
 CC leprosy, sarcoidosis and lung cancers, and disorders of the skin such as
 CC psoriasis, atopic dermatitis, eczema, allergic contact dermatitis,
 CC alopecia areata, and skin cancers such as basal carcinoma, squamous cell
 CC carcinoma and melanoma.
 XX
 SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 U; 0 other;
 Query Match 1.5%; Score 17; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1084 AAAAAAAAAAAAAAAAAA 1100
 Db 1 AAAAAAAAAAAAAAAAAA 17
 RESULT 364
 AAX27533/c
 ID AAX27533 standard; RNA; 20 BP.
 XX
 AC AAX27533;
 XX
 DT 27-MAY-1999 (first entry)
 XX
 DE Synthetic RNA sequence produced by the method of the invention.
 XX
 KW Silyloxymethyl; phosphonate; silyloxymethyl halide; diagnosis; ss;
 KW cyanoethyl phosphoramidate coupling; isomerisation; steric hindrance.
 XX
 OS Synthetic.
 OS WO9909044-A1.
 XX
 PD 25-FEB-1999.
 XX

PF 17-AUG-1998; 98WO-EP05215.
 XX
 PR 18-AUG-1997; 97CH-0001931.
 XX
 PA (JENN/) JENNY L.
 PA (PITS/) FITSCH S.
 PA (WEIS/) WEISS P A.

XX Jenny L, Pitsch S, Weiss PA;
 XX WPI; 1999-180963/15.
 XX

PT 2-Silyloxymethyl ribonucleosides and their phosphonate derivatives
 PT - have high purity, use in machine synthesis of ribonucleic acids,
 PT enable longer oligonucleotide chain construction, and larger amounts
 XX
 XX Example 6; Page 25; 38pp; English.

XX The invention relates to silyloxymethyl protected D- or L-ribonucleosides
 CC and their phosphonates (I), and silyloxymethyl halides (II). (I) are
 CC intermediates for synthesis of RNA-oligonucleotides with predetermined
 CC nucleotide sequence, particularly by machine synthesis. The groups
 CC specified above, apart from those on silyl, are those particularly for
 CC the cyanoethyl phosphoramidate coupling. Uses of the oligoribonucleotide
 CC products in diagnosis, therapy, and as research tools, are well known,
 CC and are not dealt with in detail. (II) is an intermediate for (I). The
 CC silyloxymethyl halide reagent is easy to prepare, and yields are high.
 CC Introduction of the silyloxymethyl group into the ribonucleoside is
 CC simple and rapid, and the acetal bond formed does not migrate,
 CC eliminating particularly the prior art problem of 2' to 3' isomerisation.
 CC The methylenedioxy group spacer between the silyl group and nucleoside
 CC ring results in less steric hindrance than bulky direct silyloxy
 CC linkages, enabling first, a range of choices for the silyl substituents,
 CC to provide, e.g., acid or base stability; and second, higher yields in
 CC coupling. Purer products are therefore obtained than in prior art,
 CC enabling larger quantities and longer chains of oligoribonucleotides to
 CC be synthesised successfully, and in shorter times.

XX Sequence 20 BP; 0 A; 0 C; 0 G; 20 U; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred.No. 2.1e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1084 AAAAAAAAAAAAAAAAAA 1100
 DB 20 AAAAAAAAAAAAAAAAAA 4

RESULT 365
 AAA40448/C
 ID AAA40448 standard; DNA; 20 BP.
 XX
 AC AAA40448;

XX 13-NOV-2000 (first entry)

XX Electrochemical detection method fixed probe DNA.

XX Electrochemical detection; glucose; cholesterol; urea nitrogen;
 KW bilirubin; uric acid; haemoglobin; lactic acid; body fluid; blood;
 KW plasma; serum; urine; lymph diagnosis; probe; ss.

XX Synthetic.

XX EP1018646-A2.

XX 12-JUL-2000.

XX 07-JAN-2000; 2000EP-0100126.

XX 06-JAN-1999; 99JP-0001111.

XX 24-MAY-1999; 99JP-0143599.

XX (FUJF) FUJI PHOTO FILM CO LTD.
 XX Ogawa M, Takenaka S, Takagi M;
 XX WPI; 2000-444372/39.
 XX

PT Quantitative analysis of a biochemical compound such as glucose, in
 PT body a body fluid such as blood, comprising detecting enhanced electron
 PT transfer between an oxidase and a DNA-immobilized electrode, useful for
 PT diagnosis of disease -

XX Example 1; Page 7; 14pp; English.

XX This invention describes a novel method for quantitatively analysing a
 CC biochemical compound (I) which comprises contacting (I) with double
 CC stranded DNA fixed to the surface of an electrode at their terminals in
 CC which electrochemically active threading intercalators are intercalated,
 CC in an aqueous medium under application of electric potential to the
 CC electrode in the presence of an oxidase which oxidizes the biochemical
 CC compound and becomes reduced, and detecting electric current flowing
 CC between the electrode and a second electrode in the aqueous medium. The
 CC method is useful for detection of biochemical compounds such as glucose,
 CC cholesterol, urea nitrogen, bilirubin, uric acid, haemoglobin and lactic
 CC acid in body fluids such as whole blood, plasma, serum, urine, and lymph
 CC for diagnosis of various diseases. The method allows detection of
 CC biochemical compounds quickly and easily with a high sensitivity using a
 CC simple apparatus. This sequence represents DNA fragment used as fixed
 CC probe DNA in the method of the invention.

XX Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred.No. 2.1e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1084 AAAAAAAAAAAAAAAAAA 1100
 DB 20 AAAAAAAAAAAAAAAAAA 4

RESULT 366
 AAA40449
 ID AAA40449 standard; DNA; 20 BP.
 XX
 AC AAA40449;

XX 13-NOV-2000 (first entry)

XX Electrochemical detection method sample DNA target.

XX Electrochemical detection; glucose; cholesterol; urea nitrogen;
 KW bilirubin; uric acid; haemoglobin; lactic acid; body fluid; blood;
 KW plasma; serum; urine; lymph diagnosis; ss.

XX Synthetic.

XX EP1018646-A2.

XX 12-JUL-2000.

XX 07-JAN-2000; 2000EP-0100126.

XX 06-JAN-1999; 99JP-0001111.

XX 24-MAY-1999; 99JP-0143599.

XX (FUJF) FUJI PHOTO FILM CO LTD.

XX Ogawa M, Takenaka S, Takagi M;

XX WPI; 2000-444372/39.

XX Quantitative analysis of a biochemical compound such as glucose, in

PT body a body fluid such as blood, comprising detecting enhanced electron
PT transfer between an oxidase and a DNA-immobilized electrode, useful for
PT diagnosis of disease -

XX Example 1; Page 8; 14pp; English.

CC This invention describes a novel method for quantitatively analysing a
CC biochemical compound (I) which comprises contacting (I) with double
CC stranded DNA fixed to the surface of an electrode at their terminals in
CC which electrochemically active threading intercalators are intercalated,
CC in an aqueous medium under application of electric potential to the
CC electrode in the presence of an oxidase which oxidizes the biochemical
CC compound and becomes reduced, and detecting electric current flowing
CC between the electrode and a second electrode in the aqueous medium. The
CC method is useful for detection of biochemical compounds such as glucose,
CC cholesterol, urea nitrogen, bilirubin, uric acid, haemoglobin and lactic
CC acid in body fluids such as whole blood, plasma, serum, urine, and lymph
CC for diagnosis of various diseases. The method allows detection of
CC biochemical compounds quickly and easily with a high sensitivity using a
CC simple apparatus. This sequence represents DNA fragment used as a target
CC sample in the method of the invention.

XX Sequence 20 BP; 20 A; 0 C; 0 G; 0 U; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
Db 1 AAAAAAAAAAAAAAAAAA 17

RESULT 367

ID AAA50193/c

XX AAA50193 standard; DNA; 20 BP.

AC AAA50193;

XX 07-NOV-2000 (first entry)

XX 2'-Methoxyethoxy-modified oligonucleotide.

XX Phosphodiester oligonucleotide; H-phosphonate chemistry; ss.

XX Synthetic.

XX Key Location/Qualifiers

FT modified_base 1..19

FT /*tag= a

FT /note= "2'-methoxyethoxy modified thymidine"

XX WO200047593-A1.

XX 17-AUG-2000.

XX 11-FEB-2000; 2000WO-US03543.

XX 12-FEB-1999; 99US-0250075.

XX (ISIS-) ISIS PHARM INC.

XX Manoharan M, Maier MA;

XX WPI; 2000-558188/51.

XX Preparation of mixed backbone oligomeric compounds useful as e.g.

PT primers for diagnostic tests, involves oxidation of H-phosphonate
PT internucleoside linkages to phosphodiester internucleoside linkages -

XX Example 12; Page 34; 49pp; English.

XX The present sequence is that of a phosphodiester oligonucleotide

CC containing 20 T nucleobases, 19 having a 2'-methoxyethoxy group
CC on its 5' ribose sugar moiety. It is an example of an oligomeric
CC compound produced according to the methods of the invention. The
CC invention provides compounds and methods for the preparation of
CC mixed backbone oligomeric, or chimeric, compounds having
CC phosphodiester internucleoside linkages in addition to
CC phosphorothioate and/or phosphoramidate internucleoside linkages.
CC The methods also include incorporation of boranophosphate
CC internucleoside linkages. The methods utilize H-phosphonate
CC intermediates that are coupled together forming contiguous regions
CC of 1 or more H-phosphonate internucleoside linkages. Each
CC contiguous region is subsequently oxidized to phosphodiester,
CC phosphorothioate, phosphoramidate or boranophosphate
CC internucleoside linkages prior to further elongation. Mixed
CC backbone oligomeric compounds are prepared in this manner by
CC oxidizing adjacent regions with different reagents. Oligomeric
CC compounds of the invention are prepared using novel oxidation steps
CC that oxidize a region of 1 or more H-phosphonate internucleoside
CC linkages without degrading existing linkages that have been
CC previously oxidized. The oligonucleotides obtained are useful as
CC primers in PCR, probes, linkers, gene fragments and for other
CC diagnostic tests on e.g. biological tissue, fluid, cells etc., as
CC research reagents, and as antiviral agents.

XX Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
Db 20 AAAAAAAAAAAAAAAAAA 4

RESULT 368

AAA13752/c

ID AAA13752 standard; DNA; 20 BP.

XX AAA13752;

XX 27-JUL-2000 (first entry)

XX Stem cell factor universal oligonucleotide 220-3.

XX Stem cell factor; SCF; haematopoietic progenitor cell; blood forming;
XX primitive progenitor cell; haematopoietic disorder; syngeneic;
XX allogeneic; autologous bone marrow transplant; gene therapy;
XX transfection; haematopoietic stem cell; acute blood loss; neoplasia;
XX cancer; ss.

XX Synthetic.

XX EP992579-A1.

XX 12-APR-2000.

XX 04-OCT-1990; 99EP-0122861.

XX 16-OCT-1989; 89US-0422383.

XX 11-JUN-1990; 90US-0537198.

XX 24-AUG-1990; 90US-0573616.

XX 28-SEP-1990; 90WO-US05548.

XX 01-OCT-1990; 90US-0589701.

XX 04-OCT-1990; 90EP-0310699.

XX (AMGE-) AMGEN INC.

XX Zsebo KM, Suggs SV, Bosseimann RA, Martin FH;

XX WPI; 2000-259135/23.

PT Production of hematopoietic cells suitable for administration to a

PT subject using progenitor cells and expanding the cells using stem cell
 PT factor -
 XX Example 3; Fig 12C; 123pp; English.
 XX A method has been developed of making haematopoietic cells suitable for
 CC administration to a subject. The method comprises: (a) obtaining the
 CC haematopoietic progenitor cells from a donor; and (b) expanding the
 CC cells by adding to the cells a haematopoietically effective dose of a
 CC polypeptide product having at least part of the primary structural
 CC confirmation and one or more of the biological properties of naturally
 CC occurring stem cell factor (SCF). The method is useful for stimulating
 CC primitive progenitor cells including early haematopoietic progenitor
 CC cells which are capable of maturing to erythroid, megakaryocyte,
 CC granulocyte, lymphocyte and macrophage cells. SCF results in absolute
 CC increases in haematopoietic cells of both myeloid and lymphoid lineages.
 CC SCF is useful for treating haematopoietic disorders. The method is
 CC useful for expanding early haematopoietic progenitors in syngeneic,
 CC allogeneic or autologous bone marrow transplant. SCF is useful for
 CC enhancing the efficiency of gene therapy based on transfecting the
 CC haematopoietic stem cells. SCF is also useful for combating the
 CC myelosuppressive effects of anti-HIV drugs such as AZT and for enhancing
 CC haematopoietic recovery after acute blood loss and as a boost to the
 CC immune system for fighting neoplasia (cancer). The present sequence
 CC represents a universal oligonucleotide which is used in an example from
 CC the present invention.

XX Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 other;
 SQ Query Match 1.5%; Score 17; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1084 AAAAAAAAAAAAAA 1100
 Db 18 AAAAAAAAAAAAAA 2

RESULT 369
 AAA13754/C
 ID AAA13754 standard; DNA; 20 BP.
 AC AAA13754;
 XX 27-JUL-2000 (first entry)
 XX Stem cell factor universal oligonucleotide 220-11.
 DE Stem cell factor; SCF; haematopoietic progenitor cell; blood forming;
 KW primitive progenitor cell; haematopoietic disorder; syngeneic;
 KW allogeneic; autologous bone marrow transplant; gene therapy;
 KW transfection; haematopoietic stem cell; acute blood loss; neoplasia;
 KW cancer; ss.
 XX Synthetic.
 OS EP992579-A1.
 PN 12-APR-2000.
 XX 04-OCT-1990; 99EP-0122861.
 XX 16-OCT-1989; 89US-0422383.
 PR 11-JUN-1990; 90US-0537198.
 PR 24-AUG-1990; 90US-0573616.
 PR 28-SEP-1990; 90MO-US05548.
 PR 01-OCT-1990; 90US-0589701.
 PR 04-OCT-1990; 90EP-0310899.
 XX (AMGE-) AMGEN INC.
 PA Zsebo KM, Suggs SV, Bosselmann RA, Martin FH;
 XX

DR WPI; 2000-259135/23.
 XX Production of hematopoietic cells suitable for administration to a
 PT subject using progenitor cells and expanding the cells using stem cell
 PT factor -
 XX Example 3; Fig 12C; 123pp; English.
 XX A method has been developed of making haematopoietic cells suitable for
 CC administration to a subject. The method comprises: (a) obtaining the
 CC haematopoietic progenitor cells from a donor; and (b) expanding the
 CC cells by adding to the cells a haematopoietically effective dose of a
 CC polypeptide product having at least part of the primary structural
 CC confirmation and one or more of the biological properties of naturally
 CC occurring stem cell factor (SCF). The method is useful for stimulating
 CC primitive progenitor cells including early haematopoietic progenitor
 CC cells which are capable of maturing to erythroid, megakaryocyte,
 CC granulocyte, lymphocyte and macrophage cells. SCF results in absolute
 CC increases in haematopoietic cells of both myeloid and lymphoid lineages.
 CC SCF is useful for treating haematopoietic disorders. The method is
 CC useful for expanding early haematopoietic progenitors in syngeneic,
 CC allogeneic or autologous bone marrow transplant. SCF is useful for
 CC enhancing the efficiency of gene therapy based on transfecting the
 CC haematopoietic stem cells. SCF is also useful for combating the
 CC myelosuppressive effects of anti-HIV drugs such as AZT and for enhancing
 CC haematopoietic recovery after acute blood loss and as a boost to the
 CC immune system for fighting neoplasia (cancer). The present sequence
 CC represents a universal oligonucleotide which is used in an example from
 CC the present invention.

XX Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 other;

XX Query Match 1.5%; Score 17; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1084 AAAAAAAAAAAAAA 1100
 Db 18 AAAAAAAAAAAAAA 2

RESULT 370
 AAZ91117/C
 ID AAZ91117 standard; DNA; 20 BP.
 AC AAZ91117;
 XX 06-JUN-2000 (first entry)
 XX Oligonucleotide #5 for conjugation to abietane derivative.
 DE Abietane derivative; labelling; diagnostic test; biotin substitute; ss.
 KW Synthetic.
 OS FR2781802-A1.
 PN 04-FEB-2000.
 XX 31-JUL-1998; 98FR-0010084.
 PR 31-JUL-1998; 98FR-0010084.
 XX (INMR) BIO MERIEUX.
 PA Charles MH, Piga N, Battail PN, Veron L, Delair T, Mandrand B;
 PI WPI; 2000-239603/21.
 XX Saturated and unsaturated derivatives of abietic acid and their
 PT conjugated derivatives with natural and synthetic polymers, having use
 PT in diagnostics, chemical reactions and analysis -
 XX

PS Example 5; Page 20; 39pp; French.

XX The invention relates to novel saturated and unsaturated abietane derivatives. The new compounds may be used directly or indirectly in the development of new diagnostic tests, to follow infections, CC especially viral infections, to follow and/or measure chemical products, CC especially potential pollutants. In diagnostic tests they may be used CC as markers, or to form a universal solid phase after immobilization CC on a solid support, to produce monoclonal antibodies or polyclonal CC antibodies having diagnostic uses. The oligonucleotides AA291113-291117 CC represent examples of sequences that can be labeled with the CC new abietane derivatives. The new derivatives may be used to substitute CC for biotin in diagnostic tests, but because they are not found naturally CC in humans the risk of potential interactions with biological molecules CC is eliminated.

XX Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 other;

SQ Query Match 1.5%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAA 1100
| | | | | | | | | | | | | | | | | | | | | |
Db 20 AAAAAAAAAAAAAAA 4

RESULT 371
AAS63428
ID AAS63428 standard; DNA; 20 BP.
AC AAS63428;
XX
XX 29-JAN-2002 (first entry)
DT
DE Oligonucleotide-nanoparticle probe #52.
XX
XX Oligonucleotide-nanoparticle probe; diagnostic; forensic analysis;
KW nucleic acid detection; nanostructure; biochip; biofilter;
KW drug delivery; ss.
XX
XX Synthetic.
XX
XX WO200173123-A2.
PN
XX
XX 04-OCT-2001.
PD
XX
XX 28-MAR-2001; 2001WO-US10071.
PF
XX
XX 28-MAR-2000; 2000US-192699P.
PR
XX 26-APR-2000; 2000US-200161P.
PR
XX 26-JUN-2000; 2000US-213906P.
PR
XX 26-JUN-2000; 2000US-0603830.
PR
XX 08-DEC-2000; 2000US-254392P.
PR
XX 11-DEC-2000; 2000US-25235P.
PR
XX 12-JAN-2001; 2001US-0760500.
PR
XX 28-MAR-2001; 2001US-0820279.
PR
XX (NANO-) NANOSPHERE INC.
PA
XX
XX Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;
PI Taton TA, Park S, Li Z;
PI
XX WPI; 2001-656926/75.
DR
XX Detecting and separating nucleic acid, useful e.g. for diagnosis,
PT comprises reaction with nanoparticles that carry oligonucleotides
PT complementary to parts of the target -
XX
XX Example 18; Page 158; 40pp; English.
PS
XX The invention relates to a method for detection of nucleic acid (I)
CC having at least 2 portions, comprising treatment with nanoparticles that

CC carry oligonucleotides complementary to at least 2 parts of (I), where
CC detectable change caused by hybridisation of the oligonucleotide to (I)
CC is observed. The method is used to detect (or to separate) specific (I),
CC e.g. for diagnosing a wide variety of diseases, sequencing, in forensic
CC analysis etc., and generally to detect analytes other than (I). The
CC oligonucleotide-derivatised nanoparticles are also useful for preparing
CC nanostructures useful, for example, as biochips, biofilters, mechanical
CC devices, separation membranes, chemical sensors, in computers, and for
CC drug delivery. Very stable nanoparticle-oligonucleotide conjugates
CC can be produced, allowing their direct use (as probes) in polymerase
CC chain reaction, i.e. they survive multiple heating/cooling cycles so do
CC not need to be added after amplification. (I) are detected by simple
CC colour change without the need for special equipment, making possible
CC rapid field testing for e.g. pathogens. AAS63374-AAS63448 represent
CC oligonucleotide-nanoparticle probes, and related sequences, used in the
CC method of the invention.

XX Sequence 20 BP; 20 A; 0 C; 0 G; 0 U; 0 other;

SQ Query Match 1.5%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAA 1100
| | | | | | | | | | | | | | | | | | | | | |
Db 1 AAAAAAAAAAAAAAA 17

RESULT 372
AAH78547
ID AAH78547 standard; cDNA; 20 BP.
XX
AC AAH78547;
XX
XX 10-DEC-2001 (first entry)
DT
XX
XX Nucleotide sequence of a cDNA sequence.
DE
XX
XX Nucleic acid identification; DNA library screening; ss.
KW
XX
XX Synthetic.
XX
XX US6274321-B1.
PN
XX
XX 14-AUG-2001.
PD
XX
XX 03-DEC-1999; 99US-0454704.
PF
XX
XX 03-DEC-1999; 99US-0454704.
PR
XX
XX (REGC) UNIV CALIFORNIA.
PA
XX
XX Blumberg B;
PI
XX WPI; 2001-588900/66.
DR
XX
XX Screening nucleic acids (NA) in pool of interest comprises pooling,
PT expressing NA to form expression product pool and identifying NA in NA
PT pool corresponding to expression product pool having interaction with
PT target moiety -
XX
XX Disclosure; Column 22; 19pp; English.
PS
XX The specification describes a method for identifying a nucleic acid
CC in a pool of interest. The method comprises pooling individually
CC identifiable nucleic acids into at least two pools of one nucleic acid
CC each; expressing nucleic acid pools to obtain protein expression product
CC pools; assaying protein expression product pools for products having
CC interaction with target molecule; selecting nucleic acid pools
CC corresponding to identified protein expression product pools; and
CC identifying individual nucleic acids in identified nucleic acid
CC pools. The method is useful for identifying a nucleic acid (e.g. cDNA)
CC in a pool of interest and for functionally screening several nucleic

CC acids. The method is also useful for screening genomic DNA libraries
 CC or other source of individual cDNAs, mRNAs, synthetic libraries of
 CC nucleic acids e.g. combinatorial libraries. The present sequence
 CC was used in the course of the invention.

SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 U; 0 other;
 Query Match 1.5%; Score 17; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
 |||||
 Db 1 AAAAAAAAAAAAAAAAAA 17

RESULT 373

AAS10371
 ID AAS10371 standard; DNA; 20 BP.

AC AAS10371;

XX 24-OCT-2001 (first entry)

DE Oligonucleotide-cyclic disulphide linker, d.

KW Nanoparticle; cyclic disulphide-oligonucleotide; DNA detection;
 KW DNA isolation; genetic disease; bacterial disease; viral disease;
 KW forensic science; paternity testing; gene therapy; ss.

XX Synthetic.

EH Key Location/Qualifiers
 FT misc_feature 1

FT /*tag= a
 FT /note= "A is covalently linked to a
 FT cyclic-disulphide moiety"

XX WO200151665-A2.

PD 19-JUL-2001.

PF 12-JAN-2001; 2001WO-US01190.

XX 13-JAN-2000; 2000US-0176409.

PR 26-APR-2000; 2000US-0200161.

PR 26-JUN-2000; 2000US-0603830.

PR 12-JAN-2001; 2001US-0760500.

XX (NANO-) NANOSPHERE INC.

XX Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;
 PI Taton TA, Li Z;

XX WPI; 2001-451868/48.

DR Detecting a nucleic acid useful in e.g. diagnosing genetic, bacterial
 PT or viral diseases, by contacting the nucleic acid with oligonucleotides
 PT attached to nanoparticles and having sequences complementary a portion
 PT of the nucleic acid -

XX Example 24; Fig 44; 323pp; English.

XX The sequence represents a cyclic disulphide linked oligonucleotide
 CC which may be coupled with colloidal gold particles (nanoparticles) and
 CC used to demonstrate the method of the invention. The invention relates to
 CC isolating or detecting a nucleic acid of interest, in a mixture of
 CC nucleic acids, by binding it to 2 or more complementary nucleotides which
 CC have a nanoparticle attached to their 5' ends. The nanoparticles (e.g.
 CC colloidal gold) are used to both isolate and detect (e.g. by linking the
 CC particle to a fluorescent probe) the resultant complex. The methods are
 CC useful for detecting nucleic acids, natural or synthetic, and modified or
 CC unmodified. The methods may also be applied in the diagnosis of genetic,

CC bacterial and viral diseases, in forensics, in DNA sequencing, for
 CC paternity testing, for cell line authentication, and for monitoring gene
 CC therapy. The methods are further useful in research and analytical
 CC laboratories in DNA sequencing, in the field to detect the presence of
 CC specific pathogens, for quick identification of an infection to assist in
 CC drug prescription, and in homes and health centres for inexpensive
 CC first-line screening. The methods, which are based on observing
 CC colour change with the naked eye, are cheap, fast, simple, robust
 CC (reagents are stable), do not require specialised or expensive equipment,
 CC and little or no instrumentation is required.

XX Sequence 20 BP; 20 A; 0 C; 0 G; 0 U; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 2.1e+02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100

Db 1 AAAAAAAAAAAAAAAAAA 17

RESULT 374

AAS10402/c
 ID AAS10402 standard; DNA; 20 BP.

AC AAS10402;

XX 24-OCT-2001 (first entry)

DE DNA template for 3' end labeling of an RNA molecule, #14.

KW 3' RNA end labeling; DNA template; Okazaki fragment; 5' overhang; ss.

XX Synthetic.

XX US6238865-B1.

PD 29-MAY-2001.

PF 16-OCT-1998; 98US-0173936.

PR 17-OCT-1997; 97US-0063757.

XX (CHEN/) CHEN G.

PA (HUAN/) HUANG Z.

PA (SZOS/) SZOSTAK J W.

PI Huang Z, Szostak JW;

XX WPI; 2001-366470/38.

XX Modifying a 3' terminus of a pre-selected DNA sequence, useful for
 PT labeling and modifying 3'-termini of other nucleic acids, comprises
 PT using a synthetic nucleotide template with a defined overhang
 PT nucleotide -

XX Example 5; Column 13; 22pp; English.

XX The sequence represents a synthetic DNA template molecule used to
 CC demonstrate the method of the invention. The invention relates to a
 CC method of modifying (e.g. 3' end labelling with 32P dATP) the 3'
 CC terminus of an RNA molecule by providing a DNA oligonucleotide,
 CC complementary to the 3' end of the RNA molecule, with an overhang at the
 CC 5' end which allows incorporation of the labeling nucleotide into the
 CC RNA molecule. The method, based on the synthesis of Okazaki fragments, is
 CC useful for labeling and modifying the 3'-termini of other nucleic acids
 CC such as DNA fragments. The method is a simple and efficient way of
 CC labeling or modifying RNA 3'-termini using DNA polymerase and a synthetic
 CC template with defined overhang nucleotides.

XX Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
 DB 20 AAAAAAAAAAAAAAAAAA 4

RESULT 375
 AAS10447/c
 ID AAS10447 standard; DNA; 20 BP.
 XX
 AC AAS10447;
 XX
 DT 24-OCT-2001 (first entry)
 XX
 DE Human stem cell factor (SCF) cDNA universal PCR primer 220-3.
 XX
 KW Human; stem cell factor; SCF; haematopoietic progenitor cell;
 KW blood disorder; Hodgkin's disease; vitamin B12; folic acid deficiency;
 KW hypopigmentation disorder; viral disorder; AIDS; PCR primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN USG248319-B1.
 XX
 PD 19-JUN-2001.
 XX
 PF 24-MAY-1995; 95US-0449653.
 XX
 PR 10-APR-1991; 91US-0684535.
 PR 25-NOV-1992; 92US-0982255.
 PR 16-OCT-1989; 89US-0423283.
 PR 11-JUN-1990; 90US-0537198.
 PR 24-AUG-1990; 90US-0573616.
 PR 01-OCT-1990; 90US-0589701.
 PR 21-DEC-1993; 93US-0172329.
 XX
 PA (ZSEB/) ZSEBO K M.
 PA (BOSS/) BOSSELMAN R A.
 PA (SUGG/) SUGGS S V.
 PA (MART/) MARTIN F H.
 XX
 PI Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
 XX
 DR WPI; 2001-407312/43.
 XX
 PT Increasing the number of early haematopoietic progenitor cells in the
 PT peripheral blood useful for the treatment of blood disorders including
 PT Hodgkin's disease comprises the administration of human stem cell
 PT factor -
 XX
 PS Example 3; Fig 12C; 210pp; English.
 XX
 CC The present sequence for universal PCR primer 220-3 is 1 of 19
 CC PCR primers (AAS10435-AAS10453) used to amplify various portions of
 CC the human SCF cDNA sequence. The sequence is described in an
 CC invention relating to novel stem cell factors, the polynucleotides
 CC encoding them and methods for producing the stem cell factors. The
 CC methods involve increasing the number of early haematopoietic progenitor
 CC cells in human peripheral blood by administering a haematopoietically
 CC effective human stem cell factor polypeptide. The methods are useful for
 CC the treatment of blood disorders, including myelofibrosis,
 CC myelosclerosis, osteopetrosis, metastatic carcinoma, acute leukaemia,
 CC multiple myeloma, Hodgkin's disease, lymphoma, Gaucher's disease,
 CC Niemann-Pick disease, refractory anaemia, malaria, vitamin B12 and folic
 CC acid deficiency, hypopigmentation disorders i.e. piebaldism and viral
 CC induced disorders, including AIDS.
 XX
 SQ Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;

Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
 DB 18 AAAAAAAAAAAAAAAAAA 2

RESULT 376
 AAS10449/c
 ID AAS10449 standard; DNA; 20 BP.
 XX
 AC AAS10449;
 XX
 DT 24-OCT-2001 (first entry)
 XX
 DE Human stem cell factor (SCF) cDNA universal PCR primer 220-11.
 XX
 KW Human; stem cell factor; SCF; haematopoietic progenitor cell;
 KW blood disorder; Hodgkin's disease; vitamin B12; folic acid deficiency;
 KW hypopigmentation disorder; viral disorder; AIDS; PCR primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN USG248319-B1.
 XX
 PD 19-JUN-2001.
 XX
 PF 24-MAY-1995; 95US-0449653.
 XX
 PR 10-APR-1991; 91US-0684535.
 PR 25-NOV-1992; 92US-0982255.
 PR 16-OCT-1989; 89US-0423283.
 PR 11-JUN-1990; 90US-0537198.
 PR 24-AUG-1990; 90US-0573616.
 PR 01-OCT-1990; 90US-0589701.
 PR 21-DEC-1993; 93US-0172329.
 XX
 PA (ZSEB/) ZSEBO K M.
 PA (BOSS/) BOSSELMAN R A.
 PA (SUGG/) SUGGS S V.
 PA (MART/) MARTIN F H.
 XX
 PI Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
 XX
 DR WPI; 2001-407312/43.
 XX
 PT Increasing the number of early haematopoietic progenitor cells in the
 PT peripheral blood useful for the treatment of blood disorders including
 PT Hodgkin's disease comprises the administration of human stem cell
 PT factor -
 XX
 PS Example 3; Fig 12C; 210pp; English.
 XX
 CC The present sequence for universal PCR primer 220-11 is 1 of 19
 CC PCR primers (AAS10435-AAS10453) used to amplify various portions of
 CC the human SCF cDNA sequence. The sequence is described in an
 CC invention relating to novel stem cell factors, the polynucleotides
 CC encoding them and methods for producing the stem cell factors. The
 CC methods involve increasing the number of early haematopoietic progenitor
 CC cells in human peripheral blood by administering a haematopoietically
 CC effective human stem cell factor polypeptide. The methods are useful for
 CC the treatment of blood disorders, including myelofibrosis,
 CC myelosclerosis, osteopetrosis, metastatic carcinoma, acute leukaemia,
 CC multiple myeloma, Hodgkin's disease, lymphoma, Gaucher's disease,
 CC Niemann-Pick disease, refractory anaemia, malaria, vitamin B12 and folic
 CC acid deficiency, hypopigmentation disorders i.e. piebaldism and viral
 CC induced disorders, including AIDS.
 XX
 SQ Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;

```
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1084 AAAAAAAAAAAAAAAAAA 1100
Db 18 AAAAAAAAAAAAAAAAAA 2

RESULT 377
AAH46465/C
ID AAH46465 standard; DNA; 20 BP.
XX AC
XX AAH46465;
XX
DT 14-SEP-2001 (first entry)
XX DE Oligonucleotide #13.
XX KW Phosphorothioate; anti-viral therapy; stereochemical pathway; ss.
XX OS Synthetic.
XX FH Key Location/Qualifiers
FT modified_base 1..20
FT FT /*tag= a
FT FT /mod_base= "OTHER"
FT FT /note= "All bases are phosphorothioate"
FT FT modified_base 1
FT FT /*tag= b
FT FT /mod_base= "OTHER"
FT FT /note= "Modified with 2'-O-methyl"
XX
XX US6242591-B1.
XX
XX 05-JUN-2001.
XX
XX 11-JAN-2000; 2000US-0481486.
XX
XX 15-OCT-1997; 97US-0950779.
XX (ISIS-) ISIS PHARM INC.
XX
XX Cole DL, Ravikumar VT, Cheruvallath ZS;
XX WPI; 2001-407218/43.
XX
XX Preparing sulfurized 2' substituted phosphorothioate oligonucleotides
XX useful in biological research, comprises phosphorylating the
XX 5'-hydroxyl of a nucleic acid having a nucleoside with a 2'
XX modification -
XX
XX Example 23; Column 11; 7pp; English.
XX
XX The present invention relates to a method for preparing phosphorothioate
XX oligonucleotides having at least one nucleoside with a 2' modification.
XX The method comprises phosphorylating the 5'-hydroxyl of a nucleic acid
XX group having at least one nucleoside with a 2' modification in an
XX acetonitrile. The present sequence was used to illustrate the method of
XX the present invention. The method is useful for synthesizing sulphurised
XX 2' substituted phosphorothioate oligonucleotides, which may be used in
XX molecular biological research, in applications such as anti-viral
XX therapy, and for determining the stereochemical pathways of certain
XX enzymes which recognise nucleic acids.
XX
XX Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 other;
XX
XX Query Match 1.5%; Score 17; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 2.1e+02;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1084 AAAAAAAAAAAAAAAAAA 1100
Db 20 AAAAAAAAAAAAAAAAAA 4

RESULT 377
AAH46465/C
ID AAH46465 standard; DNA; 20 BP.
XX AC
XX AAH46465;
XX
DT 14-SEP-2001 (first entry)
XX DE Oligonucleotide #13.
XX KW Phosphorothioate; anti-viral therapy; stereochemical pathway; ss.
XX OS Synthetic.
XX FH Key Location/Qualifiers
FT modified_base 1..20
FT FT /*tag= a
FT FT /mod_base= "OTHER"
FT FT /note= "All bases are phosphorothioate"
FT FT modified_base 1
FT FT /*tag= b
FT FT /mod_base= "OTHER"
FT FT /note= "Modified with 2'-O-methyl"
XX
XX US6242591-B1.
XX
XX 05-JUN-2001.
XX
XX 11-JAN-2000; 2000US-0481486.
XX
XX 15-OCT-1997; 97US-0950779.
XX (ISIS-) ISIS PHARM INC.
XX
XX Cole DL, Ravikumar VT, Cheruvallath ZS;
XX WPI; 2001-407218/43.
XX
XX Preparing sulfurized 2' substituted phosphorothioate oligonucleotides
XX useful in biological research, comprises phosphorylating the
XX 5'-hydroxyl of a nucleic acid having a nucleoside with a 2'
XX modification -
XX
XX Example 23; Column 11; 7pp; English.
XX
XX The present invention relates to a method for preparing phosphorothioate
XX oligonucleotides having at least one nucleoside with a 2' modification.
XX The method comprises phosphorylating the 5'-hydroxyl of a nucleic acid
XX group having at least one nucleoside with a 2' modification in an
XX acetonitrile. The present sequence was used to illustrate the method of
XX the present invention. The method is useful for synthesizing sulphurised
XX 2' substituted phosphorothioate oligonucleotides, which may be used in
XX molecular biological research, in applications such as anti-viral
XX therapy, and for determining the stereochemical pathways of certain
XX enzymes which recognise nucleic acids.
XX
XX Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 other;
XX
XX Query Match 1.5%; Score 17; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 2.1e+02;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
RESULT 378
AAH41331/C
ID AAH41331 standard; DNA; 20 BP.
XX AC
XX AAH41331;
XX
DT 21-AUG-2001 (first entry)
XX DE Universal stem cell factor (SCF) related oligonucleotide SEQ ID NO:32.
XX KW Stem cell factor; SCF; stem cell factor receptor; blood cell disorder;
XX KW gene therapy; PCR primer; mutagenesis; probe; ss.
XX OS Synthetic.
XX
XX US6207454-B1.
XX
XX 27-MAR-2001.
XX
XX 31-DEC-1998; 98US-0224681.
XX
XX 21-DEC-1993; 93US-0172329.
XX 24-MAY-1995; 95US-0449653.
XX 12-JAN-1998; 98US-0005893.
XX 25-NOV-1992; 92US-0982255.
XX 16-OCT-1989; 89US-0422383.
XX 11-JUN-1990; 90US-0537198.
XX 24-AUG-1990; 90US-0573616.
XX 01-OCT-1990; 90US-0589701.
XX
XX (AMGE-) AMGEN INC.
XX
XX Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
XX WPI; 2001-366062/38.
XX
XX Enhancing efficiency of transfer of polynucleotide into a target
XX mammalian cell in vitro, involves exposing cell that expresses a stem
XX cell factor receptor to stem cell factor, and introducing
XX polynucleotide into cell in vitro -
XX
XX Example 3; Fig 12C; 210pp; English.
XX
XX The present invention describes a method for enhancing (E) the
XX efficiency of transfer of a polynucleotide (I) into a target mammalian
XX cell (II) in vitro, comprising exposing (II) that expresses a stem cell
XX factor (SCF) receptor to a biologically active SCF, its analogue or
XX fragment, which induces cell proliferation, and introducing (I) to (II)
XX in vitro. Exposure of SCF to (II) results in increased uptake of (I)
XX into the cell. The method is useful for enhancing the efficiency of the
XX transfer of a polynucleotide into a target mammalian cell in vitro.
XX The method is useful in gene therapy techniques. AAH41301 to AAH41364
XX and AAH98351 to AAH98390 represent sequences used in the exemplification
XX of the present invention.
XX
XX Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 other;
XX
XX Query Match 1.5%; Score 17; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 2.1e+02;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1084 AAAAAAAAAAAAAAAAAA 1100
Db 18 AAAAAAAAAAAAAAAAAA 2

RESULT 379
AAH41333/C
ID AAH41333 standard; DNA; 20 BP.
XX AC
XX AAH41333;
XX
```

DT 21-AUG-2001 (first entry)
 XX Universal stem cell factor (SCF) related oligonucleotide SEQ ID NO:34.
 DE
 XX
 XX Stem cell factor; SCF; stem cell factor receptor; blood cell disorder;
 KW gene therapy; PCR primer; mutagenesis; probe; ss.
 XX
 XX Synthetic.
 OS
 XX US6207454-B1.
 PN
 XX 27-MAR-2001.
 PD
 XX 31-DEC-1998; 98US-0224681.
 PF
 XX 21-DEC-1993; 93US-0172329.
 PR 24-MAY-1995; 95US-0449653.
 PR 12-JAN-1998; 98US-0005893.
 PR 25-NOV-1992; 92US-0982255.
 PR 16-OCT-1989; 89US-0422383.
 PR 11-JUN-1990; 90US-0537198.
 PR 24-AUG-1990; 90US-0573616.
 PR 01-OCT-1990; 90US-0589701.
 XX (AMGE-) AMGEN INC.
 PA
 XX Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
 PI WPI; 2001-366062/38.
 XX
 XX Enhancing efficiency of transfer of polynucleotide into a target
 PT mammalian cell in vitro, involves exposing cell that expresses a stem
 PT cell factor receptor to stem cell factor, and introducing
 PT polynucleotide into cell in vitro -
 XX
 XX Example 3; Fig 12C; 210pp; English.
 PS
 XX The present invention describes a method for enhancing (E) the
 CC efficiency of transfer of a polynucleotide (I) into a target mammalian
 CC cell (II) in vitro, comprising exposing (II) that expresses a stem cell
 CC factor (SCF) receptor to a biologically active SCF, its analogue or
 CC fragment, which induces cell proliferation, and introducing (I) to (II)
 CC in vitro. Exposure of SCF to (II) results in increased uptake of (I)
 CC into the cell. The method is useful for enhancing the efficiency of the
 CC transfer of a polynucleotide into a target mammalian cell in vitro.
 CC The method is useful in gene therapy techniques. AAH41301 to AAH41364
 CC and AAB98351 to AAB98390 represent sequences used in the exemplification
 CC of the present invention.
 XX
 XX Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 other;
 SQ Query Match 1.5%; Score 17; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1084 AAAAAAAAAAAAAAAAAA 1100
 Db 18 AAAAAAAAAAAAAAAAAA 2
 RESULT 380
 AAS04111/C
 ID AAS04111 standard; DNA; 20 BP.
 XX
 AC AAS04111;
 XX
 XX 29-AUG-2001 (first entry)
 DT
 XX Human SCF (stem cell factor) cDNA universal PCR primer 220-3.
 DE
 XX Human; stem cell factor; SCF; early haematopoietic progenitor cell;
 KW blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;
 KW anaemia; Kala azar; septicemia; malaria; hypopigmentation disorder;

KW PCR primer; ss.
 XX
 XX Homo sapiens.
 XX
 PN US6207417-B1.
 XX
 XX 27-MAR-2001.
 PD
 XX 07-JUN-1995; 95US-0482918.
 PF
 XX 21-DEC-1993; 93US-0172329.
 PR 16-OCT-1989; 89US-0422383.
 PR 11-JUN-1990; 90US-0537198.
 PR 24-AUG-1990; 90US-0573616.
 PR 01-OCT-1990; 90US-0589701.
 XX (ZSEB/) ZSEBO K M.
 PA (BOSS/) BOSSELMAN R A.
 PA (SUGG/) SUGGS S V.
 PA (MART/) MARTIN F H.
 XX
 PI Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
 XX WPI; 2001-298941/31.
 DR
 XX Novel nucleic acids encoding stem cell factor useful for treating
 PT disorders involving blood cells, e.g. leukaemia, splenomegaly, Hodgkin's
 PT disease, Kala azar, anaemia and septicemia -
 XX
 XX Example 3; Fig 12C; 209pp; English.
 PS
 XX The present sequence for universal PCR primer 220-3 is 1 of 8
 CC universal oligonucleotides (AAS04110-AAS04117) used in the
 CC isolation of the human SCF (stem cell factor) cDNA sequence. The
 CC present invention relates to novel stem cell factors
 CC (AAU02453-AAU02458, AAU02460, AAU02461) and the polynucleotides
 CC encoding them. SCF stimulate primitive progenitor cells including early
 CC haematopoietic progenitor cells. The invention also describes SCF
 CC peptides (AAU02462-AAU02481) and the oligonucleotides
 CC (AAS04081-AAS04117) used in the isolation of human and rat SCF
 CC sequences. The polynucleotide encoding SCF is useful for producing SCF
 CC and useful in gene therapy. It is useful for treating disorders
 CC involving blood cells such as myelofibrosis, metastatic carcinoma,
 CC acute leukaemia, multiple myeloma, Hodgkin's disease, lymphoma,
 CC Gaucher's disease, anaemia, congestive splenomegaly, Kala azar,
 CC sarcoidosis, military tuberculosis, disseminated fungus disease,
 CC fulminating septicemia, malaria, vitamin B12 and folic acid deficiency,
 CC pyridoxine deficiency, and hypopigmentation disorders such as
 CC piebaldism and vitiligo.
 XX
 XX Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 other;
 SQ Query Match 1.5%; Score 17; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1084 AAAAAAAAAAAAAAAAAA 1100
 Db 18 AAAAAAAAAAAAAAAAAA 2
 RESULT 381
 AAS04113/C
 ID AAS04113 standard; DNA; 20 BP.
 XX
 AC AAS04113;
 XX
 XX 29-AUG-2001 (first entry)
 DT
 XX Human SCF (stem cell factor) cDNA universal PCR primer 220-11.
 DE
 XX Human; stem cell factor; SCF; early haematopoietic progenitor cell;
 KW blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;

KW anaemia; kala azar; septicemia; malaria; hypopigmentation disorder;
 KW PCR primer; ss.
 XX Homo sapiens.
 XX US6207417-B1.
 XX 27-MAR-2001.
 XX 07-JUN-1995; 95US-0482918.
 XX 21-DEC-1993; 93US-0172329.
 XX 16-OCT-1989; 89US-0422383.
 XX 11-JUN-1990; 90US-0537198.
 XX 24-AUG-1990; 90US-0573616.
 XX 01-OCT-1990; 90US-0589701.
 XX (ZSEB/) ZSEBO K M.
 XX (BOSS/) BOSSLMAN R A.
 XX (SUGG/) SUGGS S V.
 XX (MART/) MARTIN F H.
 XX Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
 XX WPI; 2001-298941/31.
 XX Novel nucleic acids encoding stem cell factor useful for treating
 XX disorders involving blood cells, e.g. leukaemia, splenomegaly, Hodgkin's
 XX disease, kala azar, anaemia and septicemia -
 XX Example 3; Fig 12C; 203pp; English.
 XX The present sequence for universal PCR primer 220-11 is 1 of 8
 XX universal oligonucleotides (AAS04110-AAS04117) used in the
 XX isolation of the human SCF (stem cell factor) cDNA sequence. The
 XX present invention relates to novel stem cell factors
 XX (AAU02453-AAU02458, AAU02460, AAU02461) and the polynucleotides
 XX encoding them. SCF stimulate primitive progenitor cells including early
 XX haematopoietic progenitor cells. The invention also describes SCF
 XX peptides (AAU02462-AAU02481) and the oligonucleotides
 XX (AAS04081-AAS04117) used in the isolation of human and rat SCF
 XX sequences. The polynucleotide encoding SCF is useful for producing SCF
 XX and useful in gene therapy. It is useful for treating disorders
 XX involving blood cells such as myelofibrosis, metastatic carcinoma,
 XX acute leukaemia, multiple myeloma, Hodgkin's disease, lymphoma,
 XX Gaucher's disease, anaemia, congestive splenomegaly, kala azar,
 XX sarcoidosis, military tuberculosis, disseminated fungus disease,
 XX Fulminating septicemia, malaria, vitamin B12 and folic acid deficiency,
 XX pyridoxine deficiency, and hypopigmentation disorders such as
 XX piebaldism and vitiligo.
 XX Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 other;
 SQ Query Match 1.5%; Score 17; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1084 AAAAAAAAAAAAAAAAAA 1100
 DB 18 AAAAAAAAAAAAAAAAAA 2
 RESULT 382
 AAS04212/C
 ID AAS04212 standard; DNA; 20 BP.
 XX AC AAS04212;
 XX 29-AUG-2001 (first entry)
 XX Human SCF (stem cell factor) cDNA universal PCR primer 220-3.
 DE Human; stem cell factor; SCF; early haematopoietic progenitor cell;
 KW blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;
 KW anaemia; kala azar; septicemia; malaria; hypopigmentation disorder;
 KW PCR primer; ss.

KW blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;
 KW anaemia; kala azar; septicemia; malaria; hypopigmentation disorder;
 XX PCR primer; ss.
 XX Homo sapiens.
 XX US6218148-B1.
 XX 17-APR-2001.
 XX 21-DEC-1993; 93US-0172329.
 XX 25-NOV-1992; 92US-0982255.
 XX 16-OCT-1989; 89US-0422383.
 XX 11-JUN-1990; 90US-0537198.
 XX 24-AUG-1990; 90US-0573616.
 XX 01-OCT-1990; 90US-0589701.
 XX (AMGE-) AMGEN INC.
 XX Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
 XX WPI; 2001-281051/29.
 XX Isolated DNA sequence, encoding polypeptide product useful for
 XX stimulating growth of early haematopoietic progenitor cells -
 XX Example 3; Fig 12C; 167pp; English.
 XX The present sequence for universal PCR primer 220-3 is 1 of 8
 XX universal oligonucleotides (AAS04211-AAS04218) used in the
 XX isolation of the human SCF (stem cell factor) cDNA sequence. The
 XX present invention relates to novel stem cell factors
 XX (AAU02761-AAU02767, AAU02770-AAU02775, AAU02797) and the polynucleotides
 XX encoding them. SCF stimulate primitive progenitor cells including early
 XX haematopoietic progenitor cells. The invention also describes SCF
 XX peptides (AAU02777-AAU02794) and the oligonucleotides
 XX (AAS04182-AAS04210) used in the isolation of human and rat SCF
 XX sequences. The polynucleotide encoding SCF is useful for producing SCF
 XX and useful in gene therapy. It is useful for treating disorders
 XX involving blood cells such as myelofibrosis, metastatic carcinoma,
 XX acute leukaemia, multiple myeloma, Hodgkin's disease, lymphoma,
 XX Gaucher's disease, anaemia, congestive splenomegaly, kala azar,
 XX sarcoidosis, military tuberculosis, disseminated fungus disease,
 XX Fulminating septicemia, malaria, vitamin B12 and folic acid deficiency,
 XX pyridoxine deficiency, and hypopigmentation disorders such as
 XX piebaldism and vitiligo.
 XX Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 other;
 SQ Query Match 1.5%; Score 17; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1084 AAAAAAAAAAAAAAAAAA 1100
 DB 18 AAAAAAAAAAAAAAAAAA 2
 RESULT 383
 AAS04214/C
 ID AAS04214 standard; DNA; 20 BP.
 XX AC AAS04214;
 XX 29-AUG-2001 (first entry)
 XX Human SCF (stem cell factor) cDNA universal PCR primer 220-11.
 DE Human; stem cell factor; SCF; early haematopoietic progenitor cell;
 KW blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;
 KW anaemia; kala azar; septicemia; malaria; hypopigmentation disorder;
 KW PCR primer; ss.

XX OS Homo sapiens.
 XX PN US6218148-B1.
 XX PD 17-APR-2001.
 XX PF 21-DEC-1993; 93US-0172329.
 XX PR 25-NOV-1992; 92US-0982255.
 XX PR 16-OCT-1989; 89US-0422383.
 XX PR 11-JUN-1990; 90US-0537198.
 XX PR 24-AUG-1990; 90US-0573616.
 XX PR 01-OCT-1990; 90US-0589701.
 XX PA (AMGE-) AMGEN INC.
 XX PI Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
 XX WPI; 2001-281051/29.
 XX DR Isolated DNA sequence, encoding polypeptide product useful for
 XX PT stimulating growth of early haematopoietic progenitor cells -
 XX PS Example 3; Fig 12C; 167pp; English.
 XX PS The present sequence for universal PCR primer 220-11 is 1 of 8
 XX CC universal oligonucleotides (AAS04211-AAS04218) used in the
 XX CC isolation of the human SCF (stem cell factor) cDNA sequence. The
 XX CC present invention relates to novel stem cell factors
 XX CC (AAU02761-AAU02767, AAU02770-AAU02775, AAU02797) and the polynucleotides
 XX CC encoding them. SCF stimulate primitive progenitor cells including early
 XX CC haematopoietic progenitor cells. The invention also describes SCF
 XX CC peptides (AAU02777-AAU02794) and the oligonucleotides
 XX CC (AAS04182-AAS04210) used in the isolation of human and rat SCF
 XX CC sequences. The polynucleotide encoding SCF is useful for producing SCF
 XX CC and useful in gene therapy. It is useful for treating disorders
 XX CC involving blood cells such as myelofibrosis, metastatic carcinoma,
 XX CC acute leukaemia, multiple myeloma, Hodgkin's disease, lymphoma,
 XX CC Gaucher's disease, anaemia, congestive splenomegaly, kala azar,
 XX CC sarcoidosis, military tuberculosis, disseminated fungus disease,
 XX CC Fulminating septicemia, malaria, vitamin B12 and folic acid deficiency,
 XX CC pyridoxine deficiency, and hypopigmentation disorders such as
 XX CC piebaldism and vitiligo.
 XX SQ Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1084 AAAAAAAAAAAAAAAAAA 1100
 Db 18 AAAAAAAAAAAAAAAAAA 2
 RESULT 384
 AAH23889/c
 ID AAH23889 standard; DNA; 20 BP.
 XX AC AAH23889;
 XX DT 07-AUG-2001 (first entry)
 XX DE Human SCF (stem cell factor) cDNA universal PCR primer 220-3.
 XX KW Human; stem cell factor; SCF; early haematopoietic progenitor cell;
 XX KW blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;
 XX KW anaemia; kala azar; septicemia; malaria; hypopigmentation disorder;
 XX KW PCR primer; ss.
 XX OS Homo sapiens.
 XX PN US6218148-B1.

PN US6204363-B1.
 XX PD 20-MAR-2001.
 XX PF 25-NOV-1992; 92US-0982255.
 XX PR 10-APR-1991; 91US-0684535.
 XX PR 16-OCT-1989; 89US-0422383.
 XX PR 11-JUN-1990; 90US-0537198.
 XX PR 24-AUG-1990; 90US-0573616.
 XX PR 01-OCT-1990; 90US-0589701.
 XX PA (AMGE-) AMGEN INC.
 XX PI Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
 XX WPI; 2001-256683/26.
 XX DR New stem cell factor polypeptides and their analogs which stimulate
 XX PT growth of early hematopoietic progenitors, useful for treating aplastic
 XX PT anemia, carcinoma, multiple myeloma, vitiligo, kala azar, Hodgkin's
 XX PT disease -
 XX PS Example 3; Fig 12C; 166pp; English.
 XX PS The present sequence for universal PCR primer 220-3 is 1 of 8
 XX CC universal oligonucleotides (AAH23888-AAH23895) used in the
 XX CC isolation of the human SCF (stem cell factor) cDNA sequence. The
 XX CC present invention relates to novel stem cell factors
 XX CC (AAH73561-AAH73568, AAH73571-AAH73576) and the polynucleotides
 XX CC encoding them. SCF stimulate primitive progenitor cells including early
 XX CC haematopoietic progenitor cells. The invention also describes SCF
 XX CC peptides (AAH73578-AAH73597) and the oligonucleotides
 XX CC (AAH23859-AAH23887) used in the isolation of human and rat SCF
 XX CC sequences. The polynucleotide encoding SCF is useful for producing SCF
 XX CC and useful in gene therapy. It is useful for treating disorders
 XX CC involving blood cells such as myelofibrosis, metastatic carcinoma,
 XX CC acute leukaemia, multiple myeloma, Hodgkin's disease, lymphoma,
 XX CC Gaucher's disease, anaemia, congestive splenomegaly, kala azar,
 XX CC sarcoidosis, military tuberculosis, disseminated fungus disease,
 XX CC Fulminating septicemia, malaria, vitamin B12 and folic acid deficiency,
 XX CC pyridoxine deficiency, and hypopigmentation disorders such as
 XX CC piebaldism and vitiligo.
 XX SQ Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1084 AAAAAAAAAAAAAAAAAA 1100
 Db 18 AAAAAAAAAAAAAAAAAA 2
 RESULT 385
 AAH23891/c
 ID AAH23891 standard; DNA; 20 BP.
 XX AC AAH23891;
 XX DT 07-AUG-2001 (first entry)
 XX DE Human SCF (stem cell factor) cDNA universal PCR primer 220-11.
 XX KW Human; stem cell factor; SCF; early haematopoietic progenitor cell;
 XX KW blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;
 XX KW anaemia; kala azar; septicemia; malaria; hypopigmentation disorder;
 XX KW PCR primer; ss.
 XX OS Homo sapiens.
 XX PN US6204363-B1.

```

XX PD 20-MAR-2001.
XX PF
XX PF 25-NOV-1992; 92US-0982255.
XX PR
XX PR 10-APR-1991; 91US-0694535.
XX PR 16-OCT-1989; 89US-0422383.
XX PR 11-JUN-1990; 90US-0537198.
XX PR 24-AUG-1990; 90US-0573616.
XX PR 01-OCT-1990; 90US-0589701.
XX PA (AMGE-) AMGEN INC.
XX PT
XX PI Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
XX PI WPI; 2001-256683/26.
XX DR
XX DR New stem cell factor polypeptides and their analogs which stimulate
XX PT growth of early hematopoietic progenitors, useful for treating aplastic
XX PT anemia, carcinoma, multiple myeloma, vitiligo, kala azar, Hodgkin's
XX PT disease -
XX PS Example 3; Fig 12C; 166pp; English.
XX SS
XX CC The present sequence for universal PCR primer 220-11 is 1 of 8
XX CC universal oligonucleotides (AAH23888-AAH23895) used in the
XX CC isolation of the human SCF (stem cell factor) cDNA sequence. The
XX CC present invention relates to novel stem cell factors
XX CC (AAB73561-AAB73568, AAB73571-AAB73576) and the polynucleotides
XX CC encoding them. SCF stimulate primitive progenitor cells including early
XX CC haematopoietic progenitor cells. The invention also describes SCF
XX CC peptides (AAB73578-AAB73597) and the oligonucleotides
XX CC (AAH23859-AAH23887) used in the isolation of human and rat SCF
XX CC sequences. The polynucleotide encoding SCF is useful for producing SCF
XX CC and useful in gene therapy. It is useful for treating disorders
XX CC involving blood cells such as myelofibrosis, metastatic carcinoma,
XX CC acute leukaemia, multiple myeloma, Hodgkin's disease, lymphoma,
XX CC Gaucher's disease, anaemia, congestive splenomegaly, Kala azar,
XX CC sarcoidosis, military tuberculosis, disseminated fungus disease,
XX CC fulminating septicemia, malaria, vitamin B12 and folic acid deficiency,
XX CC pyridoxine deficiency, and hypopigmentation disorders such as
XX CC piebaldism and vitiligo.
XX SQ Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1084 AAAAAAAAAAAAAAAAAA 1100
Db 18 AAAAAAAAAAAAAAAAAA 2

RESULT 386
AAF99099/c
ID AAF99099 standard; DNA; 20 BP.
XX AC
XX AC AAF99099;
XX DT 12-JUN-2001 (first entry)
XX DE Immunostimulatory nucleic acid #215.
XX KW Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
XX KW immunostimulatory; tumour; viral infection; bacterial infection;
XX KW fungal infection; parasitic infection; cancer; asthma;
XX KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.
XX OS Synthetic.
XX PN WO200122972-A2.
XX PR 25-SEP-1999; 99US-0156113.
XX PR 27-SEP-1999; 99US-0156135.
XX PR 23-AUG-2000; 2000US-0227436.

```

```

PD 05-APR-2001.
XX PF
XX PF 25-SEP-2000; 2000WO-US26383.
XX PR
XX PR 25-SEP-1999; 99US-0156113.
XX PR 27-SEP-1999; 99US-0156135.
XX PR 23-AUG-2000; 2000US-0227436.
XX PA (IOWA ) UNIV IOWA RES FOUND.
XX PA (COLE-) COLEY PHARM GMBH.
XX PT
XX PI Krieg AM, Schetter C, Vollmer J;
XX PI WPI; 2001-273485/28.
XX DR
XX DR Vaccinating against tumors, infectious diseases, allergies and asthma
XX PT using immunostimulatory Py-rich and TG nucleic acids -
XX PS Claim 101; Page 42; 338pp; English.
XX SS
XX CC The present invention relates to a method for stimulating an immune
XX CC response. The method comprises administering an immunostimulatory nucleic
XX CC acid to a non-rodent subject in sufficient quantity to stimulate an
XX CC immune response. The present sequence is one such immunostimulatory
XX CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
XX CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
XX CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
XX CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
XX CC haemophilus, campylobacter, clostridium, Escherichia coli and/or
XX CC staphylococcus), fungal antigens and/or parasitic antigens. The method is
XX CC also useful for preventing cancer, asthma, infectious disease, allergy or
XX CC immune deficiency. The present sequence can also be used to redirect a
XX CC Th2 to a Th1 immune response and to activate immune cells.
XX CC Note: the present sequence may have a phosphorothioate backbone.
XX SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1084 AAAAAAAAAAAAAAAAAA 1100
Db 20 AAAAAAAAAAAAAAAAAA 4

RESULT 387
AAF99427/c
ID AAF99427 standard; DNA; 20 BP.
XX AC
XX AC AAF99427;
XX DT 12-JUN-2001 (first entry)
XX DE Immunostimulatory nucleic acid #543.
XX KW Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
XX KW immunostimulatory; tumour; viral infection; bacterial infection;
XX KW fungal infection; parasitic infection; cancer; asthma;
XX KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.
XX OS Synthetic.
XX PN WO200122972-A2.
XX PR 05-APR-2001.
XX PR 25-SEP-2000; 2000WO-US26383.
XX PR 25-SEP-1999; 99US-0156113.
XX PR 27-SEP-1999; 99US-0156135.
XX PR 23-AUG-2000; 2000US-0227436.

```

PA (IOWA) UNIV IOWA RES FOUND.
 PA (COLE-) COLEY PHARM GMBH.
 XX Krieg AM, Schetter C, Vollmer J;
 XX WPI; 2001-273485/28.
 DR Vaccinating against tumors, infectious diseases, allergies and asthma
 PT using immunostimulatory Py-rich and TG nucleic acids -
 XX Claim 101; Page 49; 338pp; English.
 XX The present invention relates to a method for stimulating an immune
 CC response. The method comprises administering an immunostimulatory nucleic
 CC acid to a non-rodent subject in sufficient quantity to stimulate an
 CC immune response. The present sequence is one such immunostimulatory
 CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
 CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
 CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
 CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
 CC haemophilus, campylobacter, clostridium, Escherichia coli and/or
 CC staphylococcus), fungal antigens and/or parasitic antigens. The method is
 CC also useful for preventing cancer, asthma, infectious disease, allergy or
 CC immune deficiency. The present sequence can also be used to redirect a
 CC Th2 to a Th1 immune response and to activate immune cells.
 CC Note: the present sequence may have a phosphorothioate backbone.
 XX Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 other;
 SQ Query Match 1-5%; Score 17; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1084 AAAAAAAAAAAAAAAAAA 1100
 Db 20 AAAAAAAAAAAAAAAAAA 4
 RESULT 388
 AAF99431
 ID AAF99431 standard; DNA; 20 BP.
 AC AAF99431;
 XX 12-JUN-2001 (first entry)
 DT Immunostimulatory nucleic acid #547.
 DE Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
 KW immunostimulatory; tumour; viral infection; bacterial infection;
 KW fungal infection; parasitic infection; cancer; asthma;
 KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.
 OS Synthetic.
 XX WO200122972-A2.
 XX 05-APR-2001.
 XX 25-SEP-2000; 2000WO-US26383.
 XX 25-SEP-1999; 99US-0156113.
 PR 27-SEP-1999; 99US-0156135.
 PR 23-AUG-2000; 2000US-0227436.
 XX (IOWA) UNIV IOWA RES FOUND.
 PA (COLE-) COLEY PHARM GMBH.
 XX Krieg AM, Schetter C, Vollmer J;
 XX WPI; 2001-273485/28.
 DR Vaccinating against tumors, infectious diseases, allergies and asthma
 PT using immunostimulatory Py-rich and TG nucleic acids -
 XX Claim 101; Page 49; 338pp; English.
 XX The present invention relates to a method for stimulating an immune
 CC response. The method comprises administering an immunostimulatory nucleic
 CC acid to a non-rodent subject in sufficient quantity to stimulate an
 CC immune response. The present sequence is one such immunostimulatory
 CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
 CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
 CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
 CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
 CC haemophilus, campylobacter, clostridium, Escherichia coli and/or
 CC staphylococcus), fungal antigens and/or parasitic antigens. The method is
 CC also useful for preventing cancer, asthma, infectious disease, allergy or
 CC immune deficiency. The present sequence can also be used to redirect a
 CC Th2 to a Th1 immune response and to activate immune cells.
 CC Note: the present sequence may have a phosphorothioate backbone.
 XX Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 other;
 SQ Query Match 1-5%; Score 17; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1084 AAAAAAAAAAAAAAAAAA 1100
 Db 20 AAAAAAAAAAAAAAAAAA 4
 RESULT 388
 AAF99431
 ID AAF99431 standard; DNA; 20 BP.
 AC AAF99431;
 XX 12-JUN-2001 (first entry)
 DT Immunostimulatory nucleic acid #547.
 DE Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
 KW immunostimulatory; tumour; viral infection; bacterial infection;
 KW fungal infection; parasitic infection; cancer; asthma;
 KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.
 OS Synthetic.
 XX WO200122972-A2.
 XX 05-APR-2001.
 XX 25-SEP-2000; 2000WO-US26383.
 XX 25-SEP-1999; 99US-0156113.
 PR 27-SEP-1999; 99US-0156135.
 PR 23-AUG-2000; 2000US-0227436.
 XX (IOWA) UNIV IOWA RES FOUND.
 PA (COLE-) COLEY PHARM GMBH.
 XX Krieg AM, Schetter C, Vollmer J;
 XX WPI; 2001-273485/28.
 DR Vaccinating against tumors, infectious diseases, allergies and asthma
 PT using immunostimulatory Py-rich and TG nucleic acids -
 XX Claim 101; Page 49; 338pp; English.
 XX The present invention relates to a method for stimulating an immune
 CC response. The method comprises administering an immunostimulatory nucleic
 CC acid to a non-rodent subject in sufficient quantity to stimulate an
 CC immune response. The present sequence is one such immunostimulatory
 CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
 CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
 CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
 CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
 CC haemophilus, campylobacter, clostridium, Escherichia coli and/or
 CC staphylococcus), fungal antigens and/or parasitic antigens. The method is
 CC also useful for preventing cancer, asthma, infectious disease, allergy or
 CC immune deficiency. The present sequence can also be used to redirect a
 CC Th2 to a Th1 immune response and to activate immune cells.
 CC Note: the present sequence may have a phosphorothioate backbone.
 XX Sequence 20 BP; 0 A; 0 C; 0 G; 0 U; 0 other;
 SQ Query Match 1-5%; Score 17; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1084 AAAAAAAAAAAAAAAAAA 1100
 Db 1 AAAAAAAAAAAAAAAAAA 17
 RESULT 389
 AAF60896
 ID AAF60896 standard; DNA; 20 BP.
 AC AAF60896;
 XX 15-MAY-2001 (first entry)
 DT Conjugate forming oligonucleotide ON5 SEQ ID 5.
 DE Transport; membrane; cytostatic; virucide; vasotropic; dermatological;
 KW antiparasitic; antiasthmatic; gene therapy; tumor cell; antisense;
 KW tumor therapy; drug; phosphodiester linkage; ss.
 XX Unidentified.
 OS DE19935302-A1.
 XX 08-FEB-2001.
 XX 28-JUL-1999; 99DE-1035302.
 XX 28-JUL-1999; 99DE-1035302.
 XX (AVET) AVENTIS PHARMA DEUT GMBH.
 XX Uhlmann E, Greiner B, Unger E, Gothe G, Schwerdel M;
 PI WPI; 2001-203679/21.
 DR New substituted aryl conjugates of parent molecules, especially
 PT oligonucleotides, having improved transmembrane and intracellular
 PT transport properties, useful as medicaments or diagnostic agents -
 XX Disclosure; Page 9; 28pp; German.
 XX This invention describes a novel conjugate (I) which consists of (A) a
 CC molecule to be transported and (B) at least one aryl residue of formula
 CC -Ar-(X-C(Y)-R.1) n (II). Ar = group containing at least one aromatic
 CC ring; X = O or N (sic); Y = O, S or NH-R.2 (sic); R.1 = optionally
 CC substituted 1-23C alkyl (optionally containing double and/or triple
 CC bonds); R.2 = optionally substituted 1-18C alkyl (optionally containing
 CC double and/or triple bonds); n = integer of 1 or more. (A) is bonded to

CC (B) directly or via a chemical group, provided that the chemical group is
CC other than CH₂-S if the bond is via a phosphodiester linkage of (A). The
CC invention also describes (i) the preparation of a conjugate (I') of (A')
CC a molecule to be transported and (B') at least one aryl residue (not
CC restricted to (ii)), by preparing (A') containing a reactive function at
CC the position at which (B') is to be bonded, preparing (B') and reacting
CC (A') and (B'); and (ii) the use of aryl groups (II) (optionally bonded
CC via a chemical group) for transporting (A) across biological membranes.
CC The products of the invention have cytostatic, virucide, vasotropic,
CC dermatological, antipsoriatic and antiasthmatic activity and can be used
CC for gene therapy. Conjugation of (A) with (B) is useful for transporting
CC (A) across biological membranes or into eukaryotic or prokaryotic cells
CC (specifically bacterial, yeast or mammalian cells, including human cells,
CC particularly tumor cells). Medicaments, diagnostic agents and test kits
CC containing (I) are also claimed. Typically (I) are antisense
CC oligonucleotide derivatives for tumor therapy; oligonucleotide drugs for
CC treating viral infections or diseases associated with integrins or
CC cell-cell interactions (e.g. restenosis, vitiligo, psoriasis or asthma);
CC or labeled oligonucleotides for in vivo diagnostic use, e.g. by in situ
CC hybridization. Conjugation with (B) markedly improves the cellular uptake
CC of (A), e.g. in tumor cells. (B) include fluorescein derivative residues,
CC in which case the conjugates (I) are fluorescently labeled, allowing
CC microscopic monitoring of cellular uptake etc. The cellular uptake of (I)
CC is superior to that obtained using other conjugated groups related to
CC (ii); e.g. oligonucleotides conjugated with fluorescein diacetate (within
CC the scope of (B)) have superior uptake to corresponding fluorescein
CC conjugates.

SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 U; 0 other;
Query Match 1.5%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1084 AAAAAAAAAAAAAAAAAA 1100
Db 1 AAAAAAAAAAAAAAAAAA 17

RESULT 390
AAF28351
ID AAF28351 standard; DNA; 20 BP.
AC AAF28351;
XX
DT 02-APR-2001 (first entry)
XX
DE DNA oligomer #1.
XX
KW Deoxynucleic S-Methylthiouracil; DNmt; antisense therapy;
KW cardiovascular disease; inflammatory disease; neurocellular disease;
KW antiviral therapy; human immunodeficiency virus; human-cytomegalovirus;
KW influenza; herpes; infection; ss.
XX

OS Unidentified.
XX
EN US6169176-B1.
XX
PD 02-JAN-2001.
XX
PF 28-SEP-1999; 99US-0407675.
XX
PR 02-JUL-1998; 99US-0091481.
PR 11-DEC-1998; 99US-0111800.
PR 02-JUL-1999; 99US-0347443.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Dev AP, Bruce TC;
XX
XX WPI; 2001-122276/13.
XX
PT Preparing novel deoxynucleic alkyl thiourea oligonucleotide for use in

PT antisense therapy, by synthesizing oligonucleotides comprising backbone
PT of alkyl or alkoxy thiourea linkages in solution or on solid phase -
XX Example 7; Fig 16; 48pp; English.

PS The present sequence was used to demonstrate the ability of deoxynucleic
CC S-Methylthiouracil (DNmt) compounds to form triplexes with DNA oligomers. An
CC increase in the C content of the oligos resulted in a large decrease in
CC binding. This experiment was performed as an example of a method for
CC preparing oligonucleotides comprising a backbone of alkyl or alkoxy
CC thiourea linkages. The method is useful for preparing oligonucleotides
CC for use in antisense or antigenic therapy, to inhibit production of
CC proteins associated with genetic diseases, cardiovascular, inflammatory
CC and neurocellular diseases, and for antiviral therapy, e.g. to treat
CC human immunodeficiency virus, human-cytomegalovirus, influenza and
CC herpes infections. The compounds are also useful as diagnostic reagents
CC to detect the presence or absence of the target DNA or RNA sequences to
CC which they specifically bind and by antagonizing the normal biological
CC activity of a target protein, they can be used in the manipulation of
CC tissue e.g. tissue differentiation, both in vivo and in ex vivo tissue
CC cultures. The method provides an efficient and rapid solid-phase method
CC for the synthesis of thiourea and S-methylthiouracil.

SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 U; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1084 AAAAAAAAAAAAAAAAAA 1100
Db 1 AAAAAAAAAAAAAAAAAA 17

RESULT 391
AAF28481
ID AAF28481 standard; DNA; 20 BP.
XX
AC AAF28481;
XX
DT 03-APR-2001 (first entry)
XX
DE Random oligonucleotide, SEQ ID NO: 53.
XX
KW Nucleic acid detection; nanoparticle-oligonucleotide conjugate;
KW disease diagnosis; forensic analysis; DNA sequencing; paternity testing;
KW cell line authentication; gene therapy; ss.
XX

OS Synthetic.

XX WO200100876-A1.

XX 04-JAN-2001.

XX 26-JUN-2000; 2000WO-US17507.

XX 25-JUN-1999; 99US-0344667.

XX 26-APR-2000; 2000US-0200161.

XX (MIRK)/ MIRKIN C A.

XX (LETS)/ LETSINGER R L.

XX (MUCI)/ MUCIC R C.

XX (STOR)/ STORHOFF J J.

XX (ELGH)/ ELGHANIAN R.

XX (TATO)/ TATON T A.

XX Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;
PI Taton TA;

XX WPI; 2001-061976/07.

XX
PT Detecting nucleic acid, useful for e.g. diagnosis of diseases,
PT forensics and DNA sequencing, comprises observing detectable change

PT brought about by hybridization of nucleic acid with substrate or
 PT particle bound oligonucleotides -

XX Disclosure; Page 199; 205pp; English.

XX The present sequence is an oligonucleotide used in a method for detecting
 CC a nucleic acid having at least 2 portions. The method comprises
 CC hybridizing the nucleic acid with oligonucleotides, such as the present
 CC sequence, attached to a substrate and/or particle and detecting a change
 CC in colour, conductivity or optical density. The method is useful for the
 CC diagnosis and/or monitoring of diseases, in forensics, in DNA sequencing,
 CC for paternity testing, for cell line authentication and for monitoring
 CC gene therapy. Detecting nucleic acids based upon observing a colour
 CC change is cheap, fast, simple, and does not require specialised or
 CC expensive equipment. The nanoparticle oligonucleotide conjugates remain
 CC stable for at least 6 months. A single base mismatch and as little as 20
 CC femtomoles (fm) of target can be detected using the conjugates.

XX Sequence 20 BP; 20 A; 0 C; 0 G; 0 U; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
 DB 1 AAAAAAAAAAAAAAAAAA 17

RESULT 392
 AAC87230/C

ID AAC87230 standard; DNA; 20 BP.

XX AAC87230;

DT 09-MAR-2001 (first entry)

DE Digoxigenin-labelled poly T oligonucleotide, SEQ ID NO:9.

XX Immunostimulatory oligodeoxynucleotide; immunostimulatory ODN;
 KW immunostimulatory DNA-binding protein; nucleolin; hrNP D; AUF1;
 KW hrNP A1; lupus La protein; functional modifier identification;
 KW agonist; antagonist; mimic; inhibitor; drug screening;
 KW cellular target identification; oligonucleotide optimisation;
 KW immunotherapy; ss.

XX Synthetic.

XX WO200067023-A1.

XX 09-NOV-2000.

XX 28-APR-2000; 2000WO-US11697.

XX 29-APR-1999; 99US-0131830.

XX 03-MAR-2000; 2000US-0186845.

XX (CPGI-) CPG IMMUNOPHARMACEUTICALS GMBH.

XX (IOWA) UNIV IOWA RES FOUND.

XX Noll BO, Schetter C, Krieg AM;

XX WPI; 2001-016002/02.

XX Immunostimulatory DNA binding proteins to identify immunostimulatory
 PT DNA functional modifiers, immunostimulatory DNA binding competitors and
 PT to optimize immunostimulatory oligodeoxynucleotides for stimulation -

XX Example 1; Page 45; 95pp; English.

XX The invention relates to the use of an immunostimulatory single-stranded
 CC DNA-binding protein in screening assays to identify compounds which bind
 CC to it and thereby act as functional modifiers of immunostimulatory

CC oligodeoxynucleotide (ODN) activity. Such modifiers of ODN activity
 CC consist of immunostimulatory DNA binding inhibitors, immunostimulatory
 CC DNA mimics, and immunostimulatory DNA agonists and antagonists.

CC Immunostimulatory DNA-binding proteins can also be used in
 CC screening methods to identify immunostimulatory DNA binding competitors,
 CC and to optimize an immunostimulatory ODN for immune stimulation.

CC Isolated complexes of an immunostimulatory DNA-binding protein bound to
 CC an immunostimulatory ODN can additionally be used to screen a panel of
 CC candidate target molecules to identify the cellular target molecules of
 CC the immunostimulatory ODN. The immunostimulatory DNA-binding proteins

CC used in the methods of the invention are the RNA-binding proteins
 CC nucleolin, hrNP D, AUF1, hrNP A1 and lupus La protein. The screening
 CC methods are useful for identifying a compound that inhibits interaction
 CC between immunostimulatory DNA and an immunostimulatory DNA-binding

CC protein and for identifying agonists useful in immunotherapy. The
 CC complex is useful in screening for immunostimulatory DNA cellular target
 CC molecules. The candidate immunostimulatory ODN competitors allow the

CC investigation of structure/activity relationships of immunostimulatory
 CC DNA-binding proteins and immunostimulatory ODNs. The present sequence
 CC represents an oligonucleotide used in an exemplification of the

CC invention.

XX Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 other;
 Query Match 1.5%; Score 17; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100

DB 20 AAAAAAAAAAAAAAAAAA 4

RESULT 393

AAC87238/C

ID AAC87238 standard; DNA; 20 BP.

XX AAC87238;

XX 09-MAR-2001 (first entry)

DE Phosphorothioate poly T oligonucleotide, SEQ ID NO:17.

XX Immunostimulatory oligodeoxynucleotide; immunostimulatory ODN;
 KW immunostimulatory DNA-binding protein; nucleolin; hrNP D; AUF1;
 KW hrNP A1; lupus La protein; functional modifier identification;
 KW agonist; antagonist; mimic; inhibitor; drug screening;
 KW cellular target identification; oligonucleotide optimisation;
 KW immunotherapy; ss.

XX Synthetic.

XX WO200067023-A1.

XX 09-NOV-2000.

XX 28-APR-2000; 2000WO-US11697.

XX 29-APR-1999; 99US-0131830.

XX 03-MAR-2000; 2000US-0186845.

XX (CPGI-) CPG IMMUNOPHARMACEUTICALS GMBH.

XX (IOWA) UNIV IOWA RES FOUND.

XX Noll BO, Schetter C, Krieg AM;

XX WPI; 2001-016002/02.

XX Immunostimulatory DNA binding proteins to identify immunostimulatory
 PT DNA functional modifiers, immunostimulatory DNA binding competitors and
 PT to optimize immunostimulatory oligodeoxynucleotides for stimulation -
 XX Example 1; Page 45; 95pp; English.

XX The invention relates to the use of an immunostimulatory single-stranded
 CC DNA-binding protein in screening assays to identify compounds which bind
 CC to it and thereby act as functional modifiers of immunostimulatory
 CC oligodeoxynucleotide (ODN) activity. Such modifiers of ODN activity
 CC consist of immunostimulatory DNA binding inhibitors, immunostimulatory
 CC DNA mimics, and immunostimulatory DNA agonists and antagonists.
 CC Immunostimulatory DNA-binding proteins can also be used in
 CC screening methods to identify immunostimulatory DNA binding competitors,
 CC and to optimize an immunostimulatory ODN for immune stimulation.
 CC Isolated complexes of an immunostimulatory DNA-binding protein bound to
 CC an immunostimulatory ODN can additionally be used to screen a panel of
 CC candidate target molecules to identify the cellular target molecules of
 CC the immunostimulatory ODN. The immunostimulatory DNA-binding proteins
 CC used in the methods of the invention are the RNA-binding proteins
 CC nucleolin, hnRNP D, AUF1, hnRNP A1 and lupus La protein. The screening
 CC methods are useful for identifying a compound that inhibits interaction
 CC between immunostimulatory DNA and an immunostimulatory DNA-binding
 CC protein and for identifying agonists useful in immunotherapy. The
 CC complex is useful in screening for immunostimulatory DNA cellular target
 CC molecules. The candidate immunostimulatory ODN competitors allow the
 CC investigation of structure/activity relationships of immunostimulatory
 CC DNA-binding proteins and immunostimulatory ODNs. The present sequence
 CC represents an oligonucleotide used in an exemplification of the
 CC invention.
 XX
 SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
 |||||
 Db 20 AAAAAAAAAAAAAAAAAA 4

RESULT 394

AAAC87241/c
 ID AAC87241 standard; DNA; 20 BP.
 AC AAC87241;
 XX
 XX
 DT 09-MAR-2001 (first entry)
 XX
 XX Poly T oligonucleotide, SEQ ID NO:20.
 XX Immunostimulatory oligodeoxynucleotide; immunostimulatory ODN;
 KW immunostimulatory DNA-binding protein; nucleolin; hnRNP D; AUF1;
 KW hnRNP A1; lupus La protein; functional modifier identification;
 KW agonist; antagonist; mimic; inhibitor; drug screening;
 KW cellular target identification; oligonucleotide optimisation;
 KW immunotherapy; ss.
 KW Synthetic.
 OS
 XX WO200067023-A1.
 EN
 XX
 PD 09-NOV-2000.
 XX
 XX 28-APR-2000; 2000WO-US11697.
 PF
 XX 29-APR-1999; 99US-0131830.
 PR 03-MAR-2000; 2000US-0186845.
 XX
 XX (CPGI-) CPG IMMUNOPHARMACEUTICALS GMBH.
 PA (IOWA) UNIV IOWA RES FOUND.
 XX
 XX Noll BO, Schetter C, Krieg AM;
 PI
 XX WPI; 2001-016002/02.
 DR
 XX Immunostimulatory DNA binding proteins to identify immunostimulatory

PT DNA functional modifiers, immunostimulatory DNA binding competitors and
 PT to optimize immunostimulatory oligodeoxynucleotides for stimulation -
 XX
 XX Example 1; Page 45; 95pp; English.

CC The invention relates to the use of an immunostimulatory single-stranded
 CC DNA-binding protein in screening assays to identify compounds which bind
 CC to it and thereby act as functional modifiers of immunostimulatory
 CC oligodeoxynucleotide (ODN) activity. Such modifiers of ODN activity
 CC consist of immunostimulatory DNA binding inhibitors, immunostimulatory
 CC DNA mimics, and immunostimulatory DNA agonists and antagonists.
 CC Immunostimulatory DNA-binding proteins can also be used in
 CC screening methods to identify immunostimulatory DNA binding competitors,
 CC and to optimize an immunostimulatory ODN for immune stimulation.
 CC Isolated complexes of an immunostimulatory DNA-binding protein bound to
 CC an immunostimulatory ODN can additionally be used to screen a panel of
 CC candidate target molecules to identify the cellular target molecules of
 CC the immunostimulatory ODN. The immunostimulatory DNA-binding proteins
 CC used in the methods of the invention are the RNA-binding proteins
 CC nucleolin, hnRNP D, AUF1, hnRNP A1 and lupus La protein. The screening
 CC methods are useful for identifying a compound that inhibits interaction
 CC between immunostimulatory DNA and an immunostimulatory DNA-binding
 CC protein and for identifying agonists useful in immunotherapy. The
 CC complex is useful in screening for immunostimulatory DNA cellular target
 CC molecules. The candidate immunostimulatory ODN competitors allow the
 CC investigation of structure/activity relationships of immunostimulatory
 CC DNA-binding proteins and immunostimulatory ODNs. The present sequence
 CC represents an oligonucleotide used in an exemplification of the
 CC invention.
 XX

SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
 |||||
 Db 20 AAAAAAAAAAAAAAAAAA 4

RESULT 395

AAF89091/c
 ID AAF89091 standard; DNA; 20 BP.
 AC AAF89091;
 XX
 XX 13-JUL-2001 (first entry)
 DT
 XX Mammalian stem cell factor PCR primer SEQ ID NO: 32.
 DE
 XX Human; rat; mammal; stem cell factor; SCF; cell growth stimulation;
 KW gene therapy; haematopoietic disorder; aplastic anaemia; leukaemia;
 KW neurological damage; intestinal damage; infertility; AIDS; SCID;
 KW severe combined immunodeficiency; PCR primer; ss.
 KW Mammalia.
 OS
 XX US6207802-B1.
 EN
 XX 27-MAR-2001.
 PD
 XX 09-NOV-1994; 94US-0336728.
 PF
 XX 25-NOV-1992; 92US-0982255.
 PR 16-OCT-1989; 89US-0422383.
 PR 11-JUN-1990; 90US-0537198.
 PR 24-AUG-1990; 90US-0573616.
 PR 01-OCT-1990; 90US-0589701.
 XX
 XX (AMGE-) AMGEN INC.
 PA
 XX Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
 PI

XX DR WPI; 2001-353108/37.
 XX PT Novel isolated non-human mammalian stem cell factor polypeptide
 PT stimulating growth of early haematopoietic progenitor cells, useful for
 PT treating aplastic anaemia, lymphoma, Letterer-Siwe disease, Kala azar,
 PT sarcoidosis -
 XX PS Example 3; Fig 12C; 209pp; English.
 XX CC The present invention provides the protein and coding sequences of
 CC mammalian stem cell factors (SCFs). These are capable of stimulating the
 CC growth of early haematopoietic progenitor cells, neural stem cells and
 CC primordial germ stem cells. The sequences are useful in the treatment of
 CC leukaemias, haematopoietic disorders, aplastic anaemia, paroxysmal
 CC nocturnal haemoglobinuria, malaria, pigmentation disorders, neurological
 CC and intestinal damage, infertility, AIDS and severe combined
 CC immunodeficiency (SCID). The present sequence is primer used to amplify
 CC an SCF in the exemplification of the invention.
 XX SQ Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 other;
 CC Query Match 1.5%; Score 17; DB 1; Length 20;
 CC Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 CC Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1084 AAAAAAAAAAAAAAAAAA 1100
 DB 18 AAAAAAAAAAAAAAAAAA 2
 RESULT 396
 AAF89093/c
 ID AAF89093 standard; DNA; 20 BP.
 XX AC AAF89093;
 XX DT 13-JUL-2001 (first entry)
 XX DE Mammalian stem cell factor PCR primer SEQ ID NO: 34.
 XX KW Human; rat; mammal; stem cell factor; SCF; cell growth stimulation;
 KW gene therapy; haematopoietic disorder; aplastic anaemia; leukaemia;
 KW neurological damage; intestinal damage; infertility; AIDS; SCID;
 KW severe combined immunodeficiency; PCR primer; ss.
 XX OS Mammalia.
 XX PN US6207802-B1.
 XX PD 27-MAR-2001.
 XX PF 09-NOV-1994; 94US-0336728.
 XX PR 25-NOV-1992; 92US-0982255.
 PR 16-OCT-1989; 89US-0422383.
 PR 11-JUN-1990; 90US-0537198.
 PR 24-AUG-1990; 90US-0573616.
 PR 01-OCT-1990; 90US-0589701.
 XX PA (AMGE-) AMGEN INC.
 XX PI Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
 XX WPI; 2001-353108/37.
 XX PT Novel isolated non-human mammalian stem cell factor polypeptide
 PT stimulating growth of early haematopoietic progenitor cells, useful for
 PT treating aplastic anaemia, lymphoma, Letterer-Siwe disease, Kala azar,
 PT sarcoidosis -
 XX PS Example 3; Fig 12C; 209pp; English.

CC The present invention provides the protein and coding sequences of
 CC mammalian stem cell factors (SCFs). These are capable of stimulating the
 CC growth of early haematopoietic progenitor cells, neural stem cells and
 CC primordial germ stem cells. The sequences are useful in the treatment of
 CC leukaemias, haematopoietic disorders, aplastic anaemia, paroxysmal
 CC nocturnal haemoglobinuria, malaria, pigmentation disorders, neurological
 CC and intestinal damage, infertility, AIDS and severe combined
 CC immunodeficiency (SCID). The present sequence is primer used to amplify
 CC an SCF in the exemplification of the invention.
 XX SQ Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 other;
 CC Query Match 1.5%; Score 17; DB 1; Length 20;
 CC Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 CC Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1084 AAAAAAAAAAAAAAAAAA 1100
 DB 18 AAAAAAAAAAAAAAAAAA 2
 RESULT 397
 AAD16997/c
 ID AAD16997 standard; DNA; 20 BP.
 XX AC AAD16997;
 XX DT 29-NOV-2001 (first entry)
 XX DE Capture probe CP5'.
 XX KW Scaffold protein; antibody mimic; fibronectin type III domain;
 KW randomised loop; randomised beta-sheet; diagnostic purpose;
 KW protein designing; probe; tenth module of human Fn3; 10Fn3;
 KW fibronectin module of type III; Fn3; ss.
 XX OS Unidentified.
 XX PN WO200164942-A1.
 XX PD 07-SEP-2001.
 XX PF 28-FEB-2001; 2001WO-US06414.
 XX PR 29-FEB-2000; 2000US-0515260.
 XX PA (PHYL-) PHYLLOS INC.
 XX PI Lipovsek D, Wagner RW, Kuimelis RG;
 XX WPI; 2001-557782/62.
 XX PT Fibronectin scaffold protein array for obtaining a protein/compound
 PT which binds to a compound/protein, comprises a fibronectin type III
 PT domain having a randomised loop, a randomised beta-sheet or their
 PT combination -
 XX PS Disclosure; Page 41; 67pp; English.
 XX CC The present invention relates to an array of proteins (antibody mimics)
 CC comprising a fibronectin type III domain having a randomised loop, a
 CC randomised beta-sheet, or their combination, and has the capacity to
 CC bind to a compound that is not bound by a corresponding naturally-
 CC occurring fibronectin, immobilised onto a solid support. The antibody
 CC mimics is useful for detecting a compound preferably a protein, in a
 CC biological sample. It is also useful to detect one or more different
 CC analytes simultaneously in a sample. Hence is useful for diagnostic
 CC purposes. It is also useful for the purpose of designing proteins
 CC capable of binding to virtually any compound of interest. The present
 CC sequence is a capture probe used to self-assemble and anchor the tenth
 CC module of human fibronectin module of type III (Fn3) (10Fn3) which is
 CC used in an exemplification of the invention.

SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 other;
 Query Match 1.5%; Score 17; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
 |||||
 DB 20 AAAAAAAAAAAAAAAAAA 4

RESULT 398
 ABSQ79871/c
 ID ABQ79871 standard; DNA; 20 BP.
 AC ABQ79871;
 XX
 XX
 DT 23-DEC-2002 (first entry)
 XX
 XX Nucleotide sequence of a PCR primer #1.
 DE Polymerase chain reaction; thermal cycle; immobilisation;
 KW genetic engineering; PCR; primer; ss.
 XX
 XX Synthetic.
 OS
 XX
 PN JP2002191369-A.
 XX
 XX
 PD 09-JUL-2002.
 XX
 PF 27-DEC-2000; 2000JP-0399573.
 XX
 PR 27-DEC-2000; 2000JP-0399573.
 XX
 XX (TOJO) TOYO KOHAN CO LTD.
 PA (TAKA/) TAKAHASHI K.
 XX
 XX WPI; 2002-630904/68.
 DR
 XX
 PT Carrying out a thermal cycle of polymerase chain reaction (PCR) by
 using a substrate on which a DNA is immobilized used in medical,
 PT biochemical, molecular biological and gene engineering fields -
 XX
 XX Examples; Page 9; 13pp; Japanese.
 PS
 XX The invention relates to performing a thermal cycle of PCR by using a
 CC substrate on which a deoxyribonucleic acid (DNA) is immobilized. The
 CC method is useful in the medical, biochemical, molecular biological and
 CC genetic engineering fields. Sequences ABQ79871-881 represent PCR primers
 CC used in the method of the invention.
 XX
 SQ Sequence 20 BP; 3 A; 0 C; 0 G; 17 T; 0 other;
 Query Match 1.5%; Score 17; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
 |||||
 DB 20 AAAAAAAAAAAAAAAAAA 4

RESULT 399
 ABS73848/c
 ID ABS73848 standard; DNA; 20 BP.
 XX
 XX
 AC ABS73848;
 XX
 DT 05-DEC-2002 (first entry)
 XX
 XX SCF universal oligonucleotide 220-3.
 DE
 XX Stem cell factor; SCF; blood-forming system; blood cell disorder;
 KW

KW haematopoietic system; metastatic carcinoma; acute leukaemia;
 KW multiple myeloma; Hodgkin's disease; lymphoma; malaria; vitiligo;
 KW refractory erythroblastic anaemia; miliary tuberculosis; cytostatic;
 KW disseminated fungus disease; haematopoietic; tuberculostatic;
 KW antianemic; antifungal; antimalarial; dermatological; ss.
 XX
 OS Synthetic.
 XX
 PN EP1241258-A2.
 XX
 XX
 PD 18-SEP-2002.
 XX
 PF 04-OCT-1990; 2002EP-0008597.
 XX
 PR 16-OCT-1989; 89US-0422383.
 PR 11-JUN-1990; 90US-0537198.
 PR 24-AUG-1990; 90US-0573616.
 PR 28-SEP-1990; 90WO-US05548.
 PR 01-OCT-1990; 90US-0589701.
 PR 04-OCT-1990; 90EP-0310899.
 PR 04-OCT-1990; 95EP-0105391.
 XX
 XX (AMGE-) AMGEN INC.
 PA
 XX
 PI Zsebo KM, Suggs SV, Bosselman RA, Martin FH;
 XX
 XX WPI; 2002-684093/74.
 DR
 XX
 PT Production of a human stem cell factor (SCF) polypeptide for treating
 disorders involving blood cells, such as leukaemia, comprises culturing
 PT mammalian cells comprising non-human SCF promoter DNA linked to DNA
 PT encoding the human SCF -
 XX
 XX Example 3; Fig 12C; 120pp; English.
 PS
 XX The present invention relates to novel stem cell factors (SCFs),
 CC polynucleotide sequences encoding the SCFs, and methods of producing
 CC them. SCFs are involved in the blood-forming (haematopoietic)
 CC system in mammals, particularly humans. The method of the invention
 CC is useful for the production of human SCF. The stem cell factors are
 CC useful to treat disorders involving blood cells e.g. metastatic
 CC carcinoma, acute leukaemia, multiple myeloma, Hodgkin's disease,
 CC lymphoma, refractory erythroblastic anaemia, miliary tuberculosis,
 CC disseminated fungus disease, malaria, and vitiligo. The present
 CC sequence representing a universal oligonucleotide for SCF DNA is
 CC used in the examples of the present invention.
 XX
 SQ Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 other;
 Query Match 1.5%; Score 17; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
 |||||
 DB 18 AAAAAAAAAAAAAAAAAA 2

RESULT 400
 ABS73850/c
 ID ABS73850 standard; DNA; 20 BP.
 XX
 XX
 AC ABS73850;
 XX
 XX
 DT 05-DEC-2002 (first entry)
 XX
 XX SCF universal oligonucleotide 220-11.
 DE
 XX Stem cell factor; SCF; blood-forming system; blood cell disorder;
 KW haematopoietic system; metastatic carcinoma; acute leukaemia;
 KW multiple myeloma; Hodgkin's disease; lymphoma; malaria; vitiligo;
 KW refractory erythroblastic anaemia; miliary tuberculosis; cytostatic;
 KW disseminated fungus disease; haematopoietic; tuberculostatic;

XX 14-DEC-2000; 2000US-255534P.
 XX (COLE-) COLEY PHARM GROUP INC.
 XX Bratzler RL;
 XX WPI; 2002-566690/60.
 XX Inhibiting angiogenesis in a subject, involves administering at least
 XX one antiangiogenic nucleic acid molecule to the subject -
 XX Claim 2; Page 29; 276pp; English.
 XX The invention relates to inhibiting angiogenesis in a subject, comprising
 XX administering at least one antiangiogenic nucleic acid molecule.
 XX Also included is a kit comprising a first container housing the
 XX antiangiogenic nucleic acids, and instructions for administering them to
 XX a subject having a condition characterised by unwanted angiogenesis.
 XX The method is useful for inhibiting angiogenesis associated with solid
 XX tumour growth, tumour metastasis, precancerous lesion, rheumatoid
 XX arthritis, psoriasis, diabetic retinopathy, retinopathy of prematurity,
 XX macular degeneration, corneal graft rejection, neovascular glaucoma,
 XX retrolental fibroplasia, rubeosis, Osler-Webber Syndrome, myocardi-
 XX angiogenesis, plaque neovascularisation, telangiectasia, haemophiliac
 XX joints, angiofibroma, wound granulation, intestinal adhesions,
 XX atherosclerosis, scleroderma and hypertrophic scars. The present
 XX sequence is an antiangiogenic nucleic acid of the invention.
 XX Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 other;
 SQ

Query Match 1.5%; Score 17; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1084 AAAAAAAAAAAAAAAAAA 1100
 |||||
 Db 20 AAAAAAAAAAAAAAAAAA 4

RESULT 403
 ABS78076
 ID ABS78076 standard; DNA; 20 BP.
 XX AC ABS78076;
 XX 13-DEC-2002 (first entry)
 XX Angiogenesis inhibitory oligonucleotide #560.
 XX Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
 XX tumour metastasis; precancerous lesion; rheumatoid arthritis;
 XX psoriasis; diabetic retinopathy; retinopathy of prematurity;
 XX macular degeneration; corneal graft rejection; neovascular glaucoma;
 XX retrolental fibroplasia; rubeosis; Osler-Webber Syndrome;
 XX myocardial angiogenesis; plaque neovascularisation; telangiectasia;
 XX haemophiliac joint; angiofibroma; wound granulation;
 XX intestinal adhesion; atherosclerosis; scleroderma; hypertrophic scar.
 XX Synthetic.
 XX WO200253141-A2.
 XX 11-JUL-2002.
 XX 14-DEC-2001; 2001WO-US48458.
 XX 14-DEC-2000; 2000US-255534P.
 XX (COLE-) COLEY PHARM GROUP INC.
 XX Bratzler RL;
 XX

XX WPI; 2002-566690/60.
 XX Inhibiting angiogenesis in a subject, involves administering at least
 XX one antiangiogenic nucleic acid molecule to the subject -
 XX Claim 2; Page 29; 276pp; English.
 XX The invention relates to inhibiting angiogenesis in a subject, comprising
 XX administering at least one antiangiogenic nucleic acid molecule.
 XX Also included is a kit comprising a first container housing the
 XX antiangiogenic nucleic acids, and instructions for administering them to
 XX a subject having a condition characterised by unwanted angiogenesis.
 XX The method is useful for inhibiting angiogenesis associated with solid
 XX tumour growth, tumour metastasis, precancerous lesion, rheumatoid
 XX arthritis, psoriasis, diabetic retinopathy, retinopathy of prematurity,
 XX macular degeneration, corneal graft rejection, neovascular glaucoma,
 XX retrolental fibroplasia, rubeosis, Osler-Webber Syndrome, myocardi-
 XX angiogenesis, plaque neovascularisation, telangiectasia, haemophiliac
 XX joints, angiofibroma, wound granulation, intestinal adhesions,
 XX atherosclerosis, scleroderma and hypertrophic scars. The present
 XX sequence is an antiangiogenic nucleic acid of the invention.
 XX Sequence 20 BP; 20 A; 0 C; 0 G; 0 U; 0 other;
 SQ

Query Match 1.5%; Score 17; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1084 AAAAAAAAAAAAAAAAAA 1100
 |||||
 Db 1 AAAAAAAAAAAAAAAAAA 17

RESULT 404
 ABS64673
 ID ABS64673 standard; DNA; 20 BP.
 XX AC ABS64673;
 XX 15-NOV-2002 (first entry)
 XX Nucleic acid detection method associated polynucleotide #55.
 XX Nucleic acid detection method; nanoparticle-oligonucleotide conjugate;
 XX nanoparticle; viral RNA detection; bacterial DNA detection;
 XX fungal DNA detection; nanoprobe conjugate; ss.
 XX Synthetic.
 XX WO200246472-A2.
 XX 13-JUN-2002.
 XX 07-DEC-2001; 2001WO-US46418.
 XX 08-DEC-2000; 2000US-254392P.
 XX 08-DEC-2000; 2000US-254418P.
 XX 11-DEC-2000; 2000US-255235P.
 XX 11-DEC-2000; 2000US-255236P.
 XX 12-JAN-2001; 2001US-0760500.
 XX 28-MAR-2001; 2001US-0820279.
 XX 09-APR-2001; 2001US-282640P.
 XX 10-AUG-2001; 2001US-0927777.
 XX (NANO-) NANOSPHERE INC.
 XX Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;
 XX Taton TA, Garimella V, Li Z, Park S;
 XX WPI; 2002-608256/65.
 XX Detecting nucleic acid having two portions, by providing nanoparticles
 XX having oligonucleotides attached to it, contacting nucleic acid and

nanoparticles to allow hybridization, and observing detectable change

Example 18; Page 437; 442pp; English.

The invention describes a method of detecting (M1) a nucleic acid having two portions, involving providing nanoparticles having oligonucleotides attached to it, which has a sequence complementary to sequence of two portions of nucleic acid, contacting nucleic acid and nanoparticles, to allow hybridization of oligonucleotides with two or more portions of nucleic acid, and observing a detectable change brought about by hybridization. (M1), nanoparticles (I), nanoparticle-oligonucleotide conjugates (II) and the aggregate probe are useful for detecting two or more nucleic acids (from a biological source) having at least two portions, such as viral RNA, bacterial or fungal DNA, a gene associated with a disease, synthetic, or structurally-modified natural or synthetic RNA or DNA, or a product of a polymerase chain reaction amplification. (II) is useful for preparing a nanoprobe conjugate for detecting an analyte, and for detecting a nucleic acid bound to an electrode surface. (I) and (II) are useful for fabricating, and for separating a selected nucleic acid having two portions from other nucleic acids. (I), (II) and the aggregate probe are useful for detecting an analyte (especially polyvalent analyte) in a sample. This sequence represents a polynucleotide used to demonstrate the method of the invention.

Sequence 20 BP; 20 A; 0 C; 0 G; 0 U; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1100
DB 1 AAAAAAAAAAAAAA 17

RESULT 405
ABS64688
ID ABS64688 standard; DNA; 20 BP.
AC ABS64688;
XZ 15-NOV-2002 (first entry)
DE Nucleic acid detection method associated polynucleotide #70.
KW Nucleic acid detection method; nanoparticle-oligonucleotide conjugate;
KW nanoparticle; viral RNA detection; bacterial DNA detection;
KW fungal DNA detection; nanoprobe conjugate; ss.
OS Synthetic.
XZ WO200246472-A2.
PN 13-JUN-2002.
XZ 07-DEC-2001; 2001WO-US46418.
XZ 08-DEC-2000; 2000US-254392P.
XZ 08-DEC-2000; 2000US-254418P.
XZ 11-DEC-2000; 2000US-255235P.
XZ 11-DEC-2000; 2000US-255236P.
XZ 12-JAN-2001; 2001US-0760500.
XZ 28-MAR-2001; 2001US-0820279.
XZ 09-APR-2001; 2001US-282640P.
XZ 10-AUG-2001; 2001US-0927777.
XZ (NANO-) NANOSPHERE INC.
XZ Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghamian R;
PI Taton TA, Garimella V, Li Z, Park S;
XZ WPI; 2002-608256/65.

Detecting nucleic acid having two portions, by providing nanoparticles having oligonucleotides attached to it, contacting nucleic acid and nanoparticles to allow hybridization, and observing detectable change

Example 24; Fig 44; 442pp; English.

The invention describes a method of detecting (M1) a nucleic acid having two portions, involving providing nanoparticles having oligonucleotides attached to it, which has a sequence complementary to sequence of two portions of nucleic acid, contacting nucleic acid and nanoparticles, to allow hybridization of oligonucleotides with two or more portions of nucleic acid, and observing a detectable change brought about by hybridization. (M1), nanoparticles (I), nanoparticle-oligonucleotide conjugates (II) and the aggregate probe are useful for detecting two or more nucleic acids (from a biological source) having at least two portions, such as viral RNA, bacterial or fungal DNA, a gene associated with a disease, synthetic, or structurally-modified natural or synthetic RNA or DNA, or a product of a polymerase chain reaction amplification. (II) is useful for preparing a nanoprobe conjugate for detecting an analyte, and for detecting a nucleic acid bound to an electrode surface. (I) and (II) are useful for fabricating, and for separating a selected nucleic acid having two portions from other nucleic acids. (I), (II) and the aggregate probe are useful for detecting an analyte (especially polyvalent analyte) in a sample. This sequence represents a polynucleotide used to demonstrate the method of the invention.

Sequence 20 BP; 20 A; 0 C; 0 G; 0 U; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1100
DB 1 AAAAAAAAAAAAAA 17

RESULT 406
ABN87103/c
ID ABN87103 standard; DNA; 20 BP.
XZ ABN87103;
XZ 30-JUL-2002 (first entry)
DE Capture probe CP5' SEQ ID NO:23.
XZ Protein scaffold; antibody; binding protein; immunoglobulin;
XZ tumour necrosis factor alpha; TNF-alpha; protein framework; probe; ss.
OS Synthetic.
XZ WO200232925-A2.
XZ 25-APR-2002.
XZ 16-OCT-2001; 2001WO-US32233.
XZ 16-OCT-2000; 2000US-0688566.
XZ (PHYL-) PHYLLOS INC.
XZ Lipoveak D, Wagner RW, Kuimelis RG;
XZ WPI; 2002-444238/47.
XZ New non-antibody proteins having an immunoglobulin fold, useful in
XZ research, therapeutic or diagnostic fields, particularly as scaffolds
XZ for designing proteins with specific properties, e.g. for binding any
XZ antigen of interest

Thu Jan 8 16:51:41 2004

PS Disclosure; Page 58; 94pp; English.

XX The present invention describes a non-antibody protein, comprising a
 CC domain having an immunoglobulin-like fold, derived from a reference
 CC protein having a mutated amino acid sequence, where the non-antibody
 CC protein binds with a Kd at least as tight as 10 nM to a compound that
 CC is not bound as tightly by the reference protein. The non-antibody
 CC protein is useful as scaffolds for selecting or designing a protein
 CC framework with specific and favourable properties, e.g. for binding any
 CC antigen of interest, or for destroying or inactivating antibody
 CC molecules. The non-antibody protein is also useful in all areas where
 CC antibodies are used, e.g. research, therapeutic or diagnostic fields,
 CC and for screening novel binding proteins useful in the above-mentioned
 CC fields. The present proteins have thermodynamic properties superior to
 CC those of natural antibodies, and can be evolved rapidly in vitro. The
 CC present proteins or antibody mimics exhibit improved biophysical
 CC properties, such as stability under reducing conditions and solubility
 CC at high concentrations. In addition, these molecules are readily
 CC expressed and folded in prokaryotic systems (e.g. Escherichia coli), in
 CC eukaryotic systems (e.g. yeast), or in in vitro translation systems
 CC (e.g. rabbit reticulocyte lysate system). Furthermore, these proteins
 CC are extremely amenable to affinity maturation techniques involving
 CC multiple cycles of selection, e.g. in vitro selection using RNA-protein
 CC fusion technology, phage display or yeast display systems. The present
 CC sequence is used in the exemplification of the present invention.

XX Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 other;

SQ Query Match 1.5%; Score 17; DB 1; Length 20;

XX Best Local Similarity 100.0%; Pred. No. 2.1e+02; 0; Gaps 0;

XX Matches 17; Conservative 0; Mismatches 0; Indels 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100

DB 20 AAAAAAAAAAAAAAAAAA 4

RESULT 407

ID AAD35464/c

XX AAD35464 standard; DNA; 20 BP.

AC AAD35464;

XX 25-JUL-2002 (first entry)

XX Rat SCF 5' cDNA amplifying PCR primer, 220-3.

XX Rat; stem cell factor; SCF protein; leucopaemia; thrombocytopaenia;
 KW anaemia; myelosuppression; nerve damage; myeloproliferative disorder;
 KW infertility; neoplasia; myelofibrosis; myelocytosis; osteopetrosis;
 KW metastatic carcinoma; acute leukaemia; multiple myeloma; sarcoidosis;
 KW Hodgkin's disease; lymphoma; Gaucher's disease; Niemann-Pick disease;
 KW Letterer-Siwe disease; refractory erythroblastic anaemia; Kala azar;
 KW Di Guglielmo syndrome; congestive splenomegaly; splenic pancytopenia;
 KW disseminated fungus disease; Fulminating septicaemia; piebaldism; AIDS;
 KW acquired immune deficiency syndrome; malaria; military tuberculosis;
 KW pyridoxine deficiency; vitamin B12 deficiency; folic acid deficiency;
 KW Diamond Blackfan anaemia; hypopigmentation disorder; vitiligo; PCR;
 KW primer; ss.

XX Rattus sp.

XX US2002018763-A1.

XX 14-FEB-2002.

XX 12-JAN-1998; 98US-0005243.

XX 24-MAY-1995; 95US-0449653.

XX (ZSEB/) ZSEB K M.

XX (BOSS/) BOSSELMAN R A.

XX (SUGG/) SUGGS S V.

PA (MART/) MARTIN F H.

XX Zeebo KM, BosseLMAN RA, Suggs SV, Martin FH;

XX WPI; 2002-350789/38.

XX Novel non-naturally-occurring stem cell factor polypeptide, useful for
 CC treating leucopenia, thrombocytopenia, anemia and for enhancing
 CC engraftment of bone marrow during transplantation in a mammal -

XX Example 3; Fig 12C; 217pp; English.

XX The present invention relates to novel non-naturally-occurring stem cell
 CC factor (SCF) polypeptides having an amino acid sequence sufficiently
 CC duplicative of that of naturally-occurring SCF to allow possession of
 CC haematopoietic biological activity of naturally occurring SCF. Sequences
 CC of the invention are useful for treating leucopaemia, thrombocytopaenia,
 CC anaemia and for enhancing bone marrow recovery in treatment of radiation,
 CC engraftment of bone marrow during transplantation in mammals and chemical
 CC or chemotherapeutic induced bone marrow aplasia or myelosuppression. They
 CC are also useful for treating acquired immune deficiency in a human, nerve
 CC damage, neoplasia, infertility, myeloproliferative disorder, intestinal
 CC damage in a mammal. SCF sequences are useful for preparing biologically
 CC active polymer polypeptide adducts, for enhancing transfection of early
 CC haematopoietic progenitor cells with a gene, and transfer of a gene into
 CC a mammal. They are useful for treating myelofibrosis, myelocytosis,
 CC osteopetrosis, metastatic carcinoma, acute leukaemia, multiple myeloma,
 CC Hodgkin's disease, lymphoma, Gaucher's disease, Niemann-Pick disease,
 CC Letterer-Siwe disease, refractory erythroblastic anaemia, Di Guglielmo
 CC syndrome, congestive splenomegaly, Kala azar, sarcoidosis, primary
 CC splenic pancytopenia, disseminated fungus disease, malaria, military
 CC tuberculosis, Fulminating septicaemia, pyridoxine deficiency, vitamin
 CC B12 and folic acid deficiency, Diamond Blackfan anaemia, hypopigmentation
 CC disorders such as piebaldism, AIDS (acquired immune deficiency syndrome)
 CC and vitiligo. The present sequence is a PCR primer which is used for
 CC amplifying the 5' end of rat SCF cDNA. This sequence is used in the
 CC exemplification of the invention.

XX Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 other;

XX Query Match 1.5%; Score 17; DB 1; Length 20;

XX Best Local Similarity 100.0%; Pred. No. 2.1e+02; 0; Gaps 0;

XX Matches 17; Conservative 0; Mismatches 0; Indels 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100

DB 18 AAAAAAAAAAAAAAAAAA 2

RESULT 408

AAD35466/c

ID AAD35466 standard; DNA; 20 BP.

XX AAD35466;

XX 25-JUL-2002 (first entry)

XX Rat SCF 5' cDNA amplifying PCR primer, 220-11.

XX Rat; stem cell factor; SCF protein; leucopaemia; thrombocytopaenia;
 KW anaemia; myelosuppression; nerve damage; myeloproliferative disorder;
 KW infertility; neoplasia; myelofibrosis; myelocytosis; osteopetrosis;
 KW metastatic carcinoma; acute leukaemia; multiple myeloma; sarcoidosis;
 KW Hodgkin's disease; lymphoma; Gaucher's disease; Niemann-Pick disease;
 KW Letterer-Siwe disease; refractory erythroblastic anaemia; Kala azar;
 KW Di Guglielmo syndrome; congestive splenomegaly; splenic pancytopenia;
 KW disseminated fungus disease; Fulminating septicaemia; piebaldism; AIDS;
 KW acquired immune deficiency syndrome; malaria; military tuberculosis;
 KW pyridoxine deficiency; vitamin B12 deficiency; folic acid deficiency;
 KW Diamond Blackfan anaemia; hypopigmentation disorder; vitiligo; PCR;
 KW primer; ss.

XX Rattus sp.

us09904568-1.rng

Thu Jan 8 16:51:41 2004

```

XX OS Synthetic.
XX PN WO200218643-A2.
XX PD 07-MAR-2002.
XX PF 10-AUG-2001; 2001WO-US25237.
XX PR 11-AUG-2000; 2000US-224631P.
XX PR 08-DEC-2000; 2000US-254392P.
XX PR 11-DEC-2000; 2000US-255235P.
XX PR 12-JAN-2001; 2001US-0760500.
XX PR 28-MAR-2001; 2001US-0820279.
XX PA (NANO-) NANOSPHERE INC.
XX PI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;
XX PI Taton TA, Garimella V, Li Z, Park S;
XX DR WPI; 2002-258024/30.
XX PT Detecting nucleic acid, useful for diagnosis of genetic, viral or
XX PT bacterial disease, comprises hybridising nanoparticles with attached
XX PT oligonucleotides to nucleic acid and detecting change brought about by
XX PT hybridisation -
XX PS Example 18; Page 410; 412pp; English.
XX CC The invention relates to a method of detecting a nucleic acid (NA) having
XX CC at least 2 portions comprising: (a) providing nanoparticles (NP) with
XX CC attached oligonucleotides (OGN), where OGN has a sequence complementary
XX CC to the sequence of NA; (b) contacting NA and NP under conditions
XX CC effective to allow hybridisation of OGN with NA; and (c) observing a
XX CC detectable change brought about by hybridisation of OGN with NA.
XX CC The method is useful for detecting a nucleic acid, separating a
XX CC selected nucleic acid from others and methods of nanofabrication.
XX CC Detecting analyses such as nucleic acids and proteins are useful for the
XX CC diagnosis of genetic, bacterial and viral diseases. The OGN-NP conjugates
XX CC that use cyclic disulphide linkers improve the sensitivity of diagnostic
XX CC assays. In particular assays using OGN-NP conjugates prepared using
XX CC linkers comprising a steroid residue attached to a cyclic disulphide have
XX CC been found to be approximately 10 times more sensitive than assays
XX CC employing conjugates prepared using alkanethiols or acyclic disulphides
XX CC as the linker. The OGN-NP conjugates are stable allowing them to be used
XX CC directly in PCR solutions. Therefore conjugates added as probes to a DNA
XX CC target to be PCR amplified can be carried through the 30 or 40 heating
XX CC cooling cycles of the PCR and are still able to detect the amplicons
XX CC without opening the tubes and causing contamination. ABR64981-ABK65055
XX CC represent nanoparticle-oligonucleotides of the invention.
XX SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 U; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
DB 1 AAAAAAAAAAAAAAAAAA 17

RESULT 410
ABK65050
ID ABK65050 standard; DNA; 20 BP.
XX AC ABK65050;
XX XX 02-JUL-2002 (first entry)
XX DE Nanoparticle-oligonucleotide #70.
XX KW Nanoparticle-oligonucleotide; nanofabrication;
nucleic acid detection; ss.

```

```

XX OS Synthetic.
XX PN WO200218643-A2.
XX PD 07-MAR-2002.
XX PF 10-AUG-2001; 2001WO-US25237.
XX PR 11-AUG-2000; 2000US-224631P.
XX PR 08-DEC-2000; 2000US-254392P.
XX PR 11-DEC-2000; 2000US-255235P.
XX PR 12-JAN-2001; 2001US-0760500.
XX PR 28-MAR-2001; 2001US-0820279.
XX PA (NANO-) NANOSPHERE INC.
XX PI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;
XX PI Taton TA, Garimella V, Li Z, Park S;
XX DR WPI; 2002-258024/30.
XX PT Detecting nucleic acid, useful for diagnosis of genetic, viral or
XX PT bacterial disease, comprises hybridising nanoparticles with attached
XX PT oligonucleotides to nucleic acid and detecting change brought about by
XX PT hybridisation -
XX PS Example 18; Page 410; 412pp; English.
XX CC The invention relates to a method of detecting a nucleic acid (NA) having
XX CC at least 2 portions comprising: (a) providing nanoparticles (NP) with
XX CC attached oligonucleotides (OGN), where OGN has a sequence complementary
XX CC to the sequence of NA; (b) contacting NA and NP under conditions
XX CC effective to allow hybridisation of OGN with NA; and (c) observing a
XX CC detectable change brought about by hybridisation of OGN with NA.
XX CC The method is useful for detecting a nucleic acid, separating a
XX CC selected nucleic acid from others and methods of nanofabrication.
XX CC Detecting analyses such as nucleic acids and proteins are useful for the
XX CC diagnosis of genetic, bacterial and viral diseases. The OGN-NP conjugates
XX CC that use cyclic disulphide linkers improve the sensitivity of diagnostic
XX CC assays. In particular assays using OGN-NP conjugates prepared using
XX CC linkers comprising a steroid residue attached to a cyclic disulphide have
XX CC been found to be approximately 10 times more sensitive than assays
XX CC employing conjugates prepared using alkanethiols or acyclic disulphides
XX CC as the linker. The OGN-NP conjugates are stable allowing them to be used
XX CC directly in PCR solutions. Therefore conjugates added as probes to a DNA
XX CC target to be PCR amplified can be carried through the 30 or 40 heating
XX CC cooling cycles of the PCR and are still able to detect the amplicons
XX CC without opening the tubes and causing contamination. ABR64981-ABK65055
XX CC represent nanoparticle-oligonucleotides of the invention.
XX SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 U; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
DB 1 AAAAAAAAAAAAAAAAAA 17

RESULT 410
ABK65050
ID ABK65050 standard; DNA; 20 BP.
XX AC ABK65050;
XX XX 02-JUL-2002 (first entry)
XX DE Nanoparticle-oligonucleotide #70.
XX KW Nanoparticle-oligonucleotide; nanofabrication;
nucleic acid detection; ss.

```

KW nucleic acid detection; ss.

XX Synthetic.

XX WO200218643-A2.

XX 07-MAR-2002.

XX 10-AUG-2001; 2001WO-US25237.

XX 11-AUG-2000; 2000US-224631P.

XX 08-DEC-2000; 2000US-254392P.

XX 11-DEC-2000; 2000US-255235P.

XX 12-JAN-2001; 2001US-0760500.

XX 28-MAR-2001; 2001US-0820279.

XX (NANO-) NANOSPHERE INC.

XX Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;

XX Taton TA, Garimella V, Li Z, Park S;

XX WPI; 2002-258024/30.

XX Detecting nucleic acid, useful for diagnosis of genetic, viral or

XX bacterial disease, comprises hybridising nanoparticles with attached

XX oligonucleotides to nucleic acid and detecting change brought about by

XX hybridisation -

XX Example 24; Figure 44; 412pp; English.

XX The invention relates to a method of detecting a nucleic acid (NA) having at least 2 portions comprising: (a) providing nanoparticles (NP) with attached oligonucleotides (OGN), where OGN has a sequence complementary to the sequence of NA; (b) contacting NA and NP under conditions effective to allow hybridisation of OGN with NA; and (c) observing a detectable change brought about by hybridisation of OGN with NA.

XX The method is useful for detecting a nucleic acid, separating a selected nucleic acid from others and methods of nanofabrication.

XX Detecting analytes such as nucleic acids and proteins are useful for the diagnosis of genetic, bacterial and viral diseases. The OGN-NP conjugates that use cyclic disulphide linkers improve the sensitivity of diagnostic assays. In particular assays using OGN-NP conjugates prepared using linkers comprising a steroid residue attached to a cyclic disulphide have been found to be approximately 10 times more sensitive than assays employing conjugates prepared using alkanethiols or acyclic disulphides as the linker. The OGN-NP conjugates are stable allowing them to be used directly in PCR solutions. Therefore conjugates added as probes to a DNA target to be PCR amplified can be carried through the 30 or 40 heating cooling cycles of the PCR and are still able to detect the amplicons without opening the tubes and causing contamination. ABK64981-ABK65055 represent nanoparticle-oligonucleotides of the invention.

XX Sequence 20 BP; 20 A; 0 C; 0 G; 0 U; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 20;

Best Local Similarity 100.0%; Pred.No. 2.1e+02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100

DB 1 AAAAAAAAAAAAAAAAAA 17

RESULT 411

ID ABL54775/c

XX ABL54775 standard; DNA; 20 BP.

XX ABL54775;

XX 10-JUN-2002 (first entry)

XX CD14 receptor PCR primer SEQ ID NO 9.

KW Angiotensin-I converting enzyme; ACE; CD14; receptor; SNP;

XX single-nucleotide polymorphism; PCR; primer; ss.

XX Synthetic.

XX JP20002034599-A.

XX 05-FEB-2002.

XX 26-JUL-2000; 2000JP-0225354.

XX 26-JUL-2000; 2000JP-0225354.

XX (TOYM) TOYOCO KK.

XX WPI; 2002-275727/32.

XX Detecting 1 base polymorphism on a sequence of a chromosome or it's

XX fragment -

XX Example 2; Page 10; 10pp; Japanese.

XX The invention relates to a method for detecting 1 base polymorphism on the sequence of a chromosome or its fragment in which a sample nucleic acid is reacted with a reaction liquor containing a nucleic acid primer having a base adjacent to the polymorphic base at its 3'-end, one dideoxynucleotide corresponding to a polymorphic base having a distinguishable feature or its mixture, DNA polymerase and a composition required for its activity expression to detect the presence of taking dideoxynucleotide in the nucleic acid primer and to detect the type of the base to be specified. The method is used for detecting 1 base polymorphism on the sequence of a chromosome or its fragment. The present sequence is that of a PCR primer, useful in examples of the invention.

XX Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 20;

Best Local Similarity 100.0%; Pred.No. 2.1e+02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100

DB 20 AAAAAAAAAAAAAAAAAA 4

RESULT 412

ID AAL45122/c

XX AAL45122 standard; DNA; 20 BP.

XX AAL45122;

XX 24-MAY-2002 (first entry)

XX Oligonucleotide synthesis method related DNA #1.

XX Oligonucleotide synthesis; polynucleotide array; protecting group;

XX oxidation; ss.

XX Synthetic.

XX EP1176151-A1.

XX 30-JAN-2002.

XX 27-JUL-2001; 2001EP-0118360.

XX 28-JUL-2000; 2000US-0627249.

XX (AGIL-) AGILENT TECHNOLOGIES INC.

XX Dellinger DJ, Perbost MGM, Betley JR, Caruthers M;

XX WPI; 2002-156732/21.

XX Synthesis of polynucleotide useful during fabrication of an array
PT involves coupling nucleoside phosphoramidite and a solid-supported
PT nucleoside and treating the product with an oxidation/deprotection
PT composition -
XX
PS Example 1; Page 15; 36pp; English.
XX
CC The present invention relates to a method for the synthesis of a
CC polynucleotide which involves coupling a second nucleoside to a first
CC nucleoside through a phosphate linkage, where the second nucleoside has a
CC non-carbonate protecting group protecting a hydroxyl, and exposing the
CC product to a composition which concurrently oxidizes the phosphate formed
CC to a phosphate and deprotects the protected hydroxyl of the second
CC nucleoside. The method is useful for synthesizing the polynucleotides,
CC for carrying out either 3', to 5', or 5', to 3', synthesis and for
CC fabricating an addressable array of polynucleotides on a substrate. The
CC present sequence is an oligonucleotide produced to demonstrate the method
CC of the invention.
XX Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 other;
SQ
Query Match 1.5%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1084 AAAAAAAAAAAAAAAAAA 1100
DB 20 AAAAAAAAAAAAAAAAAA 4
RESULT 413
ABL36232
ID ABL36232 standard; DNA; 20 BP.
XX
AC ABL36232;
XX
DT 08-APR-2002 (first entry)
XX
DE M tuberculosis rRNA probe SEQ ID NO: 83.
XX
KW Skin disorder; psoriasis; atopic dermatitis; allergic contact dermatitis;
KW alopecia areata; skin cancer; Mycobacterium vaccae; melanoma; cytostatic;
KW antipsoriatic; dermatological; antiinflammatory; antiallergic;
KW Th2 immune response; immunomodulatory; probe; ss.
XX
OS Mycobacterium tuberculosis.
XX
FN US6328978-B1.
XX
PD 11-DEC-2001.
XX
PF 02-JUN-1999; 99US-0324542.
XX
PR 23-DEC-1997; 97US-0997080.
XX
PA (GENE-) GENESIS RES & DEV CORP LTD.
XX
PI Watson JD, Tan PLJ, Prestidge R;
XX
DR WPI; 2002-138361/18.
XX
PT Inhibiting skin inflammation associated with skin disorder e.g.
PT psoriasis, by administering composition comprising delipidated and
PT deglycolipidated Mycobacterium vaccae cells or Mycobacterium vaccae
PT culture filtrate -
XX
PS Example 5; Column 99-100; 116pp; English.
XX
CC The present invention relates to a method of inhibiting skin inflammation
CC associated with a skin disorder selected from psoriasis, atopic
CC dermatitis and allergic contact dermatitis, which involves administering
CC a composition containing delipidated and deglycolipidated Mycobacterium

CC vaccae cells or M. vaccae culture filtrate. The skin disorder to be
CC treated may also include alopecia areata, and skin cancers such as basal
CC cell carcinoma, squamous cell carcinoma and melanoma. The composition
CC acts by inhibiting the Th2 immune response. The present sequence is a
CC probe described in the exemplification of the invention.
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 U; 0 other;
Query Match 1.5%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1084 AAAAAAAAAAAAAAAAAA 1100
DB 1 AAAAAAAAAAAAAAAAAA 17

RESULT 414
ABL38648
ID ABL38648 standard; DNA; 20 BP.
XX
AC ABL38648;
XX
DT 16-APR-2002 (first entry)
XX
DE Immunostimulatory nucleic acid SEQ ID NO: 2.
XX
KW Antibody-induced cell lysis; cancer; immunostimulatory; CD20;
KW angiogenesis; metastasis; cytostatic; ss.
XX
OS Synthetic.
XX
FN WO200197843-A2.
XX
PD 27-DEC-2001.
XX
PF 22-JUN-2001; 2001WO-US20154.
XX
PR 22-JUN-2000; 2000US-213346P.
XX
PA (IOWA) UNIV IOWA RES FOUND.
XX
PI Weiner G, Hartmann G;
XX
DR WPI; 2002-154611/20.
XX
PT Treating or preventing cancer, such as basal cell carcinoma, comprises
PT administering immunostimulatory nucleic acids that induce expression of
PT cell surface antigens and antibodies to a subject having or at risk of
PT developing cancer -
XX
PS Disclosure; Page 95; 312pp; English.
XX
CC The present invention relates to methods for treating or preventing
CC cancer, involving administering to a subject having or at risk of
CC developing cancer immunostimulatory nucleic acids that induce expression
CC of cell surface antigens and antibodies. The methods are useful for
CC treating or preventing cancer such as basal cell carcinoma, bladder
CC cancer, bone cancer, brain and central nervous system (CNS) cancer,
CC breast cancer, cervical cancer, colon and rectum cancer, connective
CC tissue cancer, esophageal cancer, eye cancer, kidney cancer, larynx
CC cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma,
CC non-Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian
CC cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin
CC cancer, stomach cancer, testicular cancer, and uterine cancer. The
CC present sequence is an immunostimulatory oligonucleotide described in
CC the exemplification of the invention.
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 U; 0 other;
Query Match 1.5%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1084 AAAAAAAAAAAAAAAAAA 1100
Db 1 AAAAAAAAAAAAAAAAAA 17

RESULT 415
ABL39402/c
ID ABL39402 standard; DNA; 20 BP.
XX
AC ABL39402;
XX
DT 16-APR-2002 (first entry)
XX
DE Immunostimulatory nucleic acid SEQ ID NO: 838.
XX
KW Antibody-induced cell lysis; cancer; immunostimulatory; CD20;
XX angiogenesis; metastasis; cytostatic; phosphorothioate backbone; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "phosphorothioate backbone"
XX
PN WO200197843-A2.
XX
PD 27-DEC-2001.
XX
PF 22-JUN-2001; 2001WO-US20154.
XX
PR 22-JUN-2000; 2000US-213346P.
XX
PA (IOWA ) UNIV IOWA RES FOUND.
XX
PI Weiner G, Hartmann G;
XX
DR WPI; 2002-154611/20.
XX
PT Treating or preventing cancer, such as basal cell carcinoma, comprises
PT administering immunostimulatory nucleic acids that induce expression of
PT cell surface antigens and antibodies to a subject having or at risk of
PT developing cancer -
XX
PS Disclosure; Page 309; 312pp; English.
XX
CC The present invention relates to methods for treating or preventing
CC cancer, involving administering to a subject having or at risk of
CC developing cancer immunostimulatory nucleic acids that induce expression
CC of cell surface antigens and antibodies. The methods are useful for
CC treating or preventing cancer such as basal cell carcinoma, bladder
CC cancer, bone cancer, brain and central nervous system (CNS) cancer,
CC breast cancer, cervical cancer, colon and rectum cancer, connective
CC tissue cancer, esophageal cancer, eye cancer, kidney cancer, larynx
CC cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma,
CC non-Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian
CC cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin
CC cancer, stomach cancer, testicular cancer, and uterine cancer. The
CC present sequence is an immunostimulatory oligonucleotide described in
CC the exemplification of the invention.
XX
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
Db 20 AAAAAAAAAAAAAAAAAA 4

RESULT 417
ABX92177
ID ABX92177 standard; DNA; 20 BP.
XX
AC ABX92177;
XX
DT 12-MAY-2003 (first entry)
XX
DE Nanoparticle-associated oligonucleotide SEQ ID 55.
XX
```

```
RESULT 416
ABL39403/c
ID ABL39403 standard; DNA; 20 BP.
XX
AC ABL39403;
XX
DT 16-APR-2002 (first entry)
XX
DE Immunostimulatory nucleic acid SEQ ID NO: 839.
XX
KW Antibody-induced cell lysis; cancer; immunostimulatory; CD20;
XX angiogenesis; metastasis; cytostatic; ss.
XX
OS Synthetic.
XX
PN WO200197843-A2.
XX
PD 27-DEC-2001.
XX
PF 22-JUN-2001; 2001WO-US20154.
XX
PR 22-JUN-2000; 2000US-213346P.
XX
PA (IOWA ) UNIV IOWA RES FOUND.
XX
PI Weiner G, Hartmann G;
XX
DR WPI; 2002-154611/20.
XX
PT Treating or preventing cancer, such as basal cell carcinoma, comprises
PT administering immunostimulatory nucleic acids that induce expression of
PT cell surface antigens and antibodies to a subject having or at risk of
PT developing cancer -
XX
PS Disclosure; Page 309; 312pp; English.
XX
CC The present invention relates to methods for treating or preventing
CC cancer, involving administering to a subject having or at risk of
CC developing cancer immunostimulatory nucleic acids that induce expression
CC of cell surface antigens and antibodies. The methods are useful for
CC treating or preventing cancer such as basal cell carcinoma, bladder
CC cancer, bone cancer, brain and central nervous system (CNS) cancer,
CC breast cancer, cervical cancer, colon and rectum cancer, connective
CC tissue cancer, esophageal cancer, eye cancer, kidney cancer, larynx
CC cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma,
CC non-Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian
CC cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin
CC cancer, stomach cancer, testicular cancer, and uterine cancer. The
CC present sequence is an immunostimulatory oligonucleotide described in
CC the exemplification of the invention.
XX
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
Db 20 AAAAAAAAAAAAAAAAAA 4

RESULT 417
ABX92177
ID ABX92177 standard; DNA; 20 BP.
XX
AC ABX92177;
XX
DT 12-MAY-2003 (first entry)
XX
DE Nanoparticle-associated oligonucleotide SEQ ID 55.
XX
```



```
QY 1084 AAAAAAAAAAAAAAAAAA 1100
    |||||
Db 1 AAAAAAAAAAAAAAAAAA 17

RESULT 419
ABZ22916/c
ID ABZ22916 standard; DNA; 20 BP.
XX
AC ABZ22916;
XX
XX 08-APR-2003 (first entry)
XX
XX Phosphorothioate 20-mer oligonucleotide #1.
XX
XX Chiral; phosphorothioate; oligonucleotide synthesis; enantiomer; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX modified_base 1..20
XX /*tag= a
XX /*mod_base= OTHER
XX /*note= "phosphorothioate linkages"
XX
XX WO2002102815-A2.
XX
XX 27-DEC-2002.
XX
XX 13-JUN-2002; 2002WO-US18581.
XX
XX 14-JUN-2001; 2001US-0881535.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Ravikumar VT;
XX
XX WPI; 2003-157021/15.
XX
XX Preparing internucleotide phosphorothioate linkage enhanced in Sp/Rp
XX enantiomer, by coupling a synthon with 2'-substituted nucleoside in
XX presence of coupling agent having a pKa that enhances linkage in Sp/Rp
XX enantiomer -
XX
XX Example 1; Page 31; 65pp; English.
XX
XX The present invention describes a method (M1) for preparing an
XX internucleotide phosphorothioate linkage enriched in the Sp or Rp
XX enantiomer between a synthon having a hydroxyl moiety at the 5' position
XX and a 2'-substituted nucleoside having an activated phosphate moiety at
XX the 3'-position, comprising coupling a synthon with a 2'-substituted
XX nucleoside in the presence of coupling agent that is selected to enhance
XX either the Rp or Sp enantiomer according to its pKa. This method is
XX useful for preparing an oligonucleotide having at least one region of
XX internucleotide linkages that is enhanced in the Sp or Rp enantiomer,
XX which involves providing a nucleotide having a hydroxyl moiety at the
XX 5'-position or a growing oligonucleotide chain having a hydroxyl moiety
XX at the 5'-position, coupling the nucleotide or growing oligonucleotide
XX chain to a 2'-substituted nucleoside having an activated phosphate
XX moiety at the 3' position in the presence of the coupling agent, and
XX repeating the coupling step until the desired number of linkages is
XX established. The oligonucleotide having a region of internucleotide
XX linkages that is enhanced in the Sp enantiomer is further processed to
XX include another region of internucleotide linkages that is enhanced in
XX the Sp and/or Rp enantiomer. Oligonucleotides prepared by the method
XX lead to improved drugs, diagnostics and research reagents. The present
XX sequence represents an oligonucleotide used in the exemplification of
XX the present invention.
XX
XX Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 other;
XX
XX Query Match 1.5%; Score 17; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. NO. 2.1e+02;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
    |||||
Db 20 AAAAAAAAAAAAAAAAAA 4

RESULT 420
ABZ59815/c
ID ABZ59815 standard; RNA; 20 BP.
XX
XX AC ABZ59815;
XX
XX 01-APR-2003 (first entry)
XX
XX Potato gene PCR primer d720.
XX
XX Potato; plant; mitochondrial carrier protein; elongation factor EF-2;
XX transferin binding protein; receptor-like protein kinase; helicase;
XX non-long terminal repeat retroelement reverse transcriptase;
XX overwatering; transgenic; reverse transcriptase; PCR; primer; ss.
XX
XX Synthetic.
XX
XX DE10114063-A1.
XX
XX 10-OCT-2002.
XX
XX 22-MAR-2001; 2001DE-1014063.
XX
XX 22-MAR-2001; 2001DE-1014063.
XX
XX (MPBC-) MPB COLOGNE GMBH MOLECULAR PLANT & PROTE.
XX
XX Buelow L, Tschardt M, Haussuehl K;
XX
XX WPI; 2003-041808/04.
XX
XX New DNA sequences from potato, useful for producing plants with altered
XX properties, e.g. tolerance of flooding, also related proteins,
XX antibodies and inhibitory sequences -
XX
XX Example 1; Page 8; 26pp; German.
XX
XX The invention relates to DNA sequences (I) that encode six specific plant
XX proteins: (i) a protein (ABP60425) with mitochondrial carrier protein
XX activity (Iia); (ii) a protein (ABP60426) with transferrin binding
XX protein activity (Iib); (iii) a protein (ABP60427) with receptor-like
XX protein kinase activity (Iic); (iv) a protein (ABP60428) with elongation
XX factor EF-2 activity (Iid); (v) a protein (ABP60429) with non-long
XX terminal repeat retroelement reverse transcriptase activity (Iie); or
XX (vi) a protein (ABP60430) with helicase activity (Iif). (i), also related
XX sequences, derived ribozymes and antisense sequences, expression vectors,
XX encoded proteins and antibodies against the proteins, are used to produce
XX plants with altered properties, including tolerance of overwatering. The
XX antibodies are also used for isolation of the proteins and in
XX immunoassays. Also (I) or their primer or probe fragments are used to
XX screen for terminators and constitutively, aerobically or anaerobically
XX inducible plant promoters, specifically for use in potatoes and the
XX sequence that encodes (Iif) is used to alter the translation profile in
XX plants. Since (I) are derived from potato, their promoters and
XX terminators provide high level transgene expression in potato, with
XX improved tissue specificity and inducibility, and can also be used to
XX control endogenous genes. The present sequence is that of a PCR primer
XX used in the first strand synthesis of cDNAs derived from potato.
XX
XX Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 other;
XX
XX Query Match 1.5%; Score 17; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. NO. 2.1e+02;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 1084 AAAAAAAAAAAAAAAAAA 1100
 DB 20 AAAAAAAAAAAAAAAAAA 4

RESULT 421

AAQ90391
 ID AAQ90391 standard; DNA; 21 BP.

XX AC AAQ90391;

XX DT 08-JAN-1996 (first entry)

XX DE CP-1 (synthetic DNA probe with 3'ribonucleoside terminal #2).

XX KW CP-1; HLA; dQa; 3' ribonucleoside; self-addressable electronic device;

XX KW SAED; hybridisation; ss.

XX OS Synthetic.

XX FH Key Location/Qualifiers

XX FT misc_feature 21

XX FT /tag= a

XX FT /note= "3' ribonucleoside terminal"

XX FN W09512808-A1.

XX PD 11-MAY-1995.

XX PF 26-OCT-1994; 94WO-US12270.

XX PR 01-NOV-1993; 93US-0146504.

XX PA (NANO-) NANOGEN INC.

XX PI Heller MJ, Tu E;

XX DR WPI; 1995-185870/24.

XX PT New self-addressable electronic devices - used for multi-step and
 PT multiplex reactions such as DNA hybridisation(s), clinical
 PT diagnostics and bio-polymer synthesis

XX PS Example 1; Page 40; 86pp; English.

XX CC The sequences represented by, AAQ90390-90401 are synthetic DNA probes
 CC containing 3' ribonucleoside termini. The sequences shown in
 CC AAQ90402-15 are synthetic DNA probes with 5' amino termini. These
 CC sequences were specific for the polymorphisms of HLA gene dQa. The
 CC sequences were used in the device of the invention. This is a
 CC self-addressable electronic device (SAED) that can be used to carry out
 CC multi-step and multiplex reactions, such as nucleic acid hybridisations.
 CC The advantages of this method are that these reactions can be carried out
 CC with complete and precise electronic control, and that the rate,
 CC specificity and sensitivity of these reactions are greatly improved at
 CC micro-locations.

XX SQ Sequence 21 BP; 20 A; 0 C; 0 G; 1 U; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
 DB 1 AAAAAAAAAAAAAAAAAA 17

RESULT 422

AAQ75665/c
 ID AAQ75665 standard; DNA; 21 BP.

XX AC AAQ75665;

XX DT 04-AUG-1995 (first entry)
 XX DE Reverse transcription primer used in cDNA analysis technique.
 XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
 XX KW aggregate; restriction enzyme; ss.
 XX OS Synthetic.

XX PN JP06303997-A.

XX PD 01-NOV-1994.

XX PF 16-APR-1993; 93JP-0112515.

XX PR 16-APR-1993; 93JP-0112515.

XX PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

XX DR WPI; 1995-018287/03.

XX PT Analysis of cDNA and gene expression - by amplification of mRNA
 PT followed by digestion with restriction enzymes

XX PS Disclosure; Page 7; 11pp; Japanese.

XX CC A method for the analysis of cDNA comprises (a) preparing an
 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
 CC and a plural type of labelled reverse transcription primers
 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
 CC template for each reverse transcription primer; (b) digesting each of
 CC the prepared aggregates of the double-stranded cDNAs with restriction
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
 CC separate lanes. The method can be used to analyse gene expression
 CC rapidly and easily.

XX SQ Sequence 21 BP; 0 A; 1 C; 1 G; 19 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
 DB 17 AAAAAAAAAAAAAAAAAA 1

RESULT 423

AAQ75735/c

ID AAQ75735 standard; DNA; 21 BP.

XX AC AAQ75735;

XX DT 04-AUG-1995 (first entry)

XX DE Reverse transcription primer used in cDNA analysis technique.

XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
 XX KW aggregate; restriction enzyme; ss.

XX OS Synthetic.

XX PN JP06303997-A.

XX PD 01-NOV-1994.

XX PF 16-APR-1993; 93JP-0112515.

XX PR 16-APR-1993; 93JP-0112515.

XX PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

```
DR WPI; 1995-018287/03.
XX Analysis of cDNA and gene expression - by amplification of mRNA
PT followed by digestion with restriction enzymes
XX
XX PS Disclosure; Page 8; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC and a plural type of labelled reverse transcription primers
CC (GENESQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
CC template for each reverse transcription primer; (b) digesting each of
CC the prepared aggregates of the double-stranded cDNAs with restriction
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC separate lanes. The method can be used to analyse gene expression
CC rapidly and easily.
XX
XX Sequence 21 BP; 0 A; 1 C; 3 G; 17 T; 0 other;
XX
Query Match 1.5%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1084 AAAAAAAAAAAAAAAAAA 1100
DB 17 AAAAAAAAAAAAAAAAAA 1
RESULT 424
AAQ75736/c
ID AAQ75736 standard; DNA; 21 BP.
XX AC AAQ75736;
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; Gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-0112515.
XX
XX 16-APR-1993; 93JP-0112515.
XX
XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA
XX followed by digestion with restriction enzymes
XX
XX Disclosure; Page 8; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an
XX aggregate of double-stranded cDNAs by using an aggregate of mRNAs
XX and a plural type of labelled reverse transcription primers
XX (GENESQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
XX template for each reverse transcription primer; (b) digesting each of
XX the prepared aggregates of the double-stranded cDNAs with restriction
XX enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
XX separate lanes. The method can be used to analyse gene expression
XX rapidly and easily.
XX
XX Sequence 21 BP; 0 A; 1 C; 2 G; 18 T; 0 other;
XX
Query Match 1.5%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1084 AAAAAAAAAAAAAAAAAA 1100
DB 17 AAAAAAAAAAAAAAAAAA 1
RESULT 426
AAQ75738/c
ID AAQ75738 standard; DNA; 21 BP.
XX AC AAQ75738;
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; Gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
XX Sequence 21 BP; 0 A; 1 C; 2 G; 17 T; 0 other;
XX
Query Match 1.5%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1084 AAAAAAAAAAAAAAAAAA 1100
DB 17 AAAAAAAAAAAAAAAAAA 1
RESULT 426
AAQ75738/c
ID AAQ75738 standard; DNA; 21 BP.
XX AC AAQ75738;
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; Gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
```


CC separate lanes. The method can be used to analyse gene expression
 CC rapidly and easily.

SQ Sequence 21 BP; 0 A; 1 C; 2 G; 18 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
 |||||
 DB 17 AAAAAAAAAAAAAAAAAA 1

RESULT 432

AAQ75745/C
 ID AAQ75745 standard; DNA; 21 BP.

XX AC

XX AAQ75745;

XX DT 04-AUG-1995 (first entry)

XX DE Reverse transcription primer used in cDNA analysis technique.

XX XX

XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
 aggregate; restriction enzyme; ss.

XX OS Synthetic.

XX PN JP06303997-A.

XX PD 01-NOV-1994.

XX PF 16-APR-1993; 93JP-0112515.

XX PR 16-APR-1993; 93JP-0112515.

XX PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

XX WPI; 1995-018287/03.

XX DR Analysis of cDNA and gene expression - by amplification of mRNA
 followed by digestion with restriction enzymes

XX PS Disclosure; Page 8; 11pp; Japanese.

XX CC A method for the analysis of cDNA comprises (a) preparing an
 aggregate of double-stranded cDNAs by using an aggregate of mRNAs
 and a plural type of labelled reverse transcription primers
 (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
 template for each reverse transcription primer; (b) digesting each of
 the prepared aggregates of the double-stranded cDNAs with restriction
 enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
 separate lanes. The method can be used to analyse gene expression
 rapidly and easily.

SQ Sequence 21 BP; 0 A; 1 C; 1 G; 19 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
 |||||
 DB 17 AAAAAAAAAAAAAAAAAA 1

RESULT 433

AAQ75746/C
 ID AAQ75746 standard; DNA; 21 BP.

XX AC

XX AAQ75746;

DT 04-AUG-1995 (first entry)

XX DE Reverse transcription primer used in cDNA analysis technique.

XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
 aggregate; restriction enzyme; ss.

XX OS Synthetic.

XX PN JP06303997-A.

XX PD 01-NOV-1994.

XX PF 16-APR-1993; 93JP-0112515.

XX PR 16-APR-1993; 93JP-0112515.

XX PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

XX WPI; 1995-018287/03.

XX PT Analysis of cDNA and gene expression - by amplification of mRNA
 followed by digestion with restriction enzymes

XX PS Disclosure; Page 8; 11pp; Japanese.

XX CC A method for the analysis of cDNA comprises (a) preparing an
 aggregate of double-stranded cDNAs by using an aggregate of mRNAs
 and a plural type of labelled reverse transcription primers
 (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
 template for each reverse transcription primer; (b) digesting each of
 the prepared aggregates of the double-stranded cDNAs with restriction
 enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
 separate lanes. The method can be used to analyse gene expression
 rapidly and easily.

SQ Sequence 21 BP; 0 A; 2 C; 1 G; 18 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 21;

Best Local Similarity 100.0%; Pred. No. 2.3e+02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100

|||||

DB 17 AAAAAAAAAAAAAAAAAA 1

RESULT 434

AAQ75747/C

ID AAQ75747 standard; DNA; 21 BP.

XX AC AAQ75747;

XX DT 04-AUG-1995 (first entry)

XX DE Reverse transcription primer used in cDNA analysis technique.

XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
 aggregate; restriction enzyme; ss.

XX OS Synthetic.

XX PN JP06303997-A.

XX PD 01-NOV-1994.

XX PF 16-APR-1993; 93JP-0112515.

XX PR 16-APR-1993; 93JP-0112515.

XX PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

XX WPI; 1995-018287/03.

XX Analysis of cDNA and gene expression - by amplification of mRNA
PT followed by digestion with restriction enzymes
XX
PS Disclosure; Page 8; 11pp; Japanese.

XX A method for the analysis of cDNA comprises (a) preparing an
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC and a plural type of labelled reverse transcription primers
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
CC template for each reverse transcription primer; (b) digesting each of
CC the prepared aggregates of the double-stranded cDNAs with restriction
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC separate lanes. The method can be used to analyse gene expression
CC rapidly and easily.

XX Sequence 21 BP; 0 A; 2 C; 2 G; 17 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
DB 17 AAAAAAAAAAAAAAAAAA 1

RESULT 435
AAQ75748/c

ID AAQ75748 standard; DNA; 21 BP.

XX AC AAQ75748;

DT 04-AUG-1995 (first entry)

DE Reverse transcription primer used in cDNA analysis technique.

XX Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.

XX Synthetic.

XX JP06303997-A.

XX 01-NOV-1994.

XX 16-APR-1993; 93JP-0112515.

XX 16-APR-1993; 93JP-0112515.

XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

XX WPI; 1995-018287/03.

XX Analysis of cDNA and gene expression - by amplification of mRNA
PT followed by digestion with restriction enzymes

XX Disclosure; Page 8; 11pp; Japanese.

XX A method for the analysis of cDNA comprises (a) preparing an
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC and a plural type of labelled reverse transcription primers
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
CC template for each reverse transcription primer; (b) digesting each of
CC the prepared aggregates of the double-stranded cDNAs with restriction
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC separate lanes. The method can be used to analyse gene expression
CC rapidly and easily.

XX Sequence 21 BP; 1 A; 2 C; 1 G; 17 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1084 AAAAAAAAAAAAAAAAAA 1100
DB 17 AAAAAAAAAAAAAAAAAA 1

RESULT 436
AAQ75749/c

ID AAQ75749 standard; DNA; 21 BP.

XX AC AAQ75749;

DT 04-AUG-1995 (first entry)

DE Reverse transcription primer used in cDNA analysis technique.

XX Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.

XX Synthetic.

XX JP06303997-A.

XX 01-NOV-1994.

XX 16-APR-1993; 93JP-0112515.

XX 16-APR-1993; 93JP-0112515.

XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

XX WPI; 1995-018287/03.

XX Analysis of cDNA and gene expression - by amplification of mRNA
PT followed by digestion with restriction enzymes

XX Disclosure; Page 8; 11pp; Japanese.

XX A method for the analysis of cDNA comprises (a) preparing an
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC and a plural type of labelled reverse transcription primers
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
CC template for each reverse transcription primer; (b) digesting each of
CC the prepared aggregates of the double-stranded cDNAs with restriction
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC separate lanes. The method can be used to analyse gene expression
CC rapidly and easily.

XX Sequence 21 BP; 0 A; 2 C; 1 G; 18 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
DB 17 AAAAAAAAAAAAAAAAAA 1

RESULT 437
AAQ75750/c

ID AAQ75750 standard; DNA; 21 BP.

XX AC AAQ75750;

DT 04-AUG-1995 (first entry)

DE Reverse transcription primer used in cDNA analysis technique.

XX Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.

XX

CC rapidly and easily.
 XX
 SQ Sequence 21 BP; 0 A; 2 C; 1 G; 18 T; 0 other;
 Query Match 1.5%; Score 17; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1084 AAAAAAAAAAAAAAAAAA 1100
 Db 17 AAAAAAAAAAAAAAAAAA 1
 RESULT 443
 AAQ75793/c
 ID AAQ75793 standard; DNA; 21 BP.
 AC AAQ75793;
 XX
 DT 04-AUG-1995 (first entry)
 DE Reverse transcription primer used in cDNA analysis technique.
 XX
 KW Analysis; gene expression; reverse transcription; primer; cDNA;
 KW aggregate; restriction enzyme; ss.
 OS Synthetic.
 XX
 PN JP06303997-A.
 PD 01-NOV-1994.
 PF 16-APR-1993; 93JP-0112515.
 PR 16-APR-1993; 93JP-0112515.
 XX
 PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX
 DR WPI; 1995-018287/03.
 XX
 PT Analysis of cDNA and gene expression - by amplification of mRNA
 PT followed by digestion with restriction enzymes
 XX
 PS Disclosure; Page 9; 11pp; Japanese.
 XX
 CC A method for the analysis of cDNA comprises (a) preparing an
 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
 CC and a plural type of labelled reverse transcription primers
 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
 CC template for each reverse transcription primer; (b) digesting each of
 CC the prepared aggregates of the double-stranded cDNAs with restriction
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
 CC separate lanes. The method can be used to analyse gene expression
 CC rapidly and easily.
 XX
 SQ Sequence 21 BP; 0 A; 2 C; 0 G; 19 T; 0 other;
 Query Match 1.5%; Score 17; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1084 AAAAAAAAAAAAAAAAAA 1100
 Db 17 AAAAAAAAAAAAAAAAAA 1
 RESULT 444
 AAQ75794/c
 ID AAQ75794 standard; DNA; 21 BP.
 AC AAQ75794;
 XX
 DT 04-AUG-1995 (first entry)
 DE Reverse transcription primer used in cDNA analysis technique.
 XX
 KW Analysis; gene expression; reverse transcription; primer; cDNA;
 KW aggregate; restriction enzyme; ss.
 OS Synthetic.
 XX
 PN JP06303997-A.
 PD 01-NOV-1994.
 PF 16-APR-1993; 93JP-0112515.
 PR 16-APR-1993; 93JP-0112515.
 XX
 PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX
 DR WPI; 1995-018287/03.
 XX

XX
 DE Reverse transcription primer used in cDNA analysis technique.
 XX
 KW Analysis; gene expression; reverse transcription; primer; cDNA;
 KW aggregate; restriction enzyme; ss.
 OS Synthetic.
 XX
 PN JP06303997-A.
 PD 01-NOV-1994.
 PF 16-APR-1993; 93JP-0112515.
 PR 16-APR-1993; 93JP-0112515.
 XX
 PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX
 DR WPI; 1995-018287/03.
 XX
 PT Analysis of cDNA and gene expression - by amplification of mRNA
 PT followed by digestion with restriction enzymes
 XX
 PS Disclosure; Page 9; 11pp; Japanese.
 XX
 CC A method for the analysis of cDNA comprises (a) preparing an
 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
 CC and a plural type of labelled reverse transcription primers
 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
 CC template for each reverse transcription primer; (b) digesting each of
 CC the prepared aggregates of the double-stranded cDNAs with restriction
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
 CC separate lanes. The method can be used to analyse gene expression
 CC rapidly and easily.
 XX
 SQ Sequence 21 BP; 0 A; 3 C; 0 G; 18 T; 0 other;
 Query Match 1.5%; Score 17; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1084 AAAAAAAAAAAAAAAAAA 1100
 Db 17 AAAAAAAAAAAAAAAAAA 1
 RESULT 445
 AAQ75795/c
 ID AAQ75795 standard; DNA; 21 BP.
 AC AAQ75795;
 XX
 DT 04-AUG-1995 (first entry)
 DE Reverse transcription primer used in cDNA analysis technique.
 XX
 KW Analysis; gene expression; reverse transcription; primer; cDNA;
 KW aggregate; restriction enzyme; ss.
 OS Synthetic.
 XX
 PN JP06303997-A.
 PD 01-NOV-1994.
 PF 16-APR-1993; 93JP-0112515.
 PR 16-APR-1993; 93JP-0112515.
 XX
 PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX
 DR WPI; 1995-018287/03.
 XX

PT Analysis of cDNA and gene expression - by amplification of mRNA
PT followed by digestion with restriction enzymes
XX
PS
XX Disclosure; Page 9; 11pp; Japanese.

XX A method for the analysis of cDNA comprises (a) preparing an
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC and a plural type of labelled reverse transcription primers
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
CC template for each reverse transcription primer; (b) digesting each of
CC the prepared aggregates of the double-stranded cDNAs with restriction
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC separate lanes. The method can be used to analyse gene expression
CC rapidly and easily.

XX Sequence 21 BP; 0 A; 3 C; 1 G; 17 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
DB 17 AAAAAAAAAAAAAAAAAA 1

RESULT 446
AAQ75796/c
ID AAQ75796 standard; DNA; 21 BP.
XX AC AAQ75796;
XX 04-AUG-1995 (first entry)
DE Reverse transcription primer used in cDNA analysis technique.

XX Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
OS Synthetic.

XX JP06303997-A.
XX 01-NOV-1994.

XX 16-APR-1993; 93JP-0112515.
XX 16-APR-1993; 93JP-0112515.

XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX WPI; 1995-018287/03.

XX Analysis of cDNA and gene expression - by amplification of mRNA
PT followed by digestion with restriction enzymes
XX
PS Disclosure; Page 9; 11pp; Japanese.

XX A method for the analysis of cDNA comprises (a) preparing an
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC and a plural type of labelled reverse transcription primers
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
CC template for each reverse transcription primer; (b) digesting each of
CC the prepared aggregates of the double-stranded cDNAs with restriction
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC separate lanes. The method can be used to analyse gene expression
CC rapidly and easily.

XX Sequence 21 BP; 1 A; 3 C; 0 G; 17 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
DB 17 AAAAAAAAAAAAAAAAAA 1

RESULT 447
AAQ75797/c
ID AAQ75797 standard; DNA; 21 BP.
XX AC AAQ75797;
XX 04-AUG-1995 (first entry)
DE Reverse transcription primer used in cDNA analysis technique.

XX Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
OS Synthetic.

XX JP06303997-A.
XX 01-NOV-1994.

XX 16-APR-1993; 93JP-0112515.
XX 16-APR-1993; 93JP-0112515.

XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX WPI; 1995-018287/03.

XX Analysis of cDNA and gene expression - by amplification of mRNA
PT followed by digestion with restriction enzymes

XX Disclosure; Page 9; 11pp; Japanese.

XX A method for the analysis of cDNA comprises (a) preparing an
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC and a plural type of labelled reverse transcription primers
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
CC template for each reverse transcription primer; (b) digesting each of
CC the prepared aggregates of the double-stranded cDNAs with restriction
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC separate lanes. The method can be used to analyse gene expression
CC rapidly and easily.

XX Sequence 21 BP; 0 A; 3 C; 0 G; 18 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
DB 17 AAAAAAAAAAAAAAAAAA 1

RESULT 448
AAQ75798/c
ID AAQ75798 standard; DNA; 21 BP.
XX AC AAQ75798;
XX 04-AUG-1995 (first entry)
DE Reverse transcription primer used in cDNA analysis technique.

XX Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
OS Synthetic.

```
XX PN JP06303997-A.
XX CC
XX PD 01-NOV-1994.
XX CC
XX PF 16-APR-1993; 93JP-0112515.
XX CC
XX PR 16-APR-1993; 93JP-0112515.
XX CC
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX CC
XX DR WPI; 1995-018287/03.
XX CC
XX PT Analysis of cDNA and gene expression - by amplification of mRNA
XX PT followed by digestion with restriction enzymes
XX PS Disclosure; Page 9; 11pp; Japanese.
XX CC
XX CC A method for the analysis of cDNA comprises (a) preparing an
XX CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
XX CC and a plural type of labelled reverse transcription primers
XX CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
XX CC template for each reverse transcription primer; (b) digesting each of
XX CC the prepared aggregates of the double-stranded cDNAs with restriction
XX CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
XX CC separate lanes. The method can be used to analyse gene expression
XX CC rapidly and easily.
XX CC
XX CC Sequence 21 BP; 0 A; 4 C; 0 G; 17 T; 0 other;
XX CC
XX CC Query Match 1.5%; Score 17; DB 1; Length 21;
XX CC Best Local Similarity 100.0%; Pred. No. 2.3e+02;
XX CC Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX CC
QY 1084 AAAAAAAAAAAAAAAAAA 1100
DB 17 AAAAAAAAAAAAAAAAAA 1

RESULT 449
AAQ75773/c
ID AAQ75773 standard; DNA; 21 BP.
XX AC AAQ75773;
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX KW aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-0112515.
XX PR 16-APR-1993; 93JP-0112515.
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX PT Analysis of cDNA and gene expression - by amplification of mRNA
XX PT followed by digestion with restriction enzymes
XX PS Disclosure; Page 9; 11pp; Japanese.
XX CC
XX CC A method for the analysis of cDNA comprises (a) preparing an
XX CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
XX CC and a plural type of labelled reverse transcription primers
XX CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
XX CC template for each reverse transcription primer; (b) digesting each of
XX CC the prepared aggregates of the double-stranded cDNAs with restriction
XX CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
XX CC separate lanes. The method can be used to analyse gene expression
XX CC rapidly and easily.
XX CC
XX CC Sequence 21 BP; 0 A; 4 C; 0 G; 17 T; 0 other;
XX CC
XX CC Query Match 1.5%; Score 17; DB 1; Length 21;
XX CC Best Local Similarity 100.0%; Pred. No. 2.3e+02;
XX CC Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX CC
QY 1084 AAAAAAAAAAAAAAAAAA 1100
DB 17 AAAAAAAAAAAAAAAAAA 1

RESULT 450
AAQ75774/c
ID AAQ75774 standard; DNA; 21 BP.
XX AC AAQ75774;
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX KW aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-0112515.
XX PR 16-APR-1993; 93JP-0112515.
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX PT Analysis of cDNA and gene expression - by amplification of mRNA
XX PT followed by digestion with restriction enzymes
XX PS Disclosure; Page 9; 11pp; Japanese.
XX CC
XX CC A method for the analysis of cDNA comprises (a) preparing an
XX CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
XX CC and a plural type of labelled reverse transcription primers
XX CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
XX CC template for each reverse transcription primer; (b) digesting each of
XX CC the prepared aggregates of the double-stranded cDNAs with restriction
XX CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
XX CC separate lanes. The method can be used to analyse gene expression
XX CC rapidly and easily.
XX CC
XX CC Sequence 21 BP; 1 A; 2 C; 0 G; 18 T; 0 other;
XX CC
XX CC Query Match 1.5%; Score 17; DB 1; Length 21;
XX CC Best Local Similarity 100.0%; Pred. No. 2.3e+02;
XX CC Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX CC
QY 1084 AAAAAAAAAAAAAAAAAA 1100
DB 17 AAAAAAAAAAAAAAAAAA 1

RESULT 451
```

```
CC and a plural type of labelled reverse transcription primers
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
CC template for each reverse transcription primer; (b) digesting each of
CC the prepared aggregates of the double-stranded cDNAs with restriction
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC separate lanes. The method can be used to analyse gene expression
CC rapidly and easily.
XX CC
XX CC Sequence 21 BP; 1 A; 1 C; 0 G; 19 T; 0 other;
XX CC
XX CC Query Match 1.5%; Score 17; DB 1; Length 21;
XX CC Best Local Similarity 100.0%; Pred. No. 2.3e+02;
XX CC Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX CC
QY 1084 AAAAAAAAAAAAAAAAAA 1100
DB 17 AAAAAAAAAAAAAAAAAA 1

RESULT 450
AAQ75774/c
ID AAQ75774 standard; DNA; 21 BP.
XX AC AAQ75774;
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX KW aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-0112515.
XX PR 16-APR-1993; 93JP-0112515.
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX PT Analysis of cDNA and gene expression - by amplification of mRNA
XX PT followed by digestion with restriction enzymes
XX PS Disclosure; Page 9; 11pp; Japanese.
XX CC
XX CC A method for the analysis of cDNA comprises (a) preparing an
XX CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
XX CC and a plural type of labelled reverse transcription primers
XX CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
XX CC template for each reverse transcription primer; (b) digesting each of
XX CC the prepared aggregates of the double-stranded cDNAs with restriction
XX CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
XX CC separate lanes. The method can be used to analyse gene expression
XX CC rapidly and easily.
XX CC
XX CC Sequence 21 BP; 1 A; 2 C; 0 G; 18 T; 0 other;
XX CC
XX CC Query Match 1.5%; Score 17; DB 1; Length 21;
XX CC Best Local Similarity 100.0%; Pred. No. 2.3e+02;
XX CC Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX CC
QY 1084 AAAAAAAAAAAAAAAAAA 1100
DB 17 AAAAAAAAAAAAAAAAAA 1

RESULT 451
```


| | |
|------------|---|
| DE | Reverse transcription primer used in cDNA analysis technique. |
| XX | |
| XX | Analysis; gene expression; reverse transcription; primer; cDNA; |
| KW | aggregate; restriction enzyme; ss. |
| XX | |
| OS | Synthetic. |
| XX | |
| PN | JP06303997-A. |
| XX | |
| PD | 01-NOV-1994. |
| XX | |
| XX | 16-APR-1993; 93JP-0112515. |
| XX | |
| PR | 16-APR-1993; 93JP-0112515. |
| XX | |
| PA | (NITE) NIPPON TELEGRAPH & TELEPHONE CORP. |
| XX | |
| XX | WPI; 1995-018287/03. |
| XX | |
| PT | Analysis of cDNA and gene expression - by amplification of mRNA |
| PT | followed by digestion with restriction enzymes |
| XX | |
| PS | Disclosure; Page 9; lpp; Japanese. |
| XX | |
| CC | A method for the analysis of cDNA comprises (a) preparing an |
| CC | aggregate of double-stranded cDNAs by using an aggregate of mRNAs |
| CC | and a plural type of labelled reverse transcription primers |
| CC | (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the |
| CC | template for each reverse transcription primer; (b) digesting each of |
| CC | the prepared aggregates of the double-stranded cDNAs with restriction |
| CC | enzyme and; (c) electrophoresing the digested aggregate of cDNAs in |
| CC | separate lanes. The method can be used to analyse gene expression |
| CC | rapidly and easily. |
| XX | |
| SQ | Sequence 21 BP; 1 A; 2 C; 0 G; 18 T; 0 other; |
| | |
| | Query Match 1.5%; Score 17; DB 1; Length 21; |
| | Best Local Similarity 100.0%; Pred. No. 2.3e+02; |
| | Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |
| | |
| QY | 1084 AAAAAAAAAAAAAAAAAA 1100 |
| | |
| Db | 17 AAAAAAAAAAAAAAAAAA 1 |
| | |
| RESULT 456 | |
| AAQ75781/c | |
| ID | AAQ75781 standard; DNA; 21 BP. |
| XX | |
| AC | AAQ75781; |
| XX | |
| DT | 04-AUG-1995 (first entry) |
| XX | |
| DE | Reverse transcription primer used in cDNA analysis technique. |
| XX | |
| KW | Analysis; gene expression; reverse transcription; primer; cDNA; |
| KW | aggregate; restriction enzyme; ss. |
| OS | Synthetic. |
| XX | |
| PN | JP06303997-A. |
| XX | |
| PD | 01-NOV-1994. |
| XX | |
| PF | 16-APR-1993; 93JP-0112515. |
| XX | |
| PR | 16-APR-1993; 93JP-0112515. |
| XX | |
| PA | (NITE) NIPPON TELEGRAPH & TELEPHONE CORP. |
| XX | |
| XX | WPI; 1995-018287/03. |
| XX | |
| PT | Analysis of cDNA and gene expression - by amplification of mRNA |

```
PT followed by digestion with restriction enzymes
PS Disclosure; Page 9; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC and a plural type of labelled reverse transcription primers
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
CC template for each reverse transcription primer; (b) digesting each of
CC the prepared aggregates of the double-stranded cDNAs with restriction
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC separate lanes. The method can be used to analyse gene expression
CC rapidly and easily.
XX
SQ Sequence 21 BP; 0 A; 2 C; 0 G; 19 T; 0 other;
Query Match 1.5%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1084 AAAAAAAAAAAAAAAAAA 1100
Db 17 AAAAAAAAAAAAAAAAAA 1
RESULT 457
AAQ75782/c
ID AAQ75782 standard; DNA; 21 BP.
XX
AC AAQ75782;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-0112515.
XX
PR 16-APR-1993; 93JP-0112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
DE Analysis of cDNA and gene expression - by amplification of mRNA
DE followed by digestion with restriction enzymes
XX
PS Disclosure; Page 9; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC and a plural type of labelled reverse transcription primers
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
CC template for each reverse transcription primer; (b) digesting each of
CC the prepared aggregates of the double-stranded cDNAs with restriction
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC separate lanes. The method can be used to analyse gene expression
CC rapidly and easily.
XX
SQ Sequence 21 BP; 0 A; 3 C; 0 G; 18 T; 0 other;
Query Match 1.5%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1084 AAAAAAAAAAAAAAAAAA 1100
Db 17 AAAAAAAAAAAAAAAAAA 1
RESULT 457
AAQ75782/c
ID AAQ75782 standard; DNA; 21 BP.
XX
AC AAQ75782;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-0112515.
XX
PR 16-APR-1993; 93JP-0112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
DE Analysis of cDNA and gene expression - by amplification of mRNA
DE followed by digestion with restriction enzymes
XX
PS Disclosure; Page 9; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC and a plural type of labelled reverse transcription primers
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
CC template for each reverse transcription primer; (b) digesting each of
CC the prepared aggregates of the double-stranded cDNAs with restriction
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC separate lanes. The method can be used to analyse gene expression
CC rapidly and easily.
XX
SQ Sequence 21 BP; 0 A; 3 C; 0 G; 18 T; 0 other;
Query Match 1.5%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1084 AAAAAAAAAAAAAAAAAA 1100
Db 17 AAAAAAAAAAAAAAAAAA 1
RESULT 459
AAQ75784/c
ID AAQ75784 standard; DNA; 21 BP.
XX
AC AAQ75784;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
```



```
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-0112515.
XX
PR 16-APR-1993; 93JP-0112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA
XX followed by digestion with restriction enzymes
XX
PS Disclosure; Page 9; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC and a plural type of labelled reverse transcription primers
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
CC template for each reverse transcription primer; (b) digesting each of
CC the prepared aggregates of the double-stranded cDNAs with restriction
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC separate lanes. The method can be used to analyse gene expression
CC rapidly and easily.
XX
SQ Sequence 21 BP; 1 A; 2 C; 1 G; 17 T; 0 other;
XX
Query Match 1.5%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1084 AAAAAAAAAAAAAAAAAA 1100
Db 17 AAAAAAAAAAAAAAAAAA 1
XX
RESULT 460
AAQ75785/c
ID AAQ75785 standard; DNA; 21 BP.
XX
AC AAQ75785;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-0112515.
XX
PR 16-APR-1993; 93JP-0112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA
XX followed by digestion with restriction enzymes
XX
PS Disclosure; Page 9; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC and a plural type of labelled reverse transcription primers
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
CC template for each reverse transcription primer; (b) digesting each of
CC the prepared aggregates of the double-stranded cDNAs with restriction
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC separate lanes. The method can be used to analyse gene expression
CC rapidly and easily.
XX
SQ Sequence 21 BP; 1 A; 2 C; 1 G; 17 T; 0 other;
XX
Query Match 1.5%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1084 AAAAAAAAAAAAAAAAAA 1100
Db 17 AAAAAAAAAAAAAAAAAA 1
XX
RESULT 460
AAQ75785/c
ID AAQ75785 standard; DNA; 21 BP.
XX
AC AAQ75785;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-0112515.
XX
PR 16-APR-1993; 93JP-0112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA
XX followed by digestion with restriction enzymes
XX
PS Disclosure; Page 9; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC and a plural type of labelled reverse transcription primers
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
CC template for each reverse transcription primer; (b) digesting each of
CC the prepared aggregates of the double-stranded cDNAs with restriction
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC separate lanes. The method can be used to analyse gene expression
CC rapidly and easily.
XX
SQ Sequence 21 BP; 0 A; 2 C; 1 G; 17 T; 0 other;
XX
Query Match 1.5%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1084 AAAAAAAAAAAAAAAAAA 1100
Db 17 AAAAAAAAAAAAAAAAAA 1
XX
RESULT 462
AAQ75767/c
```



```
XX PS Disclosure; Page 7; 11pp; Japanese.
XX CC
XX CC A method for the analysis of cDNA comprises (a) preparing an
XX CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
XX CC and a plural type of labelled reverse transcription primers
XX CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
XX CC template for each reverse transcription primer; (b) digesting each of
XX CC the prepared aggregates of the double-stranded cDNAs with restriction
XX CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
XX CC separate lanes. The method can be used to analyse gene expression
XX CC rapidly and easily.
XX SQ Sequence 21 BP; 0 A; 2 C; 2 G; 17 T; 0 other;
XX
XX Query Match 1.5%; Score 17; DB 1; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 2.3e+02;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1084 AAAAAAAAAAAAAAAAAA 1100
XX DB 17 AAAAAAAAAAAAAAAAAA 1
XX
XX RESULT 468
XX AAQ75668/c
XX ID AAQ75668 standard; DNA; 21 BP.
XX AC AAQ75668;
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX KW aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-0112515.
XX PR 16-APR-1993; 93JP-0112515.
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX DE Analysis of cDNA and gene expression - by amplification of mRNA
XX PT followed by digestion with restriction enzymes
XX PS Disclosure; Page 7; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an
XX CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
XX CC and a plural type of labelled reverse transcription primers
XX CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
XX CC template for each reverse transcription primer; (b) digesting each of
XX CC the prepared aggregates of the double-stranded cDNAs with restriction
XX CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
XX CC separate lanes. The method can be used to analyse gene expression
XX CC rapidly and easily.
XX SQ Sequence 21 BP; 1 A; 2 C; 1 G; 17 T; 0 other;
XX
XX Query Match 1.5%; Score 17; DB 1; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 2.3e+02;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1084 AAAAAAAAAAAAAAAAAA 1100
XX PN JP06303997-A.
```

```
Db 17 AAAAAAAAAAAAAAAAAA 1
XX
XX RESULT 469
XX AAQ75669/c
XX ID AAQ75669 standard; DNA; 21 BP.
XX AC AAQ75669;
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX KW aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-0112515.
XX PR 16-APR-1993; 93JP-0112515.
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX DE Analysis of cDNA and gene expression - by amplification of mRNA
XX PT followed by digestion with restriction enzymes
XX PS Disclosure; Page 7; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an
XX CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
XX CC and a plural type of labelled reverse transcription primers
XX CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
XX CC template for each reverse transcription primer; (b) digesting each of
XX CC the prepared aggregates of the double-stranded cDNAs with restriction
XX CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
XX CC separate lanes. The method can be used to analyse gene expression
XX CC rapidly and easily.
XX SQ Sequence 21 BP; 0 A; 2 C; 1 G; 18 T; 0 other;
XX
XX Query Match 1.5%; Score 17; DB 1; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 2.3e+02;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1084 AAAAAAAAAAAAAAAAAA 1100
XX DB 17 AAAAAAAAAAAAAAAAAA 1
XX
XX RESULT 470
XX AAQ75670/c
XX ID AAQ75670 standard; DNA; 21 BP.
XX AC AAQ75670;
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX KW aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
```

```

XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-0112515.
XX PR 16-APR-1993; 93JP-0112515.
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX PT Analysis of cDNA and gene expression - by amplification of mRNA
XX FT followed by digestion with restriction enzymes
XX PS Disclosure; Page 7; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an
XX CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
XX CC and a plural type of labelled reverse transcription primers
XX CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
XX CC template for each reverse transcription primer; (b) digesting each of
XX CC the prepared aggregates of the double-stranded cDNAs with restriction
XX CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
XX CC separate lanes. The method can be used to analyse gene expression
XX CC rapidly and easily.
XX SQ Sequence 21 BP; 0 A; 3 C; 1 G; 17 T; 0 other;
      Query Match 1.5%; Score 17; DB 1; Length 21;
      Best Local Similarity 100.0%; Pred. No. 2.3e+02;
      Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
Db 17 AAAAAAAAAAAAAAAAAA 1

RESULT 471
AAQ75607/c
ID AAQ75607 standard; DNA; 21 BP.
AC AAQ75607;
XX 04-AUG-1995 (first entry)
DT Reverse transcription primer used in cDNA analysis technique.
DE Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX Synthetic.
XX JP06303997-A.
PN 01-NOV-1994.
XX 16-APR-1993; 93JP-0112515.
XX 16-APR-1993; 93JP-0112515.
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX WPI; 1995-018287/03.
XX Analysis of cDNA and gene expression - by amplification of mRNA
XX PT followed by digestion with restriction enzymes
XX PS Disclosure; Page 5; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an
XX CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
XX CC and a plural type of labelled reverse transcription primers
XX CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
XX CC template for each reverse transcription primer; (b) digesting each of
XX CC the prepared aggregates of the double-stranded cDNAs with restriction
XX CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
XX CC separate lanes. The method can be used to analyse gene expression
XX CC rapidly and easily.
XX SQ Sequence 21 BP; 1 A; 0 C; 3 G; 17 T; 0 other;
      Query Match 1.5%; Score 17; DB 1; Length 21;
      Best Local Similarity 100.0%; Pred. No. 2.3e+02;
      Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
Db 17 AAAAAAAAAAAAAAAAAA 1

RESULT 471
AAQ75607/c
ID AAQ75607 standard; DNA; 21 BP.
AC AAQ75607;
XX 04-AUG-1995 (first entry)
DT Reverse transcription primer used in cDNA analysis technique.
DE Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX Synthetic.
XX JP06303997-A.
PN 01-NOV-1994.
XX 16-APR-1993; 93JP-0112515.
XX 16-APR-1993; 93JP-0112515.
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX WPI; 1995-018287/03.
XX Analysis of cDNA and gene expression - by amplification of mRNA
XX PT followed by digestion with restriction enzymes
XX PS Disclosure; Page 5; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an
XX CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
XX CC and a plural type of labelled reverse transcription primers
XX CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the

```

```

CC template for each reverse transcription primer; (b) digesting each of
CC the prepared aggregates of the double-stranded cDNAs with restriction
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC separate lanes. The method can be used to analyse gene expression
CC rapidly and easily.
XX SQ Sequence 21 BP; 0 A; 0 C; 4 G; 17 T; 0 other;
      Query Match 1.5%; Score 17; DB 1; Length 21;
      Best Local Similarity 100.0%; Pred. No. 2.3e+02;
      Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
Db 17 AAAAAAAAAAAAAAAAAA 1

RESULT 472
AAQ75608/c
ID AAQ75608 standard; DNA; 21 BP.
XX AAQ75608;
AC AAQ75608;
XX 04-AUG-1995 (first entry)
DT Reverse transcription primer used in cDNA analysis technique.
XX 04-AUG-1995 (first entry)
DE Reverse transcription primer used in cDNA analysis technique.
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX Synthetic.
XX JP06303997-A.
PN 01-NOV-1994.
XX 16-APR-1993; 93JP-0112515.
XX 16-APR-1993; 93JP-0112515.
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX WPI; 1995-018287/03.
XX Analysis of cDNA and gene expression - by amplification of mRNA
XX PT followed by digestion with restriction enzymes
XX PS Disclosure; Page 5; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an
XX CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
XX CC and a plural type of labelled reverse transcription primers
XX CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
XX CC template for each reverse transcription primer; (b) digesting each of
XX CC the prepared aggregates of the double-stranded cDNAs with restriction
XX CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
XX CC separate lanes. The method can be used to analyse gene expression
XX CC rapidly and easily.
XX SQ Sequence 21 BP; 1 A; 0 C; 3 G; 17 T; 0 other;
      Query Match 1.5%; Score 17; DB 1; Length 21;
      Best Local Similarity 100.0%; Pred. No. 2.3e+02;
      Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
Db 17 AAAAAAAAAAAAAAAAAA 1

RESULT 473
AAQ75609/c
ID AAQ75609 standard; DNA; 21 BP.

```



```

Db      17 AAAAAAAAAAAAAAAAAA 1

RESULT 480
AAQ75612/c
ID      AAQ75612 standard; DNA; 21 BP.
XX
XX      AAQ75612;
AC
XX
XX      04-AUG-1995 (first entry)
DT
XX
XX
DE
DE
DE
XX      Reverse transcription primer used in cDNA analysis technique.
KW
KW      Analysis; gene expression; reverse transcription; primer; cDNA;
KW      aggregate; restriction enzyme; ss.
XX
XX      Synthetic.
OS
XX
XX      JPO6303997-A.
PN
XX
XX
XX
XX      01-NOV-1994.
PD
XX
XX      16-APR-1993; 93JP-0112515.
PF
XX
XX      16-APR-1993; 93JP-0112515.
PR
XX
XX      (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
PA
PA
XX      WFI; 1995-018287/03.
DR
XX
XX      Analysis of cDNA and gene expression - by amplification of mRNA
PT      followed by digestion with restriction enzymes
PT
XX
XX      Disclosure; Page 5; 11pp; Japanese.
PS
XX
XX      A method for the analysis of cDNA comprises (a) preparing an
CC      aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC      and a plural type of labelled reverse transcription primers
CC      (GENESEQ files AAQ75547-075798) and using the aggregate of mRNAs as the
CC      template for each reverse transcription primer; (b) digesting each of
CC      the prepared aggregates of the double-stranded cDNAs with restriction
CC      enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC      separate lanes. The method can be used to analyse gene expression
CC      rapidly and easily.
XX
XX      Sequence 21 BP; 2 A; 0 C; 2 G; 17 T; 0 other;
SQ      Query Match 1.5%; Score 17; DB 1; Length 21;
      Best Local Similarity 100.0%; Pred.No.2.3e+02;
      Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1084 AAAAAAAAAAAAAAAAAA 1100
      |||||||
Db      17 AAAAAAAAAAAAAAAAAA 1

RESULT 481
AAQ75613/c
ID      AAQ75613 standard; DNA; 21 BP.
XX
XX      AAQ75613;
AC
XX
XX
XX      04-AUG-1995 (first entry)
DT
XX
XX
XX      Reverse transcription primer used in cDNA analysis technique.
DE
DE
DE
XX      Analysis; gene expression; reverse transcription; primer; cDNA;
KW      aggregate; restriction enzyme; ss.
KW
XX
XX      Synthetic.
OS
XX
XX      JPO6303997-A.
FN
FN
XX

```


PD 01-NOV-1994.
 XX
 XX 16-APR-1993; 93JP-0112515.
 XX
 XX 16-APR-1993; 93JP-0112515.
 XX
 XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX
 XX WPI; 1995-018287/03.
 XX
 XX Analysis of cDNA and gene expression - by amplification of mRNA
 PT followed by digestion with restriction enzymes
 PT
 XX Disclosure; Page 5; 11pp; Japanese.
 XX
 XX A method for the analysis of cDNA comprises (a) preparing an
 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
 CC and a plural type of labelled reverse transcription primers
 CC (GENESEQ files AAQ75614-Q75798) and using the aggregate of mRNAs as the
 CC template for each reverse transcription primer; (b) digesting each of
 CC the prepared aggregates of the double-stranded cDNAs with restriction
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
 CC separate lanes. The method can be used to analyse gene expression
 CC rapidly and easily.
 XX
 XX Sequence 21 BP; 1 A; 0 C; 2 G; 18 T; 0 other;
 SQ
 Query Match 1.5%; Score 17; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1084 AAAAAAAAAAAAAAAAAA 1100
 DB 17 AAAAAAAAAAAAAAAAAA 1
 RESULT 482
 AAQ75614/c
 ID AAQ75614 standard; DNA; 21 BP.
 XX
 XX AAQ75614;
 XX
 XX 04-AUG-1995 (first entry)
 XX
 XX Reverse transcription primer used in cDNA analysis technique.
 DE
 XX Analysis; gene expression; reverse transcription; primer; cDNA;
 KW aggregate; restriction enzyme; ss.
 XX
 XX Synthetic.
 OS
 XX JP06303997-A.
 PN
 XX 01-NOV-1994.
 PD
 XX 16-APR-1993; 93JP-0112515.
 PF
 XX 16-APR-1993; 93JP-0112515.
 PR
 XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 PA
 XX WPI; 1995-018287/03.
 DR
 XX
 XX Analysis of cDNA and gene expression - by amplification of mRNA
 PT followed by digestion with restriction enzymes
 PT
 XX Disclosure; Page 6; 11pp; Japanese.
 XX
 XX A method for the analysis of cDNA comprises (a) preparing an
 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
 CC and a plural type of labelled reverse transcription primers
 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
 CC template for each reverse transcription primer; (b) digesting each of
 CC the prepared aggregates of the double-stranded cDNAs with restriction
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
 CC separate lanes. The method can be used to analyse gene expression
 CC rapidly and easily.
 XX
 XX Sequence 21 BP; 1 A; 0 C; 2 G; 18 T; 0 other;
 SQ
 Query Match 1.5%; Score 17; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1084 AAAAAAAAAAAAAAAAAA 1100
 DB 17 AAAAAAAAAAAAAAAAAA 1
 RESULT 482
 AAQ75614/c
 ID AAQ75614 standard; DNA; 21 BP.
 XX
 XX AAQ75614;
 XX
 XX 04-AUG-1995 (first entry)
 XX
 XX Reverse transcription primer used in cDNA analysis technique.
 DE
 XX Analysis; gene expression; reverse transcription; primer; cDNA;
 KW aggregate; restriction enzyme; ss.
 XX
 XX Synthetic.
 OS
 XX JP06303997-A.
 PN
 XX 01-NOV-1994.
 PD
 XX 16-APR-1993; 93JP-0112515.
 PF
 XX 16-APR-1993; 93JP-0112515.
 PR
 XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 PA
 XX WPI; 1995-018287/03.
 DR
 XX
 XX Analysis of cDNA and gene expression - by amplification of mRNA
 PT followed by digestion with restriction enzymes
 PT
 XX Disclosure; Page 6; 11pp; Japanese.
 XX
 XX A method for the analysis of cDNA comprises (a) preparing an
 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
 CC and a plural type of labelled reverse transcription primers
 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
 CC template for each reverse transcription primer; (b) digesting each of

CC the prepared aggregates of the double-stranded cDNAs with restriction
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
 CC separate lanes. The method can be used to analyse gene expression
 CC rapidly and easily.
 XX
 XX Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 other;
 SQ
 Query Match 1.5%; Score 17; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1084 AAAAAAAAAAAAAAAAAA 1100
 DB 17 AAAAAAAAAAAAAAAAAA 1
 RESULT 483
 AAQ75615/c
 ID AAQ75615 standard; DNA; 21 BP.
 XX
 XX AAQ75615;
 AC
 XX 04-AUG-1995 (first entry)
 DT
 XX Reverse transcription primer used in cDNA analysis technique.
 DE
 XX Analysis; gene expression; reverse transcription; primer; cDNA;
 KW aggregate; restriction enzyme; ss.
 XX
 XX Synthetic.
 OS
 XX JP06303997-A.
 PN
 XX 01-NOV-1994.
 PD
 XX 16-APR-1993; 93JP-0112515.
 PF
 XX 16-APR-1993; 93JP-0112515.
 PR
 XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 PA
 XX WPI; 1995-018287/03.
 DR
 XX
 XX Analysis of cDNA and gene expression - by amplification of mRNA
 PT followed by digestion with restriction enzymes
 PT
 XX Disclosure; Page 6; 11pp; Japanese.
 XX
 XX A method for the analysis of cDNA comprises (a) preparing an
 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
 CC and a plural type of labelled reverse transcription primers
 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
 CC template for each reverse transcription primer; (b) digesting each of
 CC the prepared aggregates of the double-stranded cDNAs with restriction
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
 CC separate lanes. The method can be used to analyse gene expression
 CC rapidly and easily.
 XX
 XX Sequence 21 BP; 0 A; 0 C; 3 G; 18 T; 0 other;
 SQ
 Query Match 1.5%; Score 17; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1084 AAAAAAAAAAAAAAAAAA 1100
 DB 17 AAAAAAAAAAAAAAAAAA 1
 RESULT 484
 AAQ75617/c
 ID AAQ75617 standard; DNA; 21 BP.
 XX

AC AAQ75617;
 XX
 DT 04-AUG-1995 (first entry)
 XX
 DE Reverse transcription primer used in cDNA analysis technique.
 XX
 KW Analysis; gene expression; reverse transcription; primer; cDNA;
 XX aggregate; restriction enzyme; ss.
 XX
 OS Synthetic.
 XX
 PN JP06303997-A.
 XX
 PD 01-NOV-1994.
 XX
 PF 16-APR-1993; 93JP-0112515.
 XX
 PR 16-APR-1993; 93JP-0112515.
 XX
 PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX
 DR WPI; 1995-018287/03.
 XX
 PT Analysis of cDNA and gene expression - by amplification of mRNA
 XX followed by digestion with restriction enzymes
 XX
 PS Disclosure; Page 6; 11pp; Japanese.
 XX
 CC A method for the analysis of cDNA comprises (a) preparing an
 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
 CC and a plural type of labelled reverse transcription primers
 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
 CC template for each reverse transcription primer; (b) digesting each of
 CC the prepared aggregates of the double-stranded cDNAs with restriction
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
 CC separate lanes. The method can be used to analyse gene expression
 CC rapidly and easily.
 XX
 SQ Sequence 21 BP; 0 A; 0 C; 2 G; 19 T; 0 other;
 Query Match 1.5%; Score 17; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 AC
 DT 04-AUG-1995 (first entry)
 XX
 DE Reverse transcription primer used in cDNA analysis technique.
 XX
 KW Analysis; gene expression; reverse transcription; primer; cDNA;
 XX aggregate; restriction enzyme; ss.
 XX
 OS Synthetic.
 XX
 PN JP06303997-A.
 XX
 PD 01-NOV-1994.
 XX
 PF 16-APR-1993; 93JP-0112515.
 XX
 PR 16-APR-1993; 93JP-0112515.
 XX
 PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX
 DR WPI; 1995-018287/03.
 XX
 PT Analysis of cDNA and gene expression - by amplification of mRNA
 XX followed by digestion with restriction enzymes
 XX
 PS Disclosure; Page 6; 11pp; Japanese.
 XX
 CC A method for the analysis of cDNA comprises (a) preparing an
 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
 CC and a plural type of labelled reverse transcription primers
 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
 CC template for each reverse transcription primer; (b) digesting each of
 CC the prepared aggregates of the double-stranded cDNAs with restriction
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
 CC separate lanes. The method can be used to analyse gene expression
 CC rapidly and easily.
 XX
 SQ Sequence 21 BP; 0 A; 0 C; 2 G; 19 T; 0 other;
 Query Match 1.5%; Score 17; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 AC
 DT 04-AUG-1995 (first entry)
 XX
 DE Reverse transcription primer used in cDNA analysis technique.
 XX
 KW Analysis; gene expression; reverse transcription; primer; cDNA;
 XX aggregate; restriction enzyme; ss.
 XX
 OS Synthetic.
 XX
 PN JP06303997-A.
 XX
 PD 01-NOV-1994.
 XX
 PF 16-APR-1993; 93JP-0112515.
 XX
 PR 16-APR-1993; 93JP-0112515.
 XX
 PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

XX WPI; 1995-018287/03.
 DR
 XX Analysis of cDNA and gene expression - by amplification of mRNA
 XX followed by digestion with restriction enzymes
 XX
 PS Disclosure; Page 6; 11pp; Japanese.
 XX
 CC A method for the analysis of cDNA comprises (a) preparing an
 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
 CC and a plural type of labelled reverse transcription primers
 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
 CC template for each reverse transcription primer; (b) digesting each of
 CC the prepared aggregates of the double-stranded cDNAs with restriction
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
 CC separate lanes. The method can be used to analyse gene expression
 CC rapidly and easily.
 XX
 SQ Sequence 21 BP; 0 A; 1 C; 2 G; 18 T; 0 other;
 Query Match 1.5%; Score 17; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1084 AAAAAAAAAAAAAAAAAA 1100
 |||||
 DB 17 AAAAAAAAAAAAAAAAAA 1
 RESULT 486
 AAQ75619/c
 ID AAQ75619 standard; DNA; 21 BP.
 XX
 AC AAQ75619;
 XX
 DT 04-AUG-1995 (first entry)
 XX
 DE Reverse transcription primer used in cDNA analysis technique.
 XX
 KW Analysis; gene expression; reverse transcription; primer; cDNA;
 XX aggregate; restriction enzyme; ss.
 XX
 OS Synthetic.
 XX
 PN JP06303997-A.
 XX
 PD 01-NOV-1994.
 XX
 PF 16-APR-1993; 93JP-0112515.
 XX
 PR 16-APR-1993; 93JP-0112515.
 XX
 PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX
 DR WPI; 1995-018287/03.
 XX
 PT Analysis of cDNA and gene expression - by amplification of mRNA
 XX followed by digestion with restriction enzymes
 XX
 PS Disclosure; Page 6; 11pp; Japanese.
 XX
 CC A method for the analysis of cDNA comprises (a) preparing an
 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
 CC and a plural type of labelled reverse transcription primers
 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
 CC template for each reverse transcription primer; (b) digesting each of
 CC the prepared aggregates of the double-stranded cDNAs with restriction
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
 CC separate lanes. The method can be used to analyse gene expression
 CC rapidly and easily.
 XX
 SQ Sequence 21 BP; 0 A; 1 C; 3 G; 17 T; 0 other;

XX
PN JP06303997-A.
XX
PD 01-NOV-1994.

```
XX PF 16-APR-1993; 93JP-0112515.
XX PR 16-APR-1993; 93JP-0112515.
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX PT Analysis of cDNA and gene expression - by amplification of mRNA
XX followed by digestion with restriction enzymes
XX PS Disclosure; Page 6; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC and a plural type of labelled reverse transcription primers
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
CC template for each reverse transcription primer; (b) digesting each of
CC the prepared aggregates of the double-stranded cDNAs with restriction
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC separate lanes. The method can be used to analyse gene expression
CC rapidly and easily.
XX SQ Sequence 21 BP; 1 A; 2 C; 1 G; 17 T; 0 other;
Query Match 1.5%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1084 AAAAAAAAAAAAAAA 1100
DB 17 AAAAAAAAAAAAAAA 1
RESULT 493
AAQ75663/c
ID AAQ75663 standard; DNA; 21 BP.
AC AAQ75663;
XX 04-AUG-1995 (first entry)
XX Reverse transcription primer used in cDNA analysis technique.
XX Analysis; Gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX Synthetic.
XX JP06303997-A.
XX PN 01-NOV-1994.
XX PD 16-APR-1993; 93JP-0112515.
XX PF 16-APR-1993; 93JP-0112515.
XX PR (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX PA WPI; 1995-018287/03.
XX DR Analysis of cDNA and gene expression - by amplification of mRNA
XX followed by digestion with restriction enzymes
XX PS Disclosure; Page 6; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an
XX aggregate of double-stranded cDNAs by using an aggregate of mRNAs
XX and a plural type of labelled reverse transcription primers
XX (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
XX template for each reverse transcription primer; (b) digesting each of
XX the prepared aggregates of the double-stranded cDNAs with restriction
XX enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
XX separate lanes. The method can be used to analyse gene expression
XX rapidly and easily.
XX SQ Sequence 21 BP; 1 A; 2 C; 1 G; 17 T; 0 other;
Query Match 1.5%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1084 AAAAAAAAAAAAAAA 1100
DB 17 AAAAAAAAAAAAAAA 1
RESULT 493
AAQ75663/c
ID AAQ75663 standard; DNA; 21 BP.
AC AAQ75663;
XX 04-AUG-1995 (first entry)
XX Reverse transcription primer used in cDNA analysis technique.
XX Analysis; Gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX Synthetic.
XX JP06303997-A.
XX PN 01-NOV-1994.
XX PD 16-APR-1993; 93JP-0112515.
XX PF 16-APR-1993; 93JP-0112515.
XX PR (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX PA WPI; 1995-018287/03.
XX DR Analysis of cDNA and gene expression - by amplification of mRNA
XX followed by digestion with restriction enzymes
XX PS Disclosure; Page 6; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an
XX aggregate of double-stranded cDNAs by using an aggregate of mRNAs
XX and a plural type of labelled reverse transcription primers
XX (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
XX template for each reverse transcription primer; (b) digesting each of
XX the prepared aggregates of the double-stranded cDNAs with restriction
XX enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
XX separate lanes. The method can be used to analyse gene expression
XX rapidly and easily.
XX SQ Sequence 21 BP; 1 A; 2 C; 1 G; 19 T; 0 other;
Query Match 1.5%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1084 AAAAAAAAAAAAAAA 1100
DB 17 AAAAAAAAAAAAAAA 1
RESULT 495
AAQ75646/c
ID AAQ75646 standard; DNA; 21 BP.
XX AC AAQ75646;
```

XX DT 04-AUG-1995 (first entry)

XX DE Reverse transcription primer used in cDNA analysis technique.

XX KW Analysis; gene expression; reverse transcription; primer; cDNA;

XX KW aggregate; restriction enzyme; ss.

XX OS Synthetic.

XX PN JP06303997-A.

XX PD 01-NOV-1994.

XX PF 16-APR-1993; 93JP-0112515.

XX PR 16-APR-1993; 93JP-0112515.

XX PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

XX DR WPI; 1995-018287/03.

XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes

XX PS Disclosure; Page 6; 11pp; Japanese.

XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in separate lanes. The method can be used to analyse gene expression rapidly and easily.

XX SQ Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 21;

Best Local Similarity 100.0%; Pred. No. 2.3e+02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100

DB 17 AAAAAAAAAAAAAAAAAA 1

RESULT 496

AAQ75647/c

ID AAQ75647 standard; DNA; 21 BP.

XX AC AAQ75647;

XX DT 04-AUG-1995 (first entry)

XX DE Reverse transcription primer used in cDNA analysis technique.

XX KW Analysis; gene expression; reverse transcription; primer; cDNA;

XX KW aggregate; restriction enzyme; ss.

XX OS Synthetic.

XX PN JP06303997-A.

XX PD 01-NOV-1994.

XX PF 16-APR-1993; 93JP-0112515.

XX PR 16-APR-1993; 93JP-0112515.

XX PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

XX DR WPI; 1995-018287/03.

XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes

XX PS Disclosure; Page 6; 11pp; Japanese.

XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in separate lanes. The method can be used to analyse gene expression rapidly and easily.

XX SQ Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 21;

Best Local Similarity 100.0%; Pred. No. 2.3e+02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100

DB 17 AAAAAAAAAAAAAAAAAA 1

RESULT 496

AAQ75647/c

ID AAQ75647 standard; DNA; 21 BP.

XX AC AAQ75647;

XX DT 04-AUG-1995 (first entry)

XX DE Reverse transcription primer used in cDNA analysis technique.

XX KW Analysis; gene expression; reverse transcription; primer; cDNA;

XX KW aggregate; restriction enzyme; ss.

XX OS Synthetic.

XX PN JP06303997-A.

XX PD 01-NOV-1994.

XX PF 16-APR-1993; 93JP-0112515.

XX PR 16-APR-1993; 93JP-0112515.

XX PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

DR WPI; 1995-018287/03.

XX Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes

XX PS Disclosure; Page 6; 11pp; Japanese.

XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in separate lanes. The method can be used to analyse gene expression rapidly and easily.

XX SQ Sequence 21 BP; 0 A; 0 C; 2 G; 19 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 21;

Best Local Similarity 100.0%; Pred. No. 2.3e+02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100

DB 17 AAAAAAAAAAAAAAAAAA 1

RESULT 497

AAQ75649/c

ID AAQ75649 standard; DNA; 21 BP.

XX AC AAQ75649;

XX DT 04-AUG-1995 (first entry)

XX DE Reverse transcription primer used in cDNA analysis technique.

XX KW Analysis; gene expression; reverse transcription; primer; cDNA;

XX KW aggregate; restriction enzyme; ss.

XX OS Synthetic.

XX PN JP06303997-A.

XX PD 01-NOV-1994.

XX PF 16-APR-1993; 93JP-0112515.

XX PR 16-APR-1993; 93JP-0112515.

XX PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

XX DR WPI; 1995-018287/03.

XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes

XX PS Disclosure; Page 6; 11pp; Japanese.

XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in separate lanes. The method can be used to analyse gene expression rapidly and easily.

XX SQ Sequence 21 BP; 0 A; 0 C; 1 G; 20 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 21;

```

Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
DB 17 AAAAAAAAAAAAAAAAAA 1

RESULT 498
AAQ75650/c
ID AAQ75650 standard; DNA; 21 BP.
AC AAQ75650;
XX
DT 04-AUG-1995 (first entry)
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-0112515.
XX
PR 16-APR-1993; 93JP-0112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA
PT followed by digestion with restriction enzymes
XX
PS Disclosure; Page 6; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC and a plural type of labelled reverse transcription primers
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
CC template for each reverse transcription primer; (b) digesting each of
CC the prepared aggregates of the double-stranded cDNAs with restriction
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC separate lanes. The method can be used to analyse gene expression
CC rapidly and easily.
XX
SQ Sequence 21 BP; 0 A; 1 C; 1 G; 19 T; 0 other;
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA
PT followed by digestion with restriction enzymes
XX
PS Disclosure; Page 6; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC and a plural type of labelled reverse transcription primers
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
CC template for each reverse transcription primer; (b) digesting each of
CC the prepared aggregates of the double-stranded cDNAs with restriction
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC separate lanes. The method can be used to analyse gene expression
CC rapidly and easily.
XX
SQ Sequence 21 BP; 0 A; 1 C; 1 G; 19 T; 0 other;
XX
Query Match 1.5%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
DB 17 AAAAAAAAAAAAAAAAAA 1

RESULT 499
AAQ75651/c
ID AAQ75651 standard; DNA; 21 BP.
AC AAQ75651;
XX
DT 04-AUG-1995 (first entry)
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX

```

```

XX Synthetic.
XX OS JP06303997-A.
XX PN 01-NOV-1994.
XX PD 16-APR-1993; 93JP-0112515.
XX PF 16-APR-1993; 93JP-0112515.
XX PR (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX PA WPI; 1995-018287/03.
XX DR Analysis of cDNA and gene expression - by amplification of mRNA
XX PT followed by digestion with restriction enzymes
XX PS Disclosure; Page 6; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an
XX CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
XX CC and a plural type of labelled reverse transcription primers
XX CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
XX CC template for each reverse transcription primer; (b) digesting each of
XX CC the prepared aggregates of the double-stranded cDNAs with restriction
XX CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
XX CC separate lanes. The method can be used to analyse gene expression
XX CC rapidly and easily.
XX SQ Sequence 21 BP; 0 A; 1 C; 2 G; 18 T; 0 other;
XX
Query Match 1.5%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
DB 17 AAAAAAAAAAAAAAAAAA 1

RESULT 500
AAQ75652/c
ID AAQ75652 standard; DNA; 21 BP.
XX AC AAQ75652;
XX
DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX
PN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-0112515.
XX PR 16-APR-1993; 93JP-0112515.
XX PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA
PT followed by digestion with restriction enzymes
XX PS Disclosure; Page 6; 11pp; Japanese.
XX

```

CC A method for the analysis of cDNA comprises (a) preparing an
 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
 CC and a plural type of labelled reverse transcription primers
 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
 CC template for each reverse transcription primer; (b) digesting each of
 CC the prepared aggregates of the double-stranded cDNAs with restriction
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
 CC separate lanes. The method can be used to analyse gene expression
 CC rapidly and easily.
 XX
 SQ Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 other;
 XX
 Query Match 1.5%; Score 17; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1084 AAAAAAAAAAAAAAAAAA 1100
 DB 17 AAAAAAAAAAAAAAAAAA 1
 RESULT 501
 AAQ75653/c
 ID AAQ75653 standard; DNA; 21 BP.
 XX AC AAQ75653;
 XX
 DT 04-AUG-1995 (first entry)
 XX
 DE Reverse transcription primer used in cDNA analysis technique.
 XX
 KW Analysis; gene expression; reverse transcription; primer; cDNA;
 XX aggregate; restriction enzyme; ss.
 XX Synthetic.
 OS
 XX JP06303997-A.
 PN
 XX 01-NOV-1994.
 PD
 XX
 PF 16-APR-1993; 93JP-0112515.
 XX
 PR 16-APR-1993; 93JP-0112515.
 XX
 XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 PA
 XX WPI; 1995-018287/03.
 DR
 XX
 PT Analysis of cDNA and gene expression - by amplification of mRNA
 PT followed by digestion with restriction enzymes
 XX
 PS Disclosure; Page 6; 11pp; Japanese.
 XX
 CC A method for the analysis of cDNA comprises (a) preparing an
 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
 CC and a plural type of labelled reverse transcription primers
 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
 CC template for each reverse transcription primer; (b) digesting each of
 CC the prepared aggregates of the double-stranded cDNAs with restriction
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
 CC separate lanes. The method can be used to analyse gene expression
 CC rapidly and easily.
 XX
 SQ Sequence 21 BP; 0 A; 1 C; 1 G; 19 T; 0 other;
 XX
 Query Match 1.5%; Score 17; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1084 AAAAAAAAAAAAAAAAAA 1100
 DB 17 AAAAAAAAAAAAAAAAAA 1
 RESULT 502
 AAQ75654/c
 ID AAQ75654 standard; DNA; 21 BP.
 XX AC AAQ75654;
 XX
 DT 04-AUG-1995 (first entry)
 XX
 DE Reverse transcription primer used in cDNA analysis technique.
 XX
 KW Analysis; gene expression; reverse transcription; primer; cDNA;
 XX aggregate; restriction enzyme; ss.
 XX Synthetic.
 OS
 XX JP06303997-A.
 PN
 XX 01-NOV-1994.
 PD
 XX
 PF 16-APR-1993; 93JP-0112515.
 XX
 PR 16-APR-1993; 93JP-0112515.
 XX
 XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 PA
 XX WPI; 1995-018287/03.
 DR
 XX
 PT Analysis of cDNA and gene expression - by amplification of mRNA
 PT followed by digestion with restriction enzymes
 XX
 PS Disclosure; Page 6; 11pp; Japanese.
 XX
 CC A method for the analysis of cDNA comprises (a) preparing an
 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
 CC and a plural type of labelled reverse transcription primers
 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
 CC template for each reverse transcription primer; (b) digesting each of
 CC the prepared aggregates of the double-stranded cDNAs with restriction
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
 CC separate lanes. The method can be used to analyse gene expression
 CC rapidly and easily.
 XX
 SQ Sequence 21 BP; 0 A; 1 C; 1 G; 18 T; 0 other;
 XX
 Query Match 1.5%; Score 17; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1084 AAAAAAAAAAAAAAAAAA 1100
 DB 17 AAAAAAAAAAAAAAAAAA 1
 RESULT 503
 AAQ75655/c
 ID AAQ75655 standard; DNA; 21 BP.
 XX AC AAQ75655;
 XX
 DT 04-AUG-1995 (first entry)
 XX
 DE Reverse transcription primer used in cDNA analysis technique.
 XX
 KW Analysis; gene expression; reverse transcription; primer; cDNA;
 XX aggregate; restriction enzyme; ss.
 XX Synthetic.
 OS
 XX JP06303997-A.
 PN
 XX 01-NOV-1994.
 PD
 XX

RESULT 502
 AAQ75654/c
 ID AAQ75654 standard; DNA; 21 BP.
 XX AC AAQ75654;
 XX
 DT 04-AUG-1995 (first entry)
 XX
 DE Reverse transcription primer used in cDNA analysis technique.
 XX
 KW Analysis; gene expression; reverse transcription; primer; cDNA;
 XX aggregate; restriction enzyme; ss.
 XX Synthetic.
 OS
 XX JP06303997-A.
 PN
 XX 01-NOV-1994.
 PD
 XX
 PF 16-APR-1993; 93JP-0112515.
 XX
 PR 16-APR-1993; 93JP-0112515.
 XX
 XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 PA
 XX WPI; 1995-018287/03.
 DR
 XX
 PT Analysis of cDNA and gene expression - by amplification of mRNA
 PT followed by digestion with restriction enzymes
 XX
 PS Disclosure; Page 6; 11pp; Japanese.
 XX
 CC A method for the analysis of cDNA comprises (a) preparing an
 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
 CC and a plural type of labelled reverse transcription primers
 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
 CC template for each reverse transcription primer; (b) digesting each of
 CC the prepared aggregates of the double-stranded cDNAs with restriction
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
 CC separate lanes. The method can be used to analyse gene expression
 CC rapidly and easily.
 XX
 SQ Sequence 21 BP; 0 A; 2 C; 1 G; 18 T; 0 other;
 XX
 Query Match 1.5%; Score 17; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1084 AAAAAAAAAAAAAAAAAA 1100
 DB 17 AAAAAAAAAAAAAAAAAA 1
 RESULT 503
 AAQ75655/c
 ID AAQ75655 standard; DNA; 21 BP.
 XX AC AAQ75655;
 XX
 DT 04-AUG-1995 (first entry)
 XX
 DE Reverse transcription primer used in cDNA analysis technique.
 XX
 KW Analysis; gene expression; reverse transcription; primer; cDNA;
 XX aggregate; restriction enzyme; ss.
 XX Synthetic.
 OS
 XX JP06303997-A.
 PN
 XX 01-NOV-1994.
 PD
 XX

DT 04-AUG-1995 (first entry)
 XX Reverse transcription primer used in cDNA analysis technique.
 DE Analysis; gene expression; reverse transcription; primer; cDNA;
 XX aggregate; restriction enzyme; ss.
 KW Synthetic.
 OS JP06303997-A.
 XX
 XX 01-NOV-1994.
 XX
 XX 16-APR-1993; 93JP-0112515.
 XX
 XX 16-APR-1993; 93JP-0112515.
 XX
 XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX
 XX WPI; 1995-018287/03.
 XX
 XX Analysis of cDNA and gene expression - by amplification of mRNA
 PT followed by digestion with restriction enzymes
 XX
 XX Disclosure; Page 6; 11pp; Japanese.
 XX
 XX A method for the analysis of cDNA comprises (a) preparing an
 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
 CC and a plural type of labelled reverse transcription primers
 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
 CC template for each reverse transcription primer; (b) digesting each of
 CC the prepared aggregates of the double-stranded cDNAs with restriction
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
 CC separate lanes. The method can be used to analyse gene expression
 CC rapidly and easily.
 XX
 XX Sequence 21 BP; 0 A; 2 C; 2 G; 17 T; 0 other;
 SQ
 Query Match 1.5%; Score 17; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1084 AAAAAAAAAAAAAAA 1100
 DB 17 AAAAAAAAAAAAAAA 1
 RESULT 507
 AAQ75659/c
 ID AAQ75659 standard; DNA; 21 BP.
 XX
 XX AC AAQ75659;
 XX
 XX 04-AUG-1995 (first entry)
 XX
 XX Reverse transcription primer used in cDNA analysis technique.
 DE Analysis; gene expression; reverse transcription; primer; cDNA;
 XX aggregate; restriction enzyme; ss.
 KW Synthetic.
 OS JP06303997-A.
 XX
 XX 01-NOV-1994.
 XX
 XX 16-APR-1993; 93JP-0112515.
 XX
 XX 16-APR-1993; 93JP-0112515.
 XX
 XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX
 XX WPI; 1995-018287/03.
 XX

XX Analysis of cDNA and gene expression - by amplification of mRNA
 PT followed by digestion with restriction enzymes
 XX
 XX Disclosure; Page 6; 11pp; Japanese.
 XX
 XX A method for the analysis of cDNA comprises (a) preparing an
 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
 CC and a plural type of labelled reverse transcription primers
 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
 CC template for each reverse transcription primer; (b) digesting each of
 CC the prepared aggregates of the double-stranded cDNAs with restriction
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
 CC separate lanes. The method can be used to analyse gene expression
 CC rapidly and easily.
 XX
 XX Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 other;
 SQ
 Query Match 1.5%; Score 17; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1084 AAAAAAAAAAAAAAA 1100
 DB 17 AAAAAAAAAAAAAAA 1
 RESULT 508
 AAT10743
 ID AAT10743 standard; RNA; 21 BP.
 XX
 XX AC AAT10743;
 XX
 XX 09-SEP-1996 (first entry)
 XX
 XX Oligonucleotide probe, Cp-1.
 DE Electronically self-addressable device; ED; electrode;
 KW current source; attachment layer; permeable; counterion;
 XX genetic typing; probe; detection; ss.
 XX Synthetic.
 OS
 XX Key Location/Qualifiers
 FT modified_base 21
 FT /*tag= a
 FT /note= "3'-ribonucleoside terminus"
 XX
 XX WO9601836-A1.
 XX
 XX 25-JAN-1996.
 XX
 XX 05-JUL-1995; 95WO-US08570.
 XX
 XX 07-JUL-1994; 94US-0271882.
 XX
 XX (NANO-) NANOGEN INC.
 XX
 XX Evans GA, Heller MJ, Sosnowski RG, Tu E;
 XX WPI; 1996-097582/10.
 XX
 XX Electronically self-addressable device - used for electronic control
 PT of, e.g. nucleic acid hybridisation
 XX
 XX Example 1; Page 60; 155pp; English.
 XX
 XX The sequences given in AAT10742-67 are synthetic oligonucleotides
 CC which are used in the construction of the electronically self-
 CC addressable device (ED) of the invention. The ED comprises a
 CC substrate, an electrode or opt. a number of electrodes supported by
 CC the substrate, a current source operatively connected to the
 CC electrode and an attachment layer adjacent to the electrode which is

permeable to a counterion but not permeable to a molecule capable of insulating or binding to the electrode. The attachment layer is capable of attaching a macromolecule. The PD is used for genetic typing and comprises a number of electronically addressable locations each comprising an electrode, and a binding entity, such as one of these probes, attached to each of the locations capable of detecting the presence of a genetic sequence.

Sequence 21 BP; 20 A; 0 C; 0 G; 1 U; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
DB 1 AAAAAAAAAAAAAAAAAA 17

RESULT 509
AAZ26268/c
ID AAZ26268 standard; DNA; 21 BP.
AC AAZ26268;
XX
XX 30-NOV-1999 (first entry)
XX Human polymorphic region 457.
XX
XX Polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH;
KW cell viability; loss of heterozygosity; precancerous condition; ASI;
KW allele specific inhibitor; somatic cell; diagnosis; prevention;
KW atherosclerotic plaque; premalignant metaplastic lesion; endometriosis;
KW dysplastic lesion; benign tumour; polycystic kidney disease; transplant;
KW graft versus host disease; malignant cell removal; bone marrow; ss.
XX
XX Homo sapiens.
OS
XX
XX WO9841648-A2.
XX
XX 24-SEP-1998.
PD
XX
XX 19-MAR-1998; 98WO-US05419.
XX
XX 20-MAR-1997; 97US-0041057.
XX
XX (VARI-) VARIAGENICS INC.
XX
XX Housman D, Ledley FD, Stanton VP;
PI
XX
XX WPI; 1998-521232/44.
DR
XX
XX Identifying target genes for allele-specific drugs - used for
PT diagnosis, prevention and treatment of, e.g. cancers, atherosclerotic
PT plaque, dysplastic lesions, endometriosis or graft versus host disease
XX
XX Disclosure; Figure 7; 605pp; English.
XX
XX This invention describes a novel method for identifying an inhibitor
CC potentially useful for treatment of cancer, where the inhibitor is
CC active on a gene vital for cell growth or viability, and where the gene
CC is subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is
CC used for preventing the development of cancer in a patient having a
CC precancerous condition, by administering to the patient a first allele
CC specific inhibitor (ASI) targeted to an allele of a first essential gene
CC present in cells of the precancerous condition, where the normal somatic
CC cells of the patient are heterozygous for the first gene, the inhibitor
CC is active on at least one but less than all allelic forms of the gene
CC present in a population and targets only one allelic form present in the
CC normal somatic cells, and the first gene. The products and methods can
CC be used in the diagnosis, prevention and treatment of LOH disorders,
CC e.g. cancers, atherosclerotic plaques, premalignant metaplastic or
CC dysplastic lesions, benign tumours, endometriosis, polycystic kidney

disease, and graft versus host disease. The method can also be used to remove malignant cells from bone marrow transplants. AAZ5812-226825
CC represent human polymorphic sites described in the method of the
CC invention.
XX
XX Sequence 21 BP; 5 A; 0 C; 0 G; 16 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1081 ATTAATAAAAAAAAAA 1097
DB 19 ATTAATAAAAAAAAAA 3

RESULT 510
AAV35395
ID AAV35395 standard; DNA; 21 BP.
XX
XX AAV35395;
XX
XX 13-OCT-1998 (first entry)
XX
XX HIV-1 gag protein DNA primer #8.
DE
XX
XX Hypervariable region; ENV protein; vaccinia virus; gag gene; retrovirus;
KW vaccines; infection; protection; primer; ss.
XX
XX Synthetic.
OS
XX WO9822596-A1.
XX
XX 28-MAY-1998.
XX
XX 19-NOV-1997; 97WO-JP04216.
XX
XX 19-NOV-1996; 96JP-0323412.
XX
XX (NINA-) JAPAN NAT INST INFECTIOUS DISEASES.
XX (JAPG) NIPPON ZEON KK.
XX
XX Kojima A, Kurata T, Yasuda A;
PI
XX
XX WPI; 1998-312481/27.
DR
XX
XX Recombinant vaccinia virus containing fusion HIB gag gene - for
PT production in host cells of gag protein for use as vaccine
PT
XX
XX Example 1; Page 66; 84pp; Japanese.
XX
XX AAV35388-V35414 are primers used in a method which results in a
CC recombinant vaccinia virus comprising of a gag gene from a retrovirus
CC such as HIV-1 or HIV-2, fused to a DNA fragment containing an epitope
CC region (30-300 bases in length) of a retroviral gene other than the gag
CC gene. The gag gene may be altered so as to produce a gag protein modified
CC from the natural sequence by the addition, deletion or substitution of at
CC least 1 amino acid residue. The fusion gene is inserted into a region of
CC a vaccinia virus not essential to its propagation, to give a recombinant
CC vaccinia virus vector which is used to transform a host cell (such as
CC HeLa, vero, VEF, rabbit kidney RK13 or human myeloma TK-143 cells). Upon
CC culturing the host cell produces particulate structures containing the
CC fusion gag protein. The recombinant vaccinia virus or the fusion gag
CC protein particles may be used in the production of vaccines for
CC protecting against infection with retroviruses such as HIV.
XX
XX Sequence 21 BP; 19 A; 2 C; 0 G; 0 U; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100

Db 3 AAAAAAAAAAAAAAAAAA 19
|||||

RESULT 511

AA81302
ID AAX81302 standard; DNA; 21 BP.

AC AAX81302;

DT 20-AUG-1999 (first entry)

DE 3' ribonucleoside oligonucleotide probe CP-1.

KW Microelectronic device; multi-step reaction; microscopic format;
KW ion-permeable permeation layer; electrode; electrical control;
KW transport; attachment; binding; DNA/RNA hybrid; probe; ss.

OS Synthetic.

FH Key Location/Qualifiers
FT misc_RNA 21
ET /*tag= a

PN WO929711-A1.

PD 17-JUN-1999.

PF 01-DEC-1998; 98WO-US25475.

PR 05-DEC-1997; 97US-0986065.

PA (NANO-) NANOGEN INC.

PI Butler WF, Edman CF, Heller MJ, Nerenberg MI, Sosnowski RG;
PI Tu E;

DR WPI; 1999-385567/32.

PT New microelectronic device designed to carry out and control
PT multi-step and multiplex molecular biological reactions in
PT microscopic format

PS Example 1; Page 89; 179pp; English.

CC The specification describes a self-addressable, self-assembling
CC microelectronic device which is designed to actively carry out and
CC control multi-step and multiplex molecular biological reactions in
CC microscopic formats. A key aspect of this invention is played by the
CC ion-permeable permeation layer which overlies the electrode. This
CC permeation layer allows attachment of nucleic acids to permit
CC immobilization but also separates the attached oligonucleotides and
CC hybridized target DNA sequences from the highly reactive electrochemical
CC environment generated immediately at the electrode surface. The
CC microelectronic device is designed and fabricated to actively carry
CC out and control reactions such as nucleic acid hybridizations,
CC antibody/antigen reactions, sample preparation, diagnostics and
CC biopolymer synthesis. The device can electronically control the
CC transport and attachment of specific binding entities, such as nucleic
CC acids and polypeptides, to specific micro-locations. The device can
CC subsequently control the transport and reaction of analytes or reactants
CC at the addressed specific micro-locations. The device is able to
CC concentrate analytes and reactants, remove non-specifically bound
CC molecules, provide stringency control for DNA hybridization reactions
CC and improve the detection of analytes. The present sequence
CC represents a probe used to exemplify the invention.

SQ Sequence 21 BP; 20 A; 0 C; 0 G; 1 U; 0 other;

Query Match

Best Local Similarity 1.5%; Score 17; DB 1; Length 21;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
Db 1 AAAAAAAAAAAAAAAAAA 17
|||||

RESULT 512

AA26973/c
ID AAX26973 standard; cDNA; 21 BP.

AC AAX26973;

DT 25-JUN-1999 (first entry)

DE Primer used to reverse transcribe mamaglobin RNA.

KW Human; mamary-specific protein; mamaglobin; antigen; vaccine;
KW mamaglobin-expressing cancer; breast cancer;
KW autologous tumor lymphocyte; diagnosis; marker; primer; ss.

OS Synthetic.

PN WO9914230-A1.

PD 25-MAR-1999.

PF 18-SEP-1998; 98WO-US17991.

PR 18-SEP-1997; 97US-0933149.

PA (UNIW) UNIV WASHINGTON.

PI Fleming TP, Watson MA;

DR WPI; 1999-244021/20.

PT Mamaglobin, secreted protein overexpressed in breast cancer

PS Example 2; Page 55; 60pp; English.

CC The present primer was used to reverse transcribe RNA encoding a human
CC mamary-specific protein, designated mamaglobin. The specification
CC describes a protein comprising a mamaglobin antigen that is recognized
CC by B and/or Tc cells specific for the natural, secreted and glycosylated
CC form of mamaglobin polypeptide. This protein, or recombinant vectors
CC that express it, are used in vaccines for treating mamaglobin-
CC expressing cancers, specifically of the breast. Such cancers can
CC also be treated using autologous tumor lymphocytes activated
CC ex vivo with an mamaglobin antigen, then returned to the
CC patient. Expression of mamaglobin is elevated in 27% of stage I
CC primary breast cancers, so it represents a marker useful for
CC diagnosis of this disease.

SQ Sequence 21 BP; 0 A; 0 C; 0 G; 21 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
Db 21 AAAAAAAAAAAAAAAAAA 5
|||||

RESULT 513

AA24350/c
ID AA24350 standard; DNA; 21 BP.

AC AA24350;

DT 04-APR-2000 (first entry)

DE Protein kinase inhibiting primer #12.

XX

KW Antimicrobial; cytostatic; immunosuppressive; protein kinase;
 KW prophylactic; therapy; treatment; cancer; autoimmune disease;
 KW pathogenic microorganism; primer; ss.

OS Unidentified.

PN US998596-A.

XX 07-DEC-1999.

XX 04-APR-1995; 95US-0416214.

XX 04-APR-1995; 95US-0416214.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Bergan R, Neckers L;

XX WPI; 2000-104623/09.

XX Oligonucleotides inhibiting protein kinase, useful for treating
 PT diseases such as cancer and autoimmune disease -

XX Example 8; Column 27-28; 26pp; English.

XX This invention describes novel purified aptameric oligonucleotides
 CC which have antimicrobial, cytostatic and immunosuppressive activity.
 CC The oligonucleotides are useful for binding to and preventing or
 CC inhibiting the biological function of a protein kinase or a target
 CC molecule and for detecting the presence or absence of a target molecule
 CC in biological samples. The oligonucleotides are also useful for
 CC prophylactic and therapeutic treatment of diseases such as cancer,
 CC autoimmune diseases and diseases caused by pathogenic microorganisms.
 CC This sequence represents a primer used in the method of the invention.

SQ Sequence 21 BP; 0 A; 0 C; 0 G; 21 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 21;

Best Local Similarity 100.0%; Pred. No. 2.3e+02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100

Db 21 AAAAAAAAAAAAAAAAAA 5

RESULT 514

AAH42480/c

ID AAH42480 standard; DNA; 21 BP.

XX AC AAH42480;

DT 01-OCT-2001 (first entry)

DE Oligonucleotide used to produce branched chain compounds.

KW Branched chain compound; nucleic acid synthesis; primer extension;
 KW reverse transcription; nucleic acid hybridization;
 KW nucleic acid amplification; ss.

XX Synthetic.

Key modified_base 1 Location/Qualifiers

FT /*tag= a

FT /*note= "NH2-C6 attached"

FT /*tag= b

FT /*note= "NH2-C6 attached"

FT /*tag= c

FT /*note= "branch present"

PN EP1111068-A1.

XX 27-JUN-2001.

XX 21-DEC-1999; 99EP-0125484.

XX 21-DEC-1999; 99EP-0125484.

XX (LION-) LION BIOSCIENCE AG.

XX (VBCG-) VBC GENOMICS GMBH.

XX Schmidt W, Hiller R, Huber M, Mueller M;

XX WPI; 2001-466959/51.

XX Branched compounds useful in e.g. nucleic acid synthesis reaction
 PT comprises nucleic acid moieties optionally extended by a polymerase -

XX Example 1; Page 10; 31pp; English.

XX The specification describes branched compounds containing nucleic
 CC acid moieties optionally extended by a polymerase. The branched chain
 CC compounds of the invention are used in nucleic acid synthesis reaction,
 CC primer extension reaction, reverse transcription reaction of RNA into
 CC DNA, nucleic acid hybridization experiment (for identifying sequence
 CC of a nucleic acid), and nucleic acid amplification experiment (for
 CC analysing the expression pattern of genes). The compounds are also used
 CC in solid-phase enzymatic reactions. The present sequence was used
 CC in the course of the invention to produce branched chain compounds.

SQ Sequence 21 BP; 0 A; 0 C; 0 G; 21 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 21;

Best Local Similarity 100.0%; Pred. No. 2.3e+02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100

Db 21 AAAAAAAAAAAAAAAAAA 5

RESULT 515

AAF99707/c

ID AAF99707 standard; DNA; 21 BP.

XX AC AAF99707;

DT 12-JUN-2001 (first entry)

XX Immunostimulatory nucleic acid #823.

KW Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
 KW immunostimulatory; tumour; viral infection; bacterial infection;
 KW fungal infection; parasitic infection; cancer; asthma;
 KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.

XX Synthetic.

XX WO200122972-A2.

XX 05-APR-2001.

XX 25-SEP-2000; 2000WO-US26383.

XX 25-SEP-1999; 99US-0156113.

XX 27-SEP-1999; 99US-0156135.

XX 23-AUG-2000; 2000US-0227436.

XX (IOWA) UNIV IOWA RES FOUND.

XX (COLE-) COLEY PHARM GMBH.

XX Krieg AM, Schetter C, Vollmer J;

DR WPI; 2001-273485/28.

XX Vaccinating against tumors, infectious diseases, allergies and asthma

PT using immunostimulatory Py-rich and TG nucleic acids -

XX Claim 101; Page 56; 338pp; English.

XX The present invention relates to a method for stimulating an immune

CC response. The method comprises administering an immunostimulatory nucleic

CC acid to a non-rodent subject in sufficient quantity to stimulate an

CC immune response. The present sequence is one such immunostimulatory

CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich

CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects

CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae

CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,

CC haemophilus, campylobacter, clostridium, Escherichia coli and/or

CC staphylococcus), fungal antigens and/or parasitic antigens. The method is

CC also useful for preventing cancer, asthma, infectious disease, allergy or

CC immune deficiency. The present sequence can also be used to redirect a

CC Th2 to a Th1 immune response and to activate immune cells.

CC Note: the present sequence may have a phosphorothioate backbone.

XX

SQ Sequence 21 BP; 0 A; 0 C; 0 G; 21 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 21;

Best Local Similarity 100.0%; Pred. No. 2.3e+02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1084 AAAAAAAAAAAAAAAAAA 1100

Db 21 AAAAAAAAAAAAAAAAAA 5

RESULT 516

AB578428/C

ID AB578428 standard; DNA; 21 BP.

XX

AC AB578428;

XX

DT 13-DEC-2002 (first entry)

XX

DE Angiogenesis inhibitory oligonucleotide #912.

XX

KW Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;

KW tumour metastasis; precancerous lesion; rheumatoid arthritis;

KW psoriasis; diabetic retinopathy; retinopathy of prematurity;

KW macular degeneration; corneal graft rejection; neovascular glaucoma;

KW retrolental fibroplasia; rubeosis; Osler-Webber Syndrome;

KW myocardial angiogenesis; plaque neovascularisation; telangiectasia;

KW haemophilic joint; angiofibroma; wound granulation;

KW intestinal adhesion; atherosclerosis; scleroderma; hypertrophic scar.

XX

OS Synthetic.

XX

Key modified_base Location/Qualifiers

FT 1..21

FT /*tag= a

FT /mod_base= OTHER

FT /note= "phosphorothioate backbone"

XX

PN WO200197843-A2.

XX

PD 27-DEC-2001.

XX

XX 22-JUN-2001; 2001WO-US20154.

XX

PR 22-JUN-2000; 2000US-213346P.

XX

PA (IOWA) UNIV IOWA RES FOUND.

XX

PI Weiner G, Hartmann G;

XX

DR WPI; 2002-154611/20.

XX

PT Treating or preventing cancer, such as basal cell carcinoma, comprises

PT administering immunostimulatory nucleic acids that induce expression of

PT cell surface antigens and antibodies to a subject having or at risk of

PT developing cancer -

XX

PS Disclosure; Page 309; 312pp; English.

XX

CC The present invention relates to methods for treating or preventing

CC cancer, involving administering to a subject having or at risk of

CC developing cancer immunostimulatory nucleic acids that induce expression

CC of cell surface antigens and antibodies. The methods are useful for

CC treating or preventing cancer such as basal cell carcinoma, bladder

CC The invention relates to inhibiting angiogenesis in a subject, comprising

CC administering at least one antiangiogenic nucleic acid molecule.

CC Also included is a kit comprising a first container housing the

CC antiangiogenic nucleic acids, and instructions for administering them to

CC a subject having a condition characterised by unwanted angiogenesis.

CC The method is useful for inhibiting angiogenesis associated with solid

CC tumour growth, tumour metastasis, precancerous lesion, rheumatoid

CC arthritis, psoriasis, diabetic retinopathy, retinopathy of prematurity,

CC macular degeneration, corneal graft rejection, neovascular glaucoma,

CC retrolental fibroplasia, rubeosis, Osler-Webber Syndrome, myocardial

CC angiogenesis, plaque neovascularisation, telangiectasia, haemophilic

CC joints, angiofibroma, wound granulation, intestinal adhesions,

CC atherosclerosis, scleroderma and hypertrophic scars. The present

CC sequence is an antiangiogenic nucleic acid of the invention.

XX

SQ Sequence 21 BP; 0 A; 0 C; 0 G; 21 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 21;

Best Local Similarity 100.0%; Pred. No. 2.3e+02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1084 AAAAAAAAAAAAAAAAAA 1100

Db 21 AAAAAAAAAAAAAAAAAA 5

RESULT 517

ABL39404/C

ID ABL39404 standard; DNA; 21 BP.

XX

AC ABL39404;

XX

DT 16-APR-2002 (first entry)

XX

DE Immunostimulatory nucleic acid SEQ ID NO: 840.

XX

KW Antibody-induced cell lysis; cancer; immunostimulatory; CD20;

KW angiogenesis; metastasis; cytostatic; phosphorothioate backbone; ss.

XX

OS Synthetic.

XX

Key modified_base Location/Qualifiers

FT 1..21

FT /*tag= a

FT /mod_base= OTHER

FT /note= "phosphorothioate backbone"

XX

PN WO200197843-A2.

XX

PD 27-DEC-2001.

XX

XX 22-JUN-2001; 2001WO-US20154.

XX

PR 22-JUN-2000; 2000US-213346P.

XX

PA (IOWA) UNIV IOWA RES FOUND.

XX

PI Weiner G, Hartmann G;

XX

DR WPI; 2002-154611/20.

XX

PT Treating or preventing cancer, such as basal cell carcinoma, comprises

PT administering immunostimulatory nucleic acids that induce expression of

PT cell surface antigens and antibodies to a subject having or at risk of

PT developing cancer -

XX

PS Disclosure; Page 309; 312pp; English.

XX

CC The present invention relates to methods for treating or preventing

CC cancer, involving administering to a subject having or at risk of

CC developing cancer immunostimulatory nucleic acids that induce expression

CC of cell surface antigens and antibodies. The methods are useful for

CC treating or preventing cancer such as basal cell carcinoma, bladder

CC cancer, bone cancer, brain and central nervous system (CNS) cancer,
 CC breast cancer, cervical cancer, colon and rectum cancer, connective
 CC tissue cancer, esophageal cancer, eye cancer, kidney cancer, larynx
 CC cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma,
 CC non-Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian
 CC cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin
 CC cancer, stomach cancer, testicular cancer, and uterine cancer. The
 CC present sequence is an immunostimulatory oligonucleotide described in
 CC the exemplification of the invention.

XX SQ Sequence 21 BP; 0 A; 0 C; 0 G; 21 T; 0 other;
 Query Match 1.5%; Score 17; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1100
 DB 21 AAAAAAAAAAAAAA 5

RESULT 518
 AAD51323/c
 ID AAD51323 standard; DNA; 21 BP.
 XX
 AC AAD51323;
 XX
 DT 16-APR-2003 (first entry)
 XX
 DE Regular oligo dt primer used to illustrate the method of the invention.
 XX
 XX Laminitis; viral disease; vaccine; bacterial disease; primer; epistaxis;
 KW gastritis; gastric ulcer; respiratory ailment; fracture; joint disease;
 KW musculoskeletal damage; ss.
 XX
 OS Unidentified.
 XX
 PN W0200290579-A1.
 XX
 PD 14-NOV-2002.
 XX
 PF 03-MAY-2002; 2002WO-AU00553.
 XX
 PR 04-MAY-2001; 2001AU-0004809.
 PR 29-JUN-2001; 2001US-0896941.
 XX
 PA (GENO-) GENOMICS RES PARTNERS PTY LTD.
 XX
 PI Brandon RB;
 XX
 DR WPI; 2003-120558/11.
 XX
 PT Assessing condition e.g. athletic ability, stage of disease, presence
 PT of drugs, response to exercise, response to vaccines, therapies,
 PT nutritional states, of performance animal involves analyzing nucleic
 PT acid expression
 XX
 PS Disclosure; Page 46; 87pp; English.
 XX
 CC The invention relates to a method for assessing a condition of a
 CC performance animal. The method involves determining in sample abundance
 CC of expressed target nucleic acid; transmitting digital sample signal to
 CC remote diagnostic server; processing digital sample signal at remotely
 CC located database to correlate digital signal with digital information
 CC and returning report of particular condition of animal. The method is
 CC useful for assessing a condition of a performance animal preferably
 CC human, dog or camel. The condition can be an athletic ability and a
 CC condition that enhances, hinders, impedes or does not change an expected
 CC ability of the performance animal; and also normal, pre-clinical, overt
 CC progress and/or stage of disease, undiagnosed or unclassified conditions,
 CC presence of drugs, response to exercise, response to vaccines, therapies,
 CC nutritional states and response to environmental conditions. Diseases
 CC assessed by the invention include laminitis, lameness, viral or bacterial

CC disease, gastritis, gastric ulcers, respiratory ailments, fractures,
 CC epistaxis, musculoskeletal damage or disorders and joint diseases. The
 CC present sequence is a primer used to illustrate the method of the
 CC invention.

XX SQ Sequence 21 BP; 0 A; 0 C; 0 G; 21 T; 0 other;
 Query Match 1.5%; Score 17; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1100
 DB 21 AAAAAAAAAAAAAA 5

RESULT 519
 AAQ64706/c
 ID AAQ64706 standard; cDNA to mRNA; 22 BP.
 XX
 AC AAQ64706;
 XX
 DT 25-MAR-2003 (updated)
 DT 04-JAN-1995 (first entry)
 XX
 DE 2', 5'-linked tetraadenylate-antisense oligonucleotide chimeric mol.
 XX
 KW antisense; 2', 5'-tetraadenylate; 2-5A dependent RNase activator;
 KW RNA cleavage; antiviral therapy; chimeric molecule; ss.
 XX
 OS Synthetic.
 XX
 PH Key Location/Qualifiers
 FT misc_feature 1...4
 FT /*tag= a
 FT /label= 2', 5'-linked tetraadenylate
 FT /note= "nucleotides linked through phosphodiester
 FT bonds at hydroxyl groups of 2' and 5'
 FT carbons"
 FT misc_feature 5..22
 FT /*tag= b
 FT /note= "antisense region"
 XX
 PN W09409129-A2.
 XX
 PD 28-APR-1994.
 XX
 PF 20-OCT-1993; 93WO-US10103.
 XX
 PR 21-OCT-1992; 92US-0965666.
 PR 17-SEP-1993; 93US-0123449.
 XX
 PA (CLEV-) CLEVELAND CLINIC RES INST.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Lesiak K, Maitra R, Silverman R, Torrence P;
 XX
 DR WPI; 1994-151315/18.
 XX
 FT Specific cleavage of RNA, useful partic. for treating viral
 FT infection, cancers, etc. - by using anti-sense oligo:nucleotide
 FT coupled to activator of 2-5A dependent RNase
 XX
 PS Example 1; Page 68; 86pp; English.
 XX
 CC This sequence is an example of a 2-5A-antisense oligonucleotide
 CC chimeric molecule. The antisense region targets the chimeric
 CC molecule to a particular region of RNA to be specifically
 CC cleaved and the 2', 5'-linked tetraadenylate tail activates
 CC the 2-5A RNase. Typical applications are treatment of viral
 CC infections (esp. for cleavage of an RNA virus genome), cancer;
 CC leukaemia, cardiovascular disorders (e.g. restenosis after
 CC angioplasty), genetic disorders, osteoarthritis or rheumatoid

CC arthritis.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX Sequence 22 BP; 4 A; 0 C; 0 G; 18 T; 0 other;
 SQ Query Match 1.5%; Score 17; DB 1; Length 22;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
 Db 22 AAAAAAAAAAAAAAAAAA 6

RESULT 520
 AAQ64724
 ID AAQ64724 standard; CDNA to mRNA; 22 BP.
 XX AC AAQ64724;
 XX 25-MAR-2003 (updated)
 DT 04-JAN-1995 (first entry)
 XX 2',5'-linked tetraadenylate-anti(dT)18 oligonucleotide chimeric mol.
 DE antisense; 2',5'-tetraadenylate; 2-5A dependent RNase activator;
 KW RNA cleavage; antiviral therapy; chimeric molecule; PKR;
 KW protein synthesis regulation; phosphorylation; eIF-2alpha;
 KW eukaryotic translation initiation factor; ss.
 XX Synthetic.
 OS
 XX

Key Location/Qualifiers
 FT misc_feature 1..4
 FT /tag= a
 FT /label= 2',5'-linked tetraadenylate
 FT /note= "nucleotides linked through phosphodiester
 FT bonds at hydroxyl groups of 2' and 5'
 FT carbons"
 FT misc_feature 4..5
 FT /tag= b
 FT /note= "the 2-5A moiety (*tag = a) and the antisense
 FT DNA sequence (*tag = c) are linked by two
 FT 1,4-butanediol molecules linked through
 FT phosphodiester bonds"
 FT misc_feature 5..22
 FT /tag= c
 FT /note= "antisense region, complementary to oligo dT"
 FT
 XX WO9409129-A2.
 XX 28-APR-1994.
 XX 20-OCT-1993; 93WO-US10103.
 XX 21-OCT-1992; 92US-0965666.
 XX 17-SEP-1993; 93US-0123449.
 XX (CLEV-) CLEVELAND CLINIC RES INST.
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX Lesiak K, Maitra R, Silverman R, Torrence P;
 XX WPI; 1994-151315/18.
 XX Specific cleavage of RNA, useful partic. for treating viral
 XX infection, cancers, etc. - by using anti-sense oligo:nucleotide
 XX coupled to activator of 2-5A dependent RNase
 XX Example 9; Page 66; 86pp; English.
 XX This sequence was used to determine whether 2-5A-antisense chimeric
 CC molecules are inhibitory to cell growth. The molecules AAQ64709,

CC AAQ64711 and AAQ64724 all lacked cytotoxicity. In the novel
 CC 2-5A-antisense oligonucleotide chimeric molecules, the antisense
 CC region targets the chimeric molecule to a particular region of RNA
 CC to be specifically cleaved and the 2',5'-linked tetraadenylate tail
 CC activates the 2-5A RNase. Typical applications are treatment of viral
 CC infections (esp. for cleavage of an RNA virus genome), cancer;
 CC leukaemia, cardiovascular disorders (e.g. restenosis after
 CC angioplasty), genetic disorders, osteoarthritis or rheumatoid
 CC arthritis.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX Sequence 22 BP; 22 A; 0 C; 0 G; 0 T; 0 other;
 SQ Query Match 1.5%; Score 17; DB 1; Length 22;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
 Db 1 AAAAAAAAAAAAAAAAAA 17

RESULT 521
 AAA98276/c
 ID AAA98276 standard; DNA; 22 BP.
 XX AC AAA98276;
 XX 02-FEB-2001 (first entry)
 DT
 XX Human mismatch repair gene hMSH6 intron 9 DNA fragment.
 DE
 XX Human mismatch repair gene; hMSH6; disease predisposition; genotype;
 KW mutation; carcinoma; colorectal; endometrial; ovarian; leukemia;
 KW neoplastic disease; drug development; ss.
 XX Homo sapiens.
 XX DE19909878-A1.
 XX 07-SEP-2000.
 XX 06-MAR-1999; 99DE-1009878.
 XX 06-MAR-1999; 99DE-1009878.
 XX (UYDR) UNIV DRESDEN TECH.
 XX Plaschke J, Kruppa C, Schackert H;
 XX WPI; 2000-588378/56.
 XX Novel variants of the human mismatch repair gene, MSH6, useful e.g. for
 XX determining predisposition to cancer and for development of drugs -
 XX Claim 1; Page 4; 14pp; German.

This invention describes a novel method of determining a predisposition
 CC to disease by genotyping a subject's DNA sequence (A) of the human
 CC mismatch repair gene, MSH6 at specified positions and comparing with
 CC reference DNA sequences, optionally taking into account all possible
 CC combinations of variations of the individual mutations, including any
 CC chosen absolute number of variations (A), and analysis of their
 CC sequences, are useful for the following: (i) determining a predisposition
 CC to disease, especially colorectal, endometrial and ovarian carcinoma and
 CC leukemia; (ii) determining an increased mutation rate (frequency of base
 CC substitutions, insertions and/or deletions) in eukaryotic cells; (iii)
 CC predicting the progression, severity and survival time of patients with
 CC neoplastic disease; (iv) the development of therapeutic and 'life-style'
 CC drugs; (v) predicting individual differences in response to known
 CC chemotherapeutic agents (e.g. cis-platin) or drugs developed from (iv);
 CC (vi) optimizing individual treatments and interventions against
 CC neoplasia; (vii) controlling the mutation rate in eukaryotic cells, in

CC vitro or in vivo; (viii) constructing genes and vectors, particularly for
CC development of pharmaceuticals; (ix) developing diagnostic kits and other
CC systems for genotyping; and (x) developing in vivo and in vitro test
CC systems for expressing individual forms of the MSH6 gene, e.g. for
CC studying pathophysiology of disease or processes in which MSH6 is
CC involved, and for drug development and testing.

XX Sequence 22 BP; 4 A; 1 C; 0 G; 17 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
|||||
Db 22 AAAAAAAAAAAAAAAAAA 6

RESULT 522
AAFL7413
ID AAFL7413 standard; DNA; 22 BP.
XX
AC AAFL7413;
XX
DT 09-MAR-2001 (first entry)
XX
DE L1 cleavage site related sequence #3.
XX
KW Retrotransposon; genetic defect; cystic fibrosis; ds.
XX
OS Unidentified.
XX
PN US6150160-A.
XX
PD 21-NOV-2000.
XX
PF 28-APR-1997; 97US-0847844.
XX
PR 16-NOV-1995; 95US-0006831.
XX
PR 15-NOV-1996; 96US-0749805.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PA (UYPE-) UNIV PENNSYLVANIA.
XX
PI Moran JV, Dombroski BA, Kazazian HH, Boeke JD;
XX
DR WPI; 2001-060015/07.
XX

PT DNAC comprising a promoter P and an L1 cassette sequence having a core
PT retrotransposon element, useful for random insertion of a heterologous
PT or homologous DNA sequence into a cell genome and for correcting
PT genetic defects -
XX
PS Disclosure; Fig 14; 87pp; English.
XX
CC The present invention relates to DNA for a promoter and an L1
CC cassette sequence having a core retrotransposon element. The invention
CC is useful for random insertion of a heterologous or homologous DNA
CC sequence into a cell genome, and for correction of a genetic defect
CC in the cell into which the insertion is made. Genetic defects which
CC may be corrected includes cystic fibrosis, mutations in the
CC dystrophin gene, genetic defects associated with blood clotting and
CC other genetic defects.
XX
SQ Sequence 22 BP; 22 A; 0 C; 0 G; 0 U; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
|||||
Db 1 AAAAAAAAAAAAAAAAAA 17

RESULT 523
AAQ30432/c
ID AAQ30432 standard; DNA; 23 BP.
XX
AC AAQ30432;
XX
DT 25-MAR-2003 (updated)
DT 07-DEC-1992 (first entry)
XX
DE Oligomer II6805 for forming triplex with HUMIL6 target duplex.
XX
KW Human interleukin-6 gene; herpes simplex; AIDS; modified; HIV;
KW RSV; HPV; malignancy; hepatitis; inflammation; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1
FT /*tag= a
FT /mod_base= OTHER
FT /note= "OTHER= N4 N4 ethanocytosine"
FT modified_base 23
FT /*tag= b
FT /mod_base= OTHER
FT /note= "OTHER= N4 N4 ethanocytosine"
FT misc_feature 12..23
FT /*tag= c
FT /label= inverted_polarity_region
FT misc_feature 11..12
FT /*tag= d
FT /note= "o-xyloso dimer synthon linkage"
XX
PN WO9209705-A1.
XX
PD 11-JUN-1992.
XX
PF 25-NOV-1991; 91WO-US08811.
XX
PR 23-NOV-1990; 90US-0617907.
PR 18-JAN-1991; 91US-0643382.
PR 08-APR-1991; 91US-0683420.
PR 17-APR-1991; 91US-0686544.
PR 17-APR-1991; 91US-0686546.
PR 17-APR-1991; 91US-0686547.
PR 27-SEP-1991; 91US-0766733.
XX
PA (GILE-) GILEAD SCI INC.
XX
PI Froehner B, Krawczyk S, Matteucci MD, Milligan J;
XX
DR WPI; 1992-217083/26.
XX
CC New oligomers contg. modified bases - which form a triplex with
CC G-C doublet in a DNA duplex, for treating and diagnosing HIV,
CC hepatitis, herpes, malignancy and inflammation
XX
PS Claim 12; Page 71; 77pp; English.
XX
CC The synthetic oligomer is capable of forming a triplex at
CC physiological pH with a purine rich target sequence by coupling
CC into the major groove of the duplex. The specific target sequence
CC of this oligomer is the human interleukin 6 gene untranslated
CC sequence contg. a purine rich sequence concd. on one strand
CC of the duplex. The oligomer, and others like it are useful in
CC diagnosis and therapy of diseases characterised by specific DNA
CC duplex targets, e.g. HPV, HER, HIV, hepatitis B, herpes, malignant
CC tumours and inflammation. The triple helices form under mild conditions
CC thus assays may be carried out without subjecting the test specimen to
CC harsh conditions. The oligomer contains an inverted polarity region
CC formed from an o-xyloso dimer synthon. The linking gp. is o-xyloso

CC (nucleotides have the 3'positions of xylose sugars linked via the o-
 CC xylene ring). Two nucleotides are coupled through a xylene residue
 CC to form the dimer synthon. This additional modifications may render
 CC the oligomer stable to nuclease activity. The oligomer is able to
 CC inhibit gene expression, as verified by in vitro systems.
 CC See also AAQ25452-25501 and AAQ30226-448.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 23 BP; 0 A; 2 C; 0 G; 21 T; 0 other;
 Query Match 1.5%; Score 17; DB 1; Length 23;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1084 AAAAAAAAAAAAAAAAAA 1100
 DB 22 AAAAAAAAAAAAAAAAAA 6
 RESULT 524
 AAQ45360/c
 ID AAQ45360 standard; DNA; 23 BP.
 XX
 AC AAQ45360;
 XX
 XX 25-MAR-2003 (updated)
 DT 09-OCT-1994 (first entry)
 XX
 XX Human protein-tyrosine-phosphatase-ID cDNA primer.
 DE
 XX Protein-tyrosine-phosphatase; enzyme; disease diagnosis;
 KW DNA primer; ss.
 KW
 XX Synthetic.
 OS
 PN WO9408017-A1.
 XX
 PD 14-APR-1994.
 XX
 PF 06-OCT-1993; 93WO-EP02728.
 XX
 PR 06-OCT-1992; 92US-0956315.
 PR 16-FEB-1993; 93US-0018129.
 XX
 PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
 XX
 PI Ullrich A, Vogel W;
 XX
 DR WPI; 1994-135583/16.
 XX
 PT New protein tyrosine phosphatase (PTP) protein, PTP-ID - are
 PT useful for diagnosis and treatment of diseases associated with
 PT abnormal PTP-ID levels
 XX
 PS Disclosure; Page 48; 99pp; English.
 XX
 CC This DNA primer is used in the PCR-based amplification of
 CC protein-tyrosine-phosphatase-13 cDNA.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 23 BP; 1 A; 2 C; 2 G; 18 T; 0 other;
 Query Match 1.5%; Score 17; DB 1; Length 23;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1084 AAAAAAAAAAAAAAAAAA 1100
 DB 23 AAAAAAAAAAAAAAAAAA 7
 RESULT 525
 AAQ75028

ID AAQ75028 standard; DNA; 23 BP.
 XX
 AC AAQ75028;
 XX
 DT 25-MAR-2003 (updated)
 DT 03-AUG-1995 (first entry)
 XX
 DE LCR oligo 2.
 XX
 KW Synthetic oligo; solid phase immunoassay; ss.
 XX
 OS Synthetic.
 PN WO9426932-A1.
 XX
 PD 24-NOV-1994.
 XX
 PF 13-MAY-1994; 94WO-US05407.
 XX
 PR 13-MAY-1993; 93US-0061694.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Fields HA, Khudyakov YE;
 XX
 DR WPI; 1995-006819/01.
 XX
 PT Solid phase immunoassay using oligo:nucleotide as label - also
 PT new conjugates of oligo:nucleotide coupled to antigenic peptide,
 PT partic. for diagnosing hepatitis C or E virus infection
 XX
 PS Example; Page 13; 34pp; English.
 XX
 CC AAR62941 and AAR62942 are examples of synthetic immunoreactive peptides.
 CC They are used in a method for detecting an antigen in a subject. The
 CC method involves binding the antigen to a solid support and then
 CC reacting it with an immunoreactive ligand (L) bound to an oligo;
 CC removing any unreacted L, and then detecting the presence of the
 CC oligo. A similar method can be used to detect Ab, in which case the
 CC ligand is an oligo-labelled Ag. The use of an amplifiable oligo as
 CC the label allows Ag or Ab to be detected at very low levels. An
 CC exemplary oligo is AAQ75024 which can be covalently attached by the 5'-
 CC terminus to the N- or C-terminal of a synthetic peptide. For LCR
 CC using oligo AAQ75024, oligos 1-4 (see AAQ75027-Q75030) can be used.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 23 BP; 19 A; 4 C; 0 G; 0 U; 0 other;
 Query Match 1.5%; Score 17; DB 1; Length 23;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1084 AAAAAAAAAAAAAAAAAA 1100
 DB 6 AAAAAAAAAAAAAAAAAA 22
 RESULT 526
 AAQ75029/c
 ID AAQ75029 standard; RNA; 23 BP.
 XX
 AC AAQ75029;
 XX
 DT 25-MAR-2003 (updated)
 DT 03-AUG-1995 (first entry)
 XX
 DE LCR oligo 3.
 XX
 KW Synthetic oligo; solid phase immunoassay; ss.
 XX
 OS Synthetic.
 XX
 PN WO9426932-A1.

XX PD 24-NOV-1994.
 XX PF 13-MAY-1994; 94WO-US05407.
 XX PR 13-MAY-1993; 93US-0061694.
 XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX PI Fields HA, Khudyakov YE;
 XX DR WPI; 1995-006819/01.
 XX PT Solid phase immunoassay using oligo:nucleotide as label - also
 FT new conjugates of oligo:nucleotide coupled to antigenic peptide,
 FT partic. for diagnosing hepatitis C or E virus infection
 XX Example; Page 13; 34pp; English.
 XX PS AAR62941 and AAR62942 are examples of synthetic immunoreactive peptides.
 CC They are used in a method for detecting an antigen in a subject. The
 CC method involves binding the antigen to a solid support and then
 CC reacting it with an immunoreactive ligand (L) bound to an oligo;
 CC removing any unreacted L, and then detecting the presence of the
 CC oligo. A similar method can be used to detect Abs, in which case the
 CC ligand is an oligo-labelled Ag. The use of an amplifiable oligo as
 CC the label allows Ag or Ab to be detected at very low levels. An
 CC exemplary oligo is AAQ75024 which can be covalently attached by the 5'-
 CC terminus to the N- or C-terminal of a synthetic peptide. For LCR
 CC using oligo AAQ75024, oligos 1-4 (see AAQ75027-Q75030) can be used.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX SQ Sequence 23 BP; 0 A; 0 C; 4 G; 1 T; 18 U; 0 other;
 Query Match 1.5%; Score 17; DB 1; Length 23;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1084 AAAAAAAAAAAAAAAAAA 1100
 Db 18 AAAAAAAAAAAAAAAAAA 2
 RESULT 527
 AAT33701/C
 ID AAT33701 standard; DNA; 23 BP.
 XX AC AAT33701;
 XX DT 19-MAY-1997 (first entry)
 XX DE Primer #1 for tissue or cell derived RNA.
 XX KW PCR; polymerase chain reaction; primer; amplify; reverse-transcription;
 KW molecular indexing; class IIS restriction enzyme; cancer; causative gene;
 KW viral infection; hereditary disease; agricultural gene; ss.
 OS Synthetic.
 XX FH Key Location/Qualifiers
 FT misc_feature 1
 FT /*tag= a
 FT /note= "hydroxylated"
 XX PN EP735144-A1.
 XX PD 02-OCT-1996.
 XX PF 26-MAR-1996; 96EP-0104817.
 XX PR 12-SEP-1995; 95JP-0234122.
 PR 28-MAR-1995; 95JP-0069695.
 PR 20-JUL-1995; 95JP-0184006.
 PA (SUNR) SUNTORY LTD.

XX PA (SHKJ) RES DEV CORP JAPAN.
 XX PI Kato K;
 XX DR WPI; 1996-435619/44.
 XX PT Molecular indexing of DNA - using restriction enzymes, PCR
 FT amplification and electrophoresis to analyse DNA fragments
 XX Claim 3; Page 14; 20pp; English.
 XX CC AAT33701-T33703 represent amplification primers used in the reverse-
 CC transcription of tissue or cell derived mRNA, in the method of the
 CC invention. The method of the invention is a molecular indexing method,
 CC and comprises digesting the cDNA amplified by these sequences with a
 CC class IIS restriction enzyme. Each resultant cDNA fragment is then
 CC ligated to a biotinylated adaptor (selected from a pool of 64 adaptors
 CC cohesive to all possible overhangs), and digesting the products with two
 CC further class IIS restriction enzymes. These steps are repeated (but
 CC the enzyme used for the first step is different in each) to produce two
 CC further cDNA samples. The ligation samples are then recovered using
 CC streptavidin-coated paramagnetic beads, removing the strand
 CC complementary to an adaptor-primer. The adaptor primer and an anchored
 CC oligo-dr primer (such as this sequence) are then used to amplify the cDNA
 CC samples. The amplified products are separated, and the sizes of the
 CC fragments obtained is recorded. The method can be used for the analysis
 CC and diagnosis of diseases such as cancers or viral infections, for the
 CC search and isolation of the genes of physiologically active substances
 CC that are potential pharmaceuticals, or causative genes of hereditary
 CC diseases, as well as for the isolation of genes for improving
 CC agricultural products. Using this method, it is possible to classify
 CC (index) DNA into groups in a short period of time without duplication.
 XX SQ Sequence 23 BP; 2 A; 2 C; 2 G; 17 T; 0 other;
 Query Match 1.5%; Score 17; DB 1; Length 23;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1083 TAAAAAAAAAAAAAAAAA 1099
 Db 23 TAAAAAAAAAAAAAAAAA 7
 RESULT 528
 AAT33716/C
 ID AAT33716 standard; DNA; 23 BP.
 XX AC AAT33716;
 XX DT 06-FEB-1997 (first entry)
 XX DE RT-PCR Primer for aromatic acyl transferase sequence.
 XX KW Aromatic acyl transferase; transformation; anthocyanin pigment;
 KW plants; acylation; colour; tone; colouration; colour change;
 KW Gentiana triflora; Petunia hybrida; Petilla ocimoides;
 KW Scenecio cruentus; Lavandula angustifolia; ss.
 XX OS Synthetic.
 XX PN WO9625500-A1.
 XX PD 22-AUG-1996.
 XX PF 16-FEB-1996; 96WO-JP00348.
 XX PR 30-JAN-1996; 96JP-0046534.
 PR 17-FEB-1995; 95JP-0067159.
 PR 29-JUN-1995; 95JP-0196915.
 XX PA (SUNR) SUNTORY LTD.

XX Ashikari T, Fujiwara H, Fukui Y, Kusumi T, Mizutani M;
 PI Nakao M, Tanaka Y, Yonekura K;
 XX WPI; 1996-393401/39.
 XX DNA coding for aromatic acyl transferase - for transforming plants
 PT which produce anthocyanin pigments and thus altering colour tone,
 PT e.g. of flowers
 XX
 XX Example 2; Page 21; 94pp; Japanese.
 XX Vectors containing DNA fragments encoding proteins of plant origin
 CC with aromatic acyl transferase activity may be used to transform
 CC plants which produce anthocyanin pigments. The aromatic acyl
 CC transferase acylates the pigments in the flower resulting in colour
 CC tone changes and allowing new colourations to be produced. Six
 CC specific DNA sequences encoding aromatic acyl transferase from
 CC different plants are described in AAT37308-T37313. This
 CC primer was used to reverse transcribe aromatic acyl transferase RNA
 CC to produce a cDNA ready for cloning into expression vectors.
 XX
 XX Sequence 23 BP; 1 A; 2 C; 2 G; 18 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 23;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
 |||||
 Db 23 AAAAAAAAAAAAAAAAAA 7

RESULT 529
 AAV61555/c
 ID AAV61555 standard; DNA; 23 BP.
 XX
 AC AAV61555;
 XX
 XX 08-DEC-1998 (first entry)
 DE Double-anchored oligo-dT primer, used to synthesise apolipoprotein cDNA.
 XX
 XX Primer; PCR; amplification; RT-PCR; quantitate; amount ratio; liver;
 KW kidney; apolipoprotein; ATAC-PCR; Adaptor-tagged Competitive PCR;
 KW gene expression; internal standard; calibration curve; ss.

XX Synthetic.
 OS Mus sp.
 XX
 XX EP870842-A2.
 XX 14-OCT-1998.
 XX
 XX 07-APR-1998; 98EP-0302726.
 XX
 XX 07-APR-1997; 97JP-0088495.
 XX (NISC-) JAPAN SCI & TECHNOLOGY CORP.
 XX Kato K;
 XX WPI; 1998-523164/45.
 XX
 XX Determination of gene expression levels - using combinations of
 PT different cDNA samples tagged with different PCR adaptors
 XX
 XX Example 2; Page 9; 22pp; English.

XX The present sequence represents a primer which was used to synthesise
 CC Apolipoprotein cDNA in a RT-PCR reaction. This primer as well as
 CC primers AAV61554 and AAV61556 were added to both mouse liver-derived and
 CC mouse kidney-derived total RNA to generate single-stranded cDNA. These

CC primers were used in the method of the invention to determine the amount
 CC ratio between a cDNA coding for mouse liver-derived Apolipoprotein and a
 CC cDNA that codes for the mouse kidney-derived Apolipoprotein by using
 CC Adaptor-tagged Competitive PCR (ATAC-PCR). This method allows gene
 CC expression to be quantitatively determined, and because internal
 CC standards are not required to prepare a calibration curve, it is a
 CC quicker and less laborious process.

XX Sequence 23 BP; 2 A; 2 C; 2 G; 17 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 23;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAAAAAAAAAAAAA 1099
 |||||
 Db 23 TAAAAAAAAAAAAAAAAA 7

RESULT 530
 AAV61556/c
 ID AAV61556 standard; DNA; 23 BP.

XX
 AC AAV61556;
 XX
 XX 08-DEC-1998 (first entry)
 DT Double-anchored oligo-dT primer, used to synthesise apolipoprotein cDNA.
 DE
 XX
 KW Primer; PCR; amplification; RT-PCR; quantitate; amount ratio; liver;
 KW kidney; apolipoprotein; ATAC-PCR; Adaptor-tagged Competitive PCR;
 KW gene expression; internal standard; calibration curve; ss.

XX Synthetic.
 OS Mus sp.

XX
 XX EP870842-A2.
 XX 14-OCT-1998.
 XX
 XX 07-APR-1998; 98EP-0302726.
 XX
 XX 07-APR-1997; 97JP-0088495.
 XX (NISC-) JAPAN SCI & TECHNOLOGY CORP.
 XX Kato K;

XX WPI; 1998-523164/45.

XX Determination of gene expression levels - using combinations of
 PT different cDNA samples tagged with different PCR adaptors
 XX

XX Example 2; Page 9; 22pp; English.

XX The present sequence represents a primer which was used to synthesise
 CC Apolipoprotein cDNA in a RT-PCR reaction. This primer as well as
 CC primers AAV61554 and AAV61555 were added to both mouse liver-derived and
 CC mouse kidney-derived total RNA to generate single-stranded cDNA. These
 CC primers were used in the method of the invention to determine the amount
 CC ratio between a cDNA coding for mouse liver-derived Apolipoprotein and a
 CC cDNA that codes for the mouse kidney-derived Apolipoprotein by using
 CC Adaptor-tagged Competitive PCR (ATAC-PCR). This method allows gene
 CC expression to be quantitatively determined, and because internal
 CC standards are not required to prepare a calibration curve, it is a
 CC quicker and less laborious process.

XX Sequence 23 BP; 2 A; 2 C; 2 G; 17 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 23;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAA... 1099
Db 23 TAAAAA... 7

RESULT 531
AAV61554/c
ID AAV61554 standard; DNA; 23 BP.
XX
AC AAV61554;
DT 08-DEC-1998 (first entry)
XX
DE Double-anchored oligo-dT primer, used to synthesise apolipoprotein cDNA.
XX
DE Primer; PCR; amplification; RT-PCR; quantitate; amount ratio; liver;
KW apolipoprotein; kidney; ATAC-PCR; Adaptor-tagged Competitive PCR;
KW gene expression; internal standard; calibration curve; ss.
XX
OS Synthetic.
OS Mus sp.
XX
PN EP870842-A2.
XX
PD 14-OCT-1998.
XX
PF 07-APR-1998; 98EP-0302726.
XX
PR 07-APR-1997; 97JP-0088495.
XX
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX
PI Kato K;
XX
DR WPI; 1998-523164/45.
XX
PT Determination of gene expression levels - using combinations of
PT different cDNA samples tagged with different PCR adaptors
XX
XX Example 2; Page 9; 22pp; English.
XX
XX The present sequence represents a primer which was used to synthesise
CC Apolipoprotein cDNA in a RT-PCR reaction. This primer as well as
CC primers AAV61555 and AAV61556 were added to both mouse liver-derived and
CC mouse kidney-derived total RNA to generate single-stranded cDNA. These
CC primers were used in the method of the invention to determine the amount
CC ratio between a cDNA coding for mouse liver-derived Apolipoprotein and a
CC cDNA that codes for the mouse kidney-derived Apolipoprotein by using
CC Adaptor-tagged Competitive PCR (ATAC-PCR). This method allows gene
CC expression to be quantitatively determined, and because internal
CC standards are not required to prepare a calibration curve, it is a
CC quicker and less laborious process.
XX
XX Sequence 23 BP; 2 A; 2 C; 2 G; 17 T; 0 other;
SQ

Query Match 1.5%; Score 17; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAA... 1099
Db 23 TAAAAA... 7

RESULT 532
AAC62450/c
ID AAC62450 standard; DNA; 23 BP.
XX
AC AAC62450;
DT 07-FEB-2001 (first entry)
XX
DE Cleavage of nucleic acids from solid supports assay oligonucleotide #1.

Query Match 1.5%; Score 17; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX Nucleic acid cleavage; solid support; DNA-RNA hybrid;
KW affinity chromatography; sequencing; mutagenesis; DNA preparation;
KW nucleic acid purification; ss.
XX
OS Synthetic.
FH Key Location/Qualifiers
FT misc_RNA 23
FT /*tag= a
XX
PN WO200058329-A1.
XX
PD 05-OCT-2000.
XX
PF 28-MAR-2000; 2000WO-GB01190.
XX
PR 29-MAR-1999; 99GB-0007245.
XX
PA (GOLD/) GOLDBOROUGH A.
XX
DR WPI; 2000-664908/64.
XX
PT Detaching nucleic acid molecule comprising unconventional nucleotide
PT incorporated at predetermined site from a solid support involves
PT cleaving the nucleic acid molecule at the site of unconventional
PT nucleotide -
XX
PS Disclosure; Page 16; 47pp; English.
XX
XX The present invention is concerned with the cleavage of nucleic acids
CC from solid supports. This is carried out by adding a non-conventional
CC nucleotide into the nucleic acid attached to the support, so that it is
CC recognised and cleaved by a specific DNA glycosylase and the sequence is
CC released. This is useful in many molecular biological procedures such as
CC sequencing, in vitro amplifications, cDNA and template preparation,
CC DNA-based assays, mutagenesis procedures, nucleic acid purification and
CC affinity chromatography. The present sequence is an oligonucleotide used
CC in assays to demonstrate the methods of the invention.
XX
XX Sequence 23 BP; 0 A; 0 C; 0 G; 22 T; 1 U; 0 other;
SQ

Query Match 1.5%; Score 17; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAA... 1100
Db 23 AAAAAA... 7

RESULT 533
AAC62451/c
ID AAC62451 standard; RNA; 23 BP.
XX
AC AAC62451;
DT 07-FEB-2001 (first entry)
XX
DE Cleavage of nucleic acids from solid supports assay oligonucleotide #2.
XX
KW Nucleic acid cleavage; solid support; affinity chromatography;
KW sequencing; mutagenesis; DNA preparation; nucleic acid purification; ss.
XX
OS Synthetic.
XX
PN WO200058329-A1.
XX
PD 05-OCT-2000.
XX
PF 28-MAR-2000; 2000WO-GB01190.
XX
PR 29-MAR-1999; 99GB-0007245.

Query Match 1.5%; Score 17; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Thu Jan 8 16:51:41 2004

XX PA (GOLD/) GOLDSBOROUGH A.
 XX DR WPI; 2000-664908/64.
 XX PT Detaching nucleic acid molecule comprising unconventional nucleotide
 XX PT incorporated at predetermined site from a solid support involves
 XX PT cleaving the nucleic acid molecule at the site of unconventional
 XX PT nucleotide -
 XX PS Example 1; Page 32; 47pp; English.
 XX CC The present invention is concerned with the cleavage of nucleic acids
 XX CC from solid supports. This is carried out by adding a non-conventional
 XX CC nucleotide into the nucleic acid attached to the support, so that it is
 XX CC recognised and cleaved by a specific DNA glycosylase and the sequence is
 XX CC released. This is useful in many molecular biological procedures such as
 XX CC sequencing, in vitro amplifications, cDNA and template preparation, and
 XX CC DNA-based assays, mutagenesis procedures, nucleic acid purification and
 XX CC affinity chromatography. The present sequence is an oligonucleotide used
 XX CC in assays to demonstrate the methods of the invention.
 XX SQ Sequence 23 BP; 0 A; 0 C; 0 G; 0 G; 23 U; 0 other;
 Query Match 1.5%; Score 17; DB 1; Length 23;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1084 AAAAAAAAAAAAAAAAAA 1100
 DB 23 AAAAAAAAAAAAAAAAAA 7
 RESULT 534
 AAA08407/C
 ID AAA08407 standard; DNA; 23 BP.
 AC AAA08407;
 XX 13-JUL-2000 (first entry)
 DE Oligonucleotide primer SEQ ID NO:1.
 KW Detection; primer; adapter; probe; hybridisation; gene cluster;
 KW fractionation; ss.
 XX Synthetic.
 XX JP2000055914-A.
 XX 25-FEB-2000.
 XX 13-AUG-1998; 98JP-0228944.
 XX 13-AUG-1998; 98JP-0228944.
 XX (TAIS) TAISHO PHARM CO LTD.
 XX WPI; 2000-368733/32.
 XX Gene detection method involves hybridizing probe opposite to objective
 XX gene out of fractional gene cluster -
 XX Example 1; Page 9; 11pp; Japanese.
 XX The present invention describes a gene detection method which comprises
 XX fractionating using a probe opposite to the objective gene which is
 XX hybridised out of fractioned gene cluster. The objective gene detected
 XX belongs to the group of objective genes contained in the sample. The
 XX method is used for gene detection by fractionation of cDNA by molecular
 XX index method using specific primer. It provides high detection
 XX sensitivity of objective gene. AAA08407 to AAA08414 represent
 XX oligonucleotides used in the exemplification of the present invention.

XX SQ Sequence 23 BP; 2 A; 2 C; 2 G; 17 T; 0 other;
 Query Match 1.5%; Score 17; DB 1; Length 23;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1083 TAAAAAAAAAAAAAAAAA 1099
 DB 23 TAAAAAAAAAAAAAAAAA 7
 RESULT 535
 AAF85497/C
 ID AAF85497 standard; DNA; 23 BP.
 AC AAF85497;
 XX 23-JUL-2001 (first entry)
 DE PCR primer for DNA encoding Kalata B1 polypeptide fragments.
 XX Kalata B2; transgenic plant; cotton; calcium channel binding; pain;
 KW stroke; C5a binding; antiinflammatory; PCR primer; ss.
 XX Oldenlandia affinis.
 OS WO200134829-A2.
 XX 17-MAY-2001.
 XX 03-NOV-2000; 2000WO-AU01352.
 XX 05-NOV-1999; 99AU-0003884.
 XX 25-NOV-1999; 99AU-0004235.
 XX (UYQU) UNIV QUEENSLAND.
 XX (UYLA-) UNIV LATROBE.
 XX Craik DJ, Anderson MA, Jennings CV;
 WPI; 2001-343607/36.
 Novel nucleic acid molecule encoding amino acid sequence capable of
 forming cyclic structure, for generating transgenic plants capable of
 producing cyclic knotted protein and resistant to pathogens such as
 insects -
 Example 10; Fig 1B; 112pp; English.
 PCR primers AAF85495-97 were used to amplify a DNA fragment encoding
 Kalata B1. Kalata B1 is a macrocyclic peptide with diverse biological
 activities. The Kalata B1 polynucleotide represents a nucleic acid
 molecule of the invention. The specification describes nucleic acid
 molecules which encode an amino acid sequence which is capable of being
 cyclised within a cell or a membrane of a cell to form a cyclic backbone.
 The amino acid sequence comprises sufficient disulfide bonds to confer
 a stabilized folded structure on the three-dimensional structure of the
 backbone. The nucleic acid molecules of the invention are useful for
 producing transgenic genetically modified food or non-food crop plants,
 in particular cotton. The peptides or proteins can be manipulated to
 introduce modulating activity, for modulating activity of calcium
 channel binding is useful in treatment of pain or stroke and C5a binding
 activity useful as an antiinflammatory agent. The nucleic acid molecules
 are useful in the generation of molecules having animal or plant
 therapeutic properties as well as in a range of diagnostic, industrial
 and agricultural including horticultural applications and for
 protecting plants such as crop plants from pest and/or pathogen
 infestation.
 SQ Sequence 23 BP; 2 A; 2 C; 2 G; 17 T; 0 other;
 Query Match 1.5%; Score 17; DB 1; Length 23;

```
Best Local Similarity 100.0%; Pred. No. 2.5e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 17; Conservative 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
Db 23 AAAAAAAAAAAAAAAAAA 7

RESULT 536
AAF16627/c
ID AAF16627 standard; DNA; 23 BP.
XX AC AAF16627;
XX DT 13-MAR-2001 (first entry)
XX DE Gastric acid production inhibiting oligonucleotide SEQ ID NO: 114.
XX KW Gastric acid disturbance; Gastric reflux; gastritis; dyspepsia;
XX KW stomach ulcer; duodenal ulcer; Helicobacter pylori; antisense;
XX KW DNA-RNA hybrid; ss.
XX OS Homo sapiens.
XX PN WO200071164-A1.
XX PD 30-NOV-2000.
XX PF 24-MAY-2000; 2000WO-AU00498.
XX PR 24-MAY-1999; 99AU-0000510.
XX PA (TACH/) TACHAS G.
XX PI Tachas G;
XX PS WPI; 2001-025093/03.
XX DR Treating gastric acid disturbance by administering an oligonucleotide
XX PT which modulates the activity of a polypeptide involved in gastric acid
XX PT production or secretion -
XX PS Example 3; Page 152; 164pp; English.
XX CC The present invention provides oligonucleotides, and methods for their
XX CC use, which are useful in modulating the action of proteins involved in
XX CC gastric acid production. The target protein is preferably the histamine
XX CC H2 receptor or one of the proteins which form part of the gastric proton
XX CC pump. The sequences and methods of the invention are useful in the
XX CC treatment of gastric reflux, gastritis, dyspepsia, stomach ulcers,
XX CC duodenal ulcers and other gastric acid disturbances, most of which are
XX CC caused by Helicobacter pylori.
XX SQ Sequence 23 BP; 1 A; 0 C; 0 G; 22 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
Db 23 AAAAAAAAAAAAAAAAAA 7

RESULT 537
AAD33503
ID AAD33503 standard; DNA; 23 BP.
XX AC AAD33503;
XX XX 01-JUL-2002 (first entry)
XX DT T7T18Apad_PS13-23-0001 probe for calibration of molecular array data.
XX DE
```

```
XX Molecular array; probe; ss.
XX Unidentified.
XX PN EP1186673-A2.
XX PD 13-MAR-2002.
XX PF 10-SEP-2001; 2001EP-0307665.
XX PR 11-SEP-2000; 2000US-0659173.
XX PA (AGIL-) AGILENT TECHNOLOGIES INC.
XX PI Wobler PK, Delenstarr GC;
XX WPI; 2002-282886/33.
XX DR Calibration of molecular array data by employing calibration probes
XX PT that generate signals proportional to total concentrations of labeled
XX PT target molecules, and molecular arrays incorporating sets of
XX PT calibration probes -
XX PS Disclosure; Page 14; 32pp; English.
XX CC The invention relates to a method for calibrating data scanned from a
XX CC molecular array. The method involves employing calibrations probes that
XX CC generate signals proportional to the total concentrations of labeled
XX CC target molecules to which the molecular array probes are directed over
XX CC an entire range of sample solutions and molecular arrays incorporating
XX CC sets of calibration probes. Method is useful for calibrating different
XX CC types of signals scanned from a molecular array, or calibrating signals
XX CC scanned from different molecular arrays. The present sequence is poly
XX CC (A) normalisation probe used in calibration of molecular array data.
XX SQ Sequence 23 BP; 18 A; 3 C; 0 G; 2 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
Db 1 AAAAAAAAAAAAAAAAAA 17

RESULT 538
ABL95973/c
ID ABL95973 standard; DNA; 23 BP.
XX AC ABL95973;
XX DT 19-JUN-2002 (first entry)
XX DE Probe #48 for assaying nucleic acids.
XX KW Probe; polymorphism detection; mutation detection;
XX KW disease diagnosis; microbial identification; ss.
XX OS Unidentified.
XX PN WO200208414-A1.
XX PD 31-JAN-2002.
XX PF 27-JUN-2001; 2001WO-IB01147.
XX PR 27-JUN-2000; 2000JP-0193133.
XX PR 03-AUG-2000; 2000JP-0236115.
XX PR 26-SEP-2000; 2000JP-0292483.
XX PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
```

PA (KANK-) KANKYO ENG CO LTD.
 XX Kurane R, Kanagawa T, Kamagata Y, Torimura M, Kurata S, Yamada K;
 PI Yokomaku T;
 XX WPI; 2002-195876/25.
 DR
 XX Fluorescently-labeled nucleic acid probes for assaying nucleic acids
 XX and their polymorphism and mutation, particularly useful in science and
 XX medicine for e.g. analytical applications, disease diagnosis and
 XX microbial identification -
 XX Disclosure; Fig 3; 152pp; Japanese.
 XX The present invention relates to nucleic acid probes, which are useful
 XX for assaying nucleic acids by hybridising with a target nucleic acid, in
 XX which a single-stranded oligonucleotide is labelled with a fluorescent
 XX substance and a quencher in a manner that the fluorescence intensity of
 XX the hybridisation reaction system is increased after completion of the
 XX hybridisation but no stem loop structure is formed. The probes are useful
 XX for assaying nucleic acids and their polymorphism and mutation,
 XX particularly useful for e.g. analytical applications, disease diagnosis
 XX and microbial identification. The present sequence was used to illustrate
 XX the invention.
 XX Sequence 23 BP; 0 A; 6 C; 0 G; 17 T; 0 other;
 SQ
 Query Match 1.5%; Score 17; DB 1; Length 23;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1084 AAAAAAAAAAAAAAAAAA 1100
 DB 17 AAAAAAAAAAAAAAAAAA 1
 RESULT 539
 ABA99682/C
 ID ABA99682 standard; DNA; 23 BP.
 XX
 AC ABA99682;
 DT 31-MAY-2002 (first entry)
 XX Murine osteoporosis/arthritis-rheumatism associated gene PCR primer DAPAL.
 DE Osteoporosis; murine; treatment; arthritis-rheumatism; PCR; primer; ss.
 KW Mus musculus.
 OS
 XX JP2002051782-A.
 FN
 XX 19-FEB-2002.
 PD
 XX 09-AUG-2000; 2000JP-0241413.
 PF
 XX 09-AUG-2000; 2000JP-0241413.
 PR
 XX (SANY) SANKYO CO LTD.
 PA
 XX WPI; 2002-288360/33.
 DR Preventing or treating an agent for osteoporosis or arthritis-rheumatism
 PT
 XX
 PS Example 2; Page 38; 44pp; Japanese.
 XX This invention describes a novel method for testing the effect of a
 XX substance as a preventive or treating agent for osteoporosis or
 XX arthritis-rheumatism. This sequence represents a PCR primer used in the
 XX amplification of a gene encoding a protein associated with osteoporosis
 XX or arthritis-rheumatism which is described in the disclosure of the
 XX invention.

XX Sequence 23 BP; 2 A; 2 C; 2 G; 17 T; 0 other;
 SQ
 Query Match 1.5%; Score 17; DB 1; Length 23;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1083 TAAAAAAAAAAAAAAAAA 1099
 DB 23 TAAAAAAAAAAAAAAAAA 7
 RESULT 540
 ABA97431/C
 ID ABA97431 standard; DNA; 23 BP.
 XX
 AC ABA97431;
 DT 21-MAR-2002 (first entry)
 XX Glycosyltransferase genes PCR primer #2.
 DE Glycosyltransferase; anthocyanin; flower colour; enzyme; PCR primer; ss.
 KW
 XX Unidentified.
 OS
 XX WO200192509-A1.
 FN
 XX 06-DEC-2001.
 PD
 XX 01-JUN-2001; 2001WO-JP04675.
 PF
 XX 02-JUN-2000; 2000JP-0170436.
 PR
 XX (ITFL-) INT FLOWER DEV PTY LTD.
 PA
 XX Mizutani M, Sakakibara K, Tanaka Y, Kusumi T, Ono E;
 PI WPI; 2002-114345/15.
 DR
 XX New gene encoding protein that transfers a sugar to the 3' position of
 XX anthocyanin for changing flower color -
 XX Example 3; Page 13; 50pp; Japanese.
 PS The present invention provides the genes and proteins of
 CC glycosyltransferases from Gentiana triflora, Senecio cruentus and
 CC Clitoria ternatea. The protein transfers a sugar to the 3' position of
 CC anthocyanin, and can be used for changing the colour of flowers. The
 CC present sequence is a PCR primer used to isolate glycosyltransferase
 CC coding sequences of the invention.
 XX Sequence 23 BP; 1 A; 2 C; 2 G; 18 T; 0 other;
 SQ
 Query Match 1.5%; Score 17; DB 1; Length 23;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1084 AAAAAAAAAAAAAAAAAA 1100
 DB 23 AAAAAAAAAAAAAAAAAA 7
 RESULT 541
 AAT68615/C
 ID AAT68615 standard; DNA; 24 BP.
 XX
 AC AAT68615;
 DT 20-FEB-1998 (first entry)
 XX DNA probe used in fingerprinting technique.
 DE
 XX

XX probe; screening; fingerprinting; assay; 3' termini; hybridisation; ss.
 XX Synthetic.
 XX EP778351-A2.
 XX
 XX 11-JUN-1997.
 XX 26-NOV-1996; 96EP-0118921.
 XX 30-NOV-1995; 95JP-0311949.
 XX (HITA) HITACHI LTD.
 XX Kambara H, Okano K, Uematsu C;
 XX WPI; 1997-300347/28.
 XX Nucleic acid assay methods - based on restriction fragment length
 XX determination
 XX Example 1; Page 7; 21pp; English.
 XX The present sequence is a DNA probe used in a novel method of analysis
 XX or assay for nucleotides, which comprises: (i) digesting DNA with a
 XX restriction enzyme; (ii) discriminating a difference in sequences of the
 XX DNA fragments obtained around the 3' termini with a DNA probe and
 XX extending the DNA probe by a complementary strand synthesis to
 XX fractionate the DNA fragments into groups; and (iii) measuring lengths
 XX of the DNA fragments which belong to the groups, or length of the
 XX extended DNA probe, and using the lengths obtained for the fragments
 XX around the 3' termini as fingerprints. Where polyA is present, the
 XX presence of recognition sequence GCG is critical for clarifying the
 XX terminal site, this is because the length of polyA cannot be controlled.
 XX The method is useful for assaying a large number of cDNA molecules or
 XX DNA fragments and for assaying long DNA sequences.
 XX Sequence 24 BP; 0 A; 2 C; 1 G; 19 T; 2 other;
 XX
 XX Query Match 1.5%; Score 17; DB 1; Length 24;
 XX Best Local Similarity 100.0%; Pred. No. 2.6e+02;
 XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX 1084 AAAAAAAAAAAAAAAAAA 1100
 XX |||||
 XX 19 AAAAAAAAAAAAAAAAAA 3
 XX
 XX RESULT 542
 XX AAH43079/c
 XX ID AAH43079 standard; DNA; 24 BP.
 XX AC
 XX AAH43079;
 XX 15-OCT-2001 (first entry)
 XX DE Nucleotide sequence of a synthetic oligonucleotide.
 XX KW Nucleic acid immobilisation; ss.
 XX OS Synthetic.
 XX WO200155365-A1.
 XX 02-AUG-2001.
 XX 24-JAN-2001; 2001WO-JP00443.
 XX 27-JAN-2000; 2000JP-0019301.
 XX (TOJO) TOYO KOHAN CO LTD.
 XX Tanga M, Okamura H, Takagi K, Takahashi K;

XX WPI; 2001-488794/53.
 XX Support for immobilizing nucleotides -
 XX Example 1; Page 8; 18pp; Japanese.
 XX The specification describes a support for immobilizing nucleotides
 XX which contributes to the efficient clarification of DNA without damaging
 XX the terminal parts of the DNA. The support is a chemically treated
 XX modified substrate on which oligonucleotides with restriction enzyme
 XX cleavage sites are immobilised. The support is useful for immobilizing
 XX nucleic acids such as DNA. The present sequence represents a synthetic
 XX oligonucleotide used in the course of the invention.
 XX Sequence 24 BP; 3 A; 0 C; 3 G; 18 T; 0 other;
 XX
 XX Query Match 1.5%; Score 17; DB 1; Length 24;
 XX Best Local Similarity 100.0%; Pred. No. 2.6e+02;
 XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX 1084 AAAAAAAAAAAAAAAAAA 1100
 XX |||||
 XX 23 AAAAAAAAAAAAAAAAAA 7
 XX
 XX RESULT 543
 XX AAH24266/c
 XX ID AAH24266 standard; DNA; 24 BP.
 XX AC
 XX AAH24266;
 XX 11-SEP-2001 (first entry)
 XX DE Human phosphatase 79 RT-PCR primer, SEQ ID NO:4.
 XX KW Phosphatase 79; human; BAC clone CTS-54D4-encoded protein homologue;
 XX recombinant production; malignant tumour; cancer; blood disease;
 XX HIV infection; human immunodeficiency virus; immune disorder;
 XX inflammatory condition; cytostatic; anti-HIV; antiinflammatory;
 XX immunomodulator; reverse transcription-PCR; RT-PCR primer; ss.
 XX OS Homo sapiens.
 XX WO200138385-A1.
 XX 31-MAY-2001.
 XX 20-NOV-2000; 2000WO-CN00459.
 XX 22-NOV-1999; 99CN-0124059.
 XX (BIOR-) BIOROAD GENE DEV LTD SHANGHAI.
 XX Mao Y, Xie Y;
 XX WPI; 2001-355903/37.
 XX Human phosphatase 79 and encoded polynucleotide, applicable in
 XX diagnosis and treatment of malignant tumor, hemopathy, HIV infection,
 XX immunological diseases and various inflammation -
 XX Example 3; Page 12; 38pp; Chinese.
 XX The invention relates to human phosphatase 79 (AAB73700), nucleic acids
 XX encoding it (AAH24264), and a method for the recombinant production of
 XX human phosphatase 79. The present invention additionally discloses an
 XX agonist of phosphatase 79 for therapeutic use, and an antibody which
 XX specifically binds to human phosphatase 79. Human phosphatase 79, and
 XX nucleotides which encode it may be used for treating a variety of
 XX diseases, such as malignant tumours, blood diseases, HIV (human
 XX immunodeficiency virus) infection, immune disorders and inflammatory
 XX conditions. The protein may also be used to screen for modulators of its

CC activity or for peptide fingerprinting identification. The polynucleotide
CC can be used as a primer for nucleic acid amplification reaction or as a
CC probe for hybridisation reactions, or in producing gene chips or
CC microarrays. Sequences AAH24265-AAH24266 represent reverse
CC transcription-PCR (RT-PCR) primers used in an exemplification of the
CC invention to isolate human phosphatase 79 cDNA.
XX
SQ Sequence 24 BP; 2 A; 0 C; 0 G; 22 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
DB 24 AAAAAAAAAAAAAAAAAA 8

RESULT 544
ABQ79878/c
ID ABQ79878 standard; DNA; 24 BP.
XX
AC ABQ79878;
XX
DT 23-DEC-2002 (first entry)
DE Nucleotide sequence of a PCR primer #8.
XX
KW Polymerase chain reaction; thermal cycle; immobilisation;
KW genetic engineering; PCR; primer; ss.
XX
OS Synthetic.
XX
PN JP2002191369-A.
XX
PD 09-JUL-2002.
XX
PF 27-DEC-2000; 2000JP-0399573.
XX
PR 27-DEC-2000; 2000JP-0399573.
XX
PA (TOJO) TOYO KOHAN CO LTD.
PA (TAKA) TAKAHASHI K.
XX
DR WPI; 2002-630904/68.
XX
PT Carrying out a thermal cycle of polymerase chain reaction (PCR) by
PT using a substrate on which a DNA is immobilized used in medical,
PT biochemical, molecular biological and gene engineering fields -
XX
PS Examples; Page 10; 13pp; Japanese.
XX
CC The invention relates to performing a thermal cycle of PCR by using a
CC substrate on which a deoxyribonucleic acid (DNA) is immobilized. The
CC method is useful in the medical, biochemical, molecular biological and
CC genetic engineering fields. Sequences ABQ79871-881 represent PCR primers
CC used in the method of the invention.
XX
SQ Sequence 24 BP; 3 A; 0 C; 3 G; 18 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
DB 23 AAAAAAAAAAAAAAAAAA 7

RESULT 545
ABK86172/c
ID ABK86172 standard; DNA; 24 BP.
XX

AC ABK86172;
XX
DT 24-SEP-2002 (first entry)
XX
DE Oligo dT primer #4 used in method to study gene expression.
XX
KW Oligo dT primer; gene expression analysis; primer; ss.
XX
OS Synthetic.
XX
FN WO200236828-A2.
XX
PD 10-MAY-2002.
XX
PF 01-NOV-2001; 2001WO-US45401.
XX
PR 01-NOV-2000; 2000US-244933P.
XX
PA (GENO-) GENOMIC SOLUTIONS INC.
XX
PI Kane MD, Dombkowski AA, Nagel AC;
XX
DR WPI; 2002-508123/54.
XX
PT Identifying and characterizing gene expression in samples, for
PT identifying mRNAs expressed at different levels, comprises employing an
PT identifier having a oligo-dT primer of a specific sequence and a
PT detectable marker at its 5' end -
XX
PS Example 1; Page 15; 45pp; English.
XX
CC The invention relates to systems for identification and characterisation
CC of gene expression in one or more samples, comprising an identifier having
CC a specific oligo-dT primer sequence, where the identifier comprises a
CC detectable marker at its 5' end. The system is useful for identifying any
CC or all genes expressed in a given in vivo or in vitro RNA sample, as well
CC as the relative differences in mRNA between 2 or more samples, where
CC desired, for supporting discovery of new genes, and for identifying mRNAs
CC that are expressed at different levels between 2 or more samples. The new
CC system or method addresses limitations of prior methods by comprising
CC compositions and systems that incorporate new strategies where molecular
CC or biochemical assay compositions and systems are linked to DNA or RNA
CC sequence databases for optimal resource efficiency in assaying gene
CC expression. The system has the following advantages over existing
CC methods: (a) prior sequence information or clone library construction is
CC not needed to enable the assay; (b) provides immediate sequence
CC information in addition to information concerning changes or differences
CC in mRNA level, to determine mRNA expression level and mRNA identification
CC in one assay; (c) generates cDNA fragments from all mRNAs present in the
CC sample for subsequent investigation by common molecular biology
CC techniques; and (d) does not require prior knowledge of the sequence of
CC the genome of the organism under investigation and can be employed in
CC organisms lacking significant genomic sequence information. The present
CC invention represents an oligo dT primer used in the method of the
XX
SQ Sequence 24 BP; 0 A; 0 C; 0 G; 20 T; 4 other;

Query Match 1.5%; Score 17; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
DB 24 AAAAAAAAAAAAAAAAAA 8

RESULT 546
ABN85073/c
ID ABN85073 standard; DNA; 24 BP.
XX
AC ABN85073;
XX

DT 05-SEP-2002 (first entry)
 XX Human S4 ribosomal protein 13.97 PCR primer #2.
 XX
 XX Human; S4 ribosomal protein 13.97; malignant tumour; haemopathy;
 KW HIV infection; immunological disease; inflammation; cytostatic; anti-HIV;
 KW PCR; primer; ss.
 XX
 XX Homo sapiens.
 OS
 XX CN1333268-A.
 PN
 XX 30-JAN-2002.
 PD
 XX 07-JUL-2000; 2000CN-0117077.
 PF
 XX 07-JUL-2000; 2000CN-0117077.
 PR
 XX (SHAN-) SHANGHAI BIODOOR GENE DEV CO LTD.
 PA
 XX Mao Y, Xie Y;
 PI
 XX WPI; 2002-292916/34.
 DR
 XX Human S4 ribosomal protein 13.97 polypeptide and encoding
 PT polynucleotide, useful for treating malignant tumor, inflammation,
 PT hemopathy, human immunodeficiency virus infection, immunological
 PT disease and inflammation -
 XX
 XX Example 2; Page 16 (Disclosure); 33pp; Chinese.
 PS
 XX The present invention relates to human S4 ribosomal protein 13.97 (see
 CC ABB83379). The ribosomal protein and its coding sequence are useful
 CC for treating malignant tumours, haemopathy, HIV infection, immunological
 CC diseases and various inflammations. The present sequence is a PCR primer,
 CC which was used in an example from the invention.
 XX
 XX Sequence 24 BP; 1 A; 2 C; 1 G; 20 T; 0 other;
 SQ
 Query Match 1.5%; Score 17; DB 1; Length 24;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1084 AAAAAAAAAAAAAA 1100
 DB 24 AAAAAAAAAAAAAA 8
 RESULT 547
 AAD33505
 ID AAD33505 standard; DNA; 24 BP.
 XX
 AC AAD33505;
 XX
 XX 01-JUL-2002 (first entry)
 DT
 XX T7718Apad_PS12-24-0001 probe for calibration of molecular array data.
 DE
 XX Molecular array; probe; ss.
 KW
 XX Unidentified.
 OS
 XX EP1186673-A2.
 PN
 XX 13-MAR-2002.
 PD
 XX 10-SEP-2001; 2001EP-0307665.
 XX
 XX 11-SEP-2000; 2000US-0659173.
 PR
 XX (AGIL-) AGILENT TECHNOLOGIES INC.
 PA
 XX Wobler PK, Delenstarr GC;
 PI

XX WPI; 2002-282886/33.
 DR
 XX Calibration of molecular array data by employing calibration probes
 PT that generate signals proportional to total concentrations of labeled
 PT target molecules, and molecular arrays incorporating sets of
 PT calibration probes -
 XX
 XX Disclosure; Page 14; 32pp; English.
 PS
 XX The invention relates to a method for calibrating data scanned from a
 CC molecular array. The method involves employing calibration probes that
 CC generate signals proportional to the total concentrations of labeled
 CC target molecules to which the molecular array probes are directed over
 CC an entire range of sample solutions and molecular arrays incorporating
 CC sets of calibration probes. Method is useful for calibrating different
 CC types of signals scanned from a molecular array, or calibrating signals
 CC scanned from different molecular arrays. The present sequence is poly
 CC (A) normalisation probe used in calibration of molecular array data.
 XX
 XX Sequence 24 BP; 18 A; 4 C; 0 G; 2 T; 0 other;
 SQ
 Query Match 1.5%; Score 17; DB 1; Length 24;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1084 AAAAAAAAAAAAAA 1100
 DB 1 AAAAAAAAAAAAAA 17
 RESULT 548
 ABL55130/C
 ID ABL55130 standard; DNA; 24 BP.
 XX
 AC ABL55130;
 XX
 XX 31-MAY-2002 (first entry)
 DT
 XX Human gonadotropin-releasing hormone 10 RT-PCR primer, SEQ ID NO:4.
 DE
 XX Human; gonadotropin-releasing hormone 10; recombinant production;
 KW cancer; HIV infection; human immunodeficiency virus; gene therapy;
 KW cytostatic; anti-HIV; reverse transcription-PCR; RT-PCR; primer; ss.
 XX
 OS Homo sapiens.
 XX
 XX CN1325900-A.
 FN
 XX 12-DEC-2001.
 PD
 XX 31-MAY-2000; 2000CN-0116266.
 PF
 XX 31-MAY-2000; 2000CN-0116266.
 PR
 XX (BODE-) BODE GENE DEV CO LTD SHANGHAI.
 PA
 XX Mao Y, Xie Y;
 PI
 XX WPI; 2002-196660/26.
 DR
 XX Polypeptide-human gonadotropin-releasing hormone 10 and polynucleotide
 PT encoding it -
 XX
 XX Example 2; Page 17 (Disclosure); 32pp; Chinese.
 PS
 XX The invention relates to human gonadotropin-releasing hormone 10
 CC (AAW49158) and to nucleic acids encoding it (ABL55128). The protein has
 CC a molecular weight of 10 kD. The invention also relates to a method for
 CC the recombinant production of the protein, an antagonist of the protein,
 CC and the use of the protein, gene and antagonist in therapeutic
 CC applications. Gonadotropin-releasing hormone 10 can be used in the
 CC treatment of a variety of diseases such as cancer and HIV (human

Thu Jan 8 16:51:41 2004

CC immunodeficiency virus) infection. Sequences ABL55129-ABL55130 represent
 CC reverse transcription-PCR (RT-PCR) primers used in an exemplification of
 CC the invention to isolate human gonadotropin-releasing hormone 10 cDNA.
 XX
 SQ Sequence 24 BP; 1 A; 1 C; 3 G; 19 T; 0 other;
 Query Match 1.5%; Score 17; DB 1; Length 24;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1084 AAAAAAAAAAAAAAAAAA 1100
 Db 19 AAAAAAAAAAAAAAAAAA 3
 RESULT 549
 ABX79809/C
 ID ABX79809 standard; cDNA; 24 BP.
 XX
 AC ABX79809;
 DT 17-APR-2003 (first entry)
 XX
 DE EST polymorphic DNA repeat polynucleotide #134.
 KW EST; expressed sequence tag; ss; polymorphic repeat; tandem repeat;
 KW polymorphic marker prediction of ubiquitous simple sequences; POMPOUS;
 KW Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;
 KW Haw River syndrome; Huntington's disease; fragile-X syndrome;
 KW Friedrich's ataxia; myotonic dystrophy; hyperandrogenaemia;
 KW spinal atrophy; bulbar atrophy; spinocerebellar ataxia.
 XX
 OS Homo sapiens.
 XX
 PN US6472154-B1.
 XX
 PD 29-OCT-2002.
 XX
 PF 31-DEC-1999; 99US-0475947.
 XX
 PR 31-DEC-1999; 99US-0475947.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX
 PI Garner HR, Wren JD, Minna JD, Fondon JW;
 XX
 PT WPI; 2003-208818/20.
 DR
 DR Identifying a candidate polymorphic repeat within a coding sequence,
 PT for understanding or treating genetic disease, comprises detecting
 PT tandem repeats in a target coding sequence and scoring the repeats for
 PT polymorphic probability -
 PT
 PS Examples; Column 579; 588pp; English.
 XX
 CC The invention discloses a method for identifying a candidate polymorphic
 CC repeat within a coding sequence (expressed sequence tag, EST), which
 CC comprises detecting tandem repeats in a target coding sequence, scoring
 CC the repeats for polymorphic probability and generating a dataset
 CC correlating the repeats with polymorphic probability to identify a
 CC candidate polymorphic repeat. The computational methods (polymorphic
 CC marker prediction of ubiquitous simple sequences, POMPOUS, and Rep-X) are
 CC useful for identifying and detecting candidate polymorphic repeats in
 CC human genes, which can be used to understand, treat or eliminate genetic
 CC diseases, predispositions or adverse drug-treatment reactions. Examples
 CC of diseases linked to nucleotide repeats are Machado-Joseph, Haw River
 CC syndrome, Huntington's disease, fragile-X syndrome, Friedrich's ataxia,
 CC myotonic dystrophy, hyperandrogenaemia, spinal and bulbar atrophy and
 CC spinocerebellar ataxia. The sequences presented in ABX79676-ABX80022 are
 CC the polymorphic repeats identified for a search of human ESTs.
 XX
 SQ Sequence 24 BP; 0 A; 1 C; 0 G; 23 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 24;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1084 AAAAAAAAAAAAAAAAAA 1100
 Db 23 AAAAAAAAAAAAAAAAAA 7
 RESULT 550
 AAZ37719
 ID AAZ37719 standard; DNA; 20 BP.
 XX
 AC AAZ37719;
 DT 07-JAN-2000 (first entry)
 XX
 DE Human mdm2 phosphorothioate oligodeoxynucleotide #249.
 XX
 KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53;
 KW cancer; antisense; modulation; oligonucleotide; expression;
 KW inhibition; hyperproliferation; blood cancer; brain cancer;
 KW breast cancer; lung cancer; soft tissue cancer; psoriasis; fibrosis;
 KW atherosclerosis; restenosis; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO9949065-A1.
 XX
 PD 30-SEP-1999.
 XX
 PF 26-MAR-1999; 99WO-US06702.
 XX
 PR 26-MAR-1998; 98US-0048810.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Miraglia LJ, Nero P, Graham MJ, Monia BP, Cowsett LM;
 XX
 DR WPI; 1999-610754/52.
 XX
 PT New antisense compounds used to treat eg. hyperproliferative conditions
 PT -
 XX
 PS Example 9; Page 54; 157pp; English.
 CC
 CC AAZ37473-Z37738 represent human mdm2 phosphorothioate oligonucleotides.
 CC AAZ37471, AAZ37472, AAZ37739, AAZ37740 and AAZ37741 are used in the
 CC exemplification of the present invention. The present invention
 CC describes novel nucleotide antisense compounds, targeted to the 5',
 CC untranslated, translation termination codon, or 3' untranslated region
 CC of a nucleic acid encoding human mdm2, that modulates expression of
 CC human mdm2. The oligonucleotides mediate their effect by antisense
 CC inhibition of hyperproliferative gene expression. The antisense compound
 CC is used to treat an animal having a disease or condition associated
 CC with mdm2, particularly a hyperproliferative condition, more
 CC particularly cancer, especially of the blood, brain, breast, lung or soft
 CC tissue, or psoriasis, fibrosis, atherosclerosis or restenosis.
 XX
 SQ Sequence 20 BP; 6 A; 2 C; 10 G; 2 T; 0 other;
 Query Match 1.5%; Score 16.8; DB 1; Length 20;
 Best Local Similarity 90.0%; Pred. No. 2.3e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 996 AGCTGAGCGTGGAGATGG 1015
 Db 1 AGGCTGAGCGAGGAGATGG 20
 RESULT 551
 AAS29488

ID AAS29488 standard; DNA; 20 BP.
 AC AAS29488;
 XX 21-NOV-2001 (first entry)
 DT
 DE Human mdm2 antisense oligonucleotide 31623.
 XX
 XX Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
 KW atherosclerosis; tumour; cytostatic; anti psoriatic;
 KW anti arteriosclerotic; vasotropic; antisense; phosphorothioate; ss.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH modified_base 1..20
 FT /*tag= a
 FT /mcd_base= OTHER
 FT /note= "OTHER= All phosphorothioate linkages,
 FT additionally bases 1-6 and bases 15-20 are
 FT 2'-O-methoxyethyl bases, and bases 7-14 are
 FT deoxynucleotides"
 FT
 XX US2001016575-A1.
 PN
 XX
 XX 23-AUG-2001.
 PD
 XX
 XX 02-JAN-2001; 2001US-0752983.
 PF
 XX 26-MAR-1999; 99US-0280805.
 PR
 XX 26-MAR-1998; 98US-0048810.
 PR
 XX (MIRA/) MIRAGLIA L J.
 PA (NERO/) NERO P.
 PA (GRAH/) GRAHAM M J.
 PA (MONI/) MONIA B P.
 PA (COWS/) COWSERT L M.
 XX
 XX Miraglia LJ, Nero P, Graham MJ, Monia BP, Cowsert LM;
 FI WPI; 2001-535565/59.
 DR
 XX
 XX An antisense compound, useful for treating e.g. cancer, comprises
 PT nucleobases targeted a region (e.g. translation termination codon
 PT region) of a nucleic acid encoding human mdm2 -
 XX
 XX Example 9; Page 18; 81pp; English.
 PS
 XX The present invention relates to antisense compounds, 8-30 nucleobases
 CC in length targeted to the 5' untranslated region, translation
 CC termination codon region, 3' untranslated region, coding region or
 CC translation start site of a nucleic acid encoding human mdm2, where
 CC the antisense compound modulates the expression of human mdm2. The
 CC antisense oligonucleotides of the invention are useful for encoding
 CC human mdm2 and for inhibiting the expression of human mdm2. They may be
 CC used for treating an animal having a disease or condition associated
 CC with amplification of mdm2 gene or overexpression of mdm2 e.g. a
 CC hyperproliferative disorder such as cancer (blood, brain, breast, lung,
 CC or a soft tissue cancer) and psoriasis, fibrosis, atherosclerosis or
 CC restenosis, tumours, colorectal carcinoma and chronic myelogenous
 CC leukemia. The antisense compound may be administered with a
 CC chemotherapeutic agent to overcome drug resistance. The antisense
 CC compound reduces hyperproliferation of human cells. The method, which
 CC involves the use of the antisense compound, is also useful for detecting
 CC the role of mdm2 expression in various cell functions and physiological
 CC processes and useful in both clinical research and diagnostic tools.
 CC AAS29242-AAS29507 represent the human mdm2 antisense oligonucleotides
 CC of the present invention.
 XX
 XX Sequence 20 BP; 6 A; 2 C; 10 G; 2 T; 0 other;
 SQ
 Query Match 1.5%; Score 16.8; DB 1; Length 20;
 Best Local Similarity 90.0%; Pred. No. 2.3e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 996 AGCTGAGGCTGGAGATGG 1015
 DB 1 AGGCTGAGGAGGAGATGG 20
 RESULT 552
 AAF83959/c
 ID AAF83959 standard; DNA; 20 BP.
 XX
 AC AAF83959;
 XX
 XX 06-AUG-2001 (first entry)
 DT
 DE BAP28 gene fragment amplifying primer BAP28polyTcourt.
 XX
 XX BAP28; prostate; tumour; cancer; diagnostic; genetic analysis;
 KW PCTA-1; PCR primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200100669-A2.
 XX
 XX 04-JAN-2001.
 PD
 XX
 XX 23-JUN-2000; 2000WO-IB01183.
 PF
 XX 25-JUN-1999; 99US-0141323.
 PR
 XX 18-JAN-2000; 2000US-0176860.
 PR
 XX (GEST) GENSET.
 PA
 XX Barry C, Bougueleret L, Chumakov I, Cohen-Akenine A;
 PI WPI; 2001-367032/38.
 DR
 XX
 XX New BAP28 polynucleotides and polypeptides overexpressed in prostate
 PT cancer cells for diagnosing prostate tumors, e.g. by hybridization or
 PT polymerase chain reaction assays -
 PT
 XX Examples; Page 347; 349pp; English.
 PS
 XX The invention is directed to BAP28 polypeptides, BAP28 polynucleotide
 CC sequences and regulatory region located at the 3' and 5' ends of the
 CC BAP28 coding region. The BAP28 polypeptides can be expressed by standard
 CC recombinant methodology. BAP28 polynucleotides and polypeptides have been
 CC found to be over expressed in prostate tumour cells, therefore levels of
 CC BAP28 expression and/or activity may be assayed (e.g. by polymerase chain
 CC reaction (PCR)) to diagnose patient suffering from or susceptible to
 CC prostate cancer. Antibodies specific for the BAP28 polypeptides are
 CC useful as diagnostic reagents. Biallelic markers of the BAP28 gene are
 CC useful in genetic analysis. Sequences AAF83934-963 represent primers for
 CC the BAP28 gene and PCTA-1 gene (the coding strand of PCTA-1 gene is on
 CC the opposite of the coding strand of BAP28).
 XX
 XX Sequence 20 BP; 2 A; 0 C; 1 G; 17 T; 0 other;
 SQ
 Query Match 1.5%; Score 16.8; DB 1; Length 20;
 Best Local Similarity 90.0%; Pred. No. 2.3e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1080 TATTAAAAA 1099
 DB 20 TATACAAAAA 1
 RESULT 553
 AAF80873
 ID AAF80873 standard; DNA; 20 BP.
 XX
 AC AAF80873;
 XX

02-MAY-2001 (first entry)
Human mdm2 phosphorothioate oligonucleotide #247.
Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
Homo sapiens.
US6184212-B1.
06-FEB-2001.
26-MAR-1999; 99US-0280805.
26-MAR-1998; 98US-0048810.
(ISIS-) ISIS PHARM INC.
Miraglia LJ, Nero P, Graham MJ, Monia BP, Cowse LM;
WPI; 2001-190948/19.
Novel antisense compound 8-30 nucleobases in length targeted to a
nucleic acid molecule encoding human mdm-2 useful for modulating the
expression of human mdm-2 and reducing hyperproliferation of human
cells -
Example 9; Column 31; 77pp; English.
The present invention relates to an antisense compound 8-30
nucleobases in length targeted to nucleobases 1-308 of the
5' untranslated region, 1776-1806 of the translation termination
codon region or 1818-2370 of the 3' untranslated region of a
nucleic acid molecule encoding human mdm-2. The invention is
useful for reducing hyperproliferation of human cells,
modulating the expression of mdm2 in human cells or tissues
or in vitro. The hyperproliferative disorder includes cancer or
psoriasis.
Sequence 20 BP; 6 A; 2 C; 10 G; 2 T; 0 other;
Query Match 1.5%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 2.3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 996 AGTCTGAGCTGAGAAATGG 1015
||| ||||| ||||| |||||
Db 1 AGGCTGAGCGAGGAAATGG 20
RESULT 554
AAS97833
ID AAS97833 standard; DNA; 20 BP.
AC AAS97833;
XX
XX
XX 12-MAR-2002 (first entry)
DE Murine SAC1 gene-specific oligonucleotide PCR primer #400.
XX Human; mouse; SAC1; carbohydrate; sweetener; ethanol; alcoholism; ss;
KW obesity; diabetes; transgenic embryo; body tissue; body fluid; pancreas;
KW blood; tongue; PCR primer; anorectic; antidiabetic; gene therapy;
KW protein replacement therapy.
XX Mus sp.
XX WO200183749-A2.
XX PN
XX PD 08-NOV-2001.
XX PF 25-APR-2001; 2001WO-US13387.
XX PR 25-APR-2001; 2001WO-US13387.
XX

28-APR-2000; 2000US-200794P.
28-JUL-2000; 2000US-221419P.
10-NOV-2000; 2000US-247443P.
XX
XX (WARN) WARNER LAMBERT CO.
XX (MONE-) MONELL CHEM SENSES CENT.
XX Bachmanov AA, Beauchamp GK, Chatterjee A, De Jong PJ, Li S, Li X;
XX Ohmen JD, Reed DR, Ross D, Tordoff MG;
XX WPI; 2002-075162/10.
XX Novel isolated polypeptide comprising variant form of mouse or human
XX SAC1 polypeptide, and is associated with altered preference for
XX carbohydrates or other sweeteners, useful for preventing obesity,
XX diabetes, alcoholism -
XX Claim 14; Page 89; 239pp; English.
XX The invention relates to an isolated polypeptide, comprising a variant
XX form of mouse or human SAC1 polypeptide. The variant form is associated
XX with altered preference for carbohydrates, other sweeteners or ethanol.
XX The polypeptide and its associated DNA sequence can be produced by
XX recombinant techniques and is useful for preventing obesity, diabetes or
XX alcoholism associated with SAC1 expression. The sequences are useful in
XX screening for drugs and sweeteners. Recombinant cell lines and transgenic
XX embryos may be used in screening for and identifying agents that induce
XX or repress function of SAC1. Predisposition to diabetes, obesity or
XX alcoholism can be ascertained by testing any fluid or tissue of a human
XX (such as blood, pancreas or tongue) for sequence variations of the SAC1
XX gene. A sequence variation of the SAC1 locus may indicate a
XX predisposition to diabetes, obesity and/or alcoholism and may provide a
XX diagnostic mark. The polynucleotide can be detected in a biological
XX sample by contacting the DNA with a probe to form a hybridisation complex
XX which is then detected. The sequences represent cDNA encoding human and
XX mouse SAC1 polypeptides and PCR primers specific for the SAC1 genes.
XX Sequence 20 BP; 7 A; 0 C; 10 G; 3 T; 0 other;
Query Match 1.5%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 2.3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1000 TGAGGCTGGAGAAATGGGAG 1019
||| ||||| ||||| |||||
Db 1 TGAGGCTGGAGAAATGGGAG 20
RESULT 555
AAS97860/c
ID AAS97860 standard; DNA; 20 BP.
XX
XX AAS97860;
AC AAS97860;
XX
XX 12-MAR-2002 (first entry)
DE Murine SAC1 gene-specific oligonucleotide PCR primer #427.
XX Human; mouse; SAC1; carbohydrate; sweetener; ethanol; alcoholism; ss;
KW obesity; diabetes; transgenic embryo; body tissue; body fluid; pancreas;
KW blood; tongue; PCR primer; anorectic; antidiabetic; gene therapy;
KW protein replacement therapy.
XX Mus sp.
XX WO200183749-A2.
XX PN
XX PD 08-NOV-2001.
XX PF 25-APR-2001; 2001WO-US13387.
XX PR 28-APR-2000; 2000US-200794P.
XX 28-JUL-2000; 2000US-221419P.
XX

PR 10-NOV-2000; 2000US-247443P.
 XX (WARN) WARNER LAMBERT CO.
 PA (MONE-) MONELL CHEM SENSES CENT.
 XX
 PI Bachmanov AA, Beauchamp GK, Chatterjee A, De Jong PJ, Li S, Li X;
 PI Ohmen JD, Reed DR, Ross D, Tordoff MG;
 XX WPI; 2002-075162/10.
 XX Novel isolated polypeptide comprising variant form of mouse or human
 PT SACL polypeptide, and is associated with altered preference for
 PT carbohydrates or other sweeteners, useful for preventing obesity,
 PT diabetes, alcoholism -
 XX Claim 14; Page 90; 239pp; English.
 XX The invention relates to an isolated polypeptide, comprising a variant
 CC form of mouse or human SACL polypeptide. The variant form is associated
 CC with altered preference for carbohydrates, other sweeteners or ethanol.
 CC The polypeptide and its associated DNA sequence can be produced by
 CC recombinant techniques and is useful for preventing obesity, diabetes or
 CC alcoholism associated with SACL expression. The sequences are useful in
 CC screening for drugs and sweeteners. Recombinant cell lines and transgenic
 CC embryos may be used in screening for and identifying agents that induce
 CC or repress function of SACL. Predisposition to diabetes, obesity or
 CC alcoholism can be ascertained by testing any fluid or tissue of a human
 CC (such as blood, pancreas or tongue) for sequence variations of the SACL
 CC gene. A sequence variation of the SACL locus may indicate a
 CC predisposition to diabetes, obesity and/or alcoholism and may provide a
 CC diagnostic mark. The polynucleotide can be detected in a biological
 CC sample by contacting the DNA with a probe to form a hybridisation complex
 CC which is then detected. The sequences represent cDNA encoding human and
 CC mouse SACL polypeptides and PCR primers specific for the SACL genes.
 XX
 SQ Sequence 20 BP; 3 A; 10 C; 0 G; 7 T; 0 other;
 Query Match 1.5%; Score 16.8; DB 1; Length 20;
 Best Local Similarity 90.0%; Pred. No. 2.3e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 1000 TGAGGCTGGAGATGGGAAG 1019
 Db 20 TGAGGCTGGAGATGGGAAG 1
 RESULT 556
 AAZ26500
 ID AAZ26500 standard; DNA; 21 BP.
 XX
 AC AAZ26500;
 XX
 DT 30-NOV-1999 (first entry)
 XX Human polymorphic region 689.
 XX Polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH;
 XX cell viability; loss of heterozygosity; precancerous condition; ASI;
 XX allele specific inhibitor; somatic cell; diagnosis; prevention;
 XX atherosclerotic plaque; premalignant metaplastic lesion; endometriosis;
 XX dysplastic lesion; benign tumour; polycystic kidney disease; transplant;
 XX graft versus host disease; malignant cell removal; bone marrow; ss.
 XX
 OS Homo sapiens.
 XX
 XX WO9841648-A2.
 PN
 XX 24-SEP-1998.
 PD
 XX 19-MAR-1998; 98WO-US05419.
 PF
 XX 20-MAR-1997; 97US-0041057.
 PR

PA (VARI-) VARIAGENICS INC.
 XX Housman D, Ledley FD, Stanton VP;
 PI WPI; 1998-521232/44.
 DR
 XX Identifying target genes for allele-specific drugs - used for
 PT diagnosis, prevention and treatment of, e.g. cancers, atherosclerotic
 PT plaque, dysplastic lesions, endometriosis or graft versus host disease
 XX
 PS Disclosure; Figure 7; 605pp; English.
 XX
 XX This invention describes a novel method for identifying an inhibitor
 CC potentially useful for treatment of cancer, where the inhibitor is
 CC active on a gene vital for cell growth or viability, and where the gene
 CC is subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is
 CC used for preventing the development of cancer in a patient having a
 CC precancerous condition, by administering to an allele of a first essential
 CC specific inhibitor (ASI) targeted to an allele of a first essential gene
 CC present in cells of the precancerous condition, where the normal somatic
 CC cells of the patient are heterozygous for the first gene, the inhibitor
 CC is active on at least one but less than all allelic forms of the gene
 CC present in a population and targets only one allelic form present in the
 CC normal somatic cells, and the first gene. The products and methods can
 CC be used in the diagnosis, prevention and treatment of LOH disorders,
 CC e.g. cancers, atherosclerotic plaques, premalignant metaplastic or
 CC dysplastic lesions, benign tumours, endometriosis, polycystic kidney
 CC disease, and graft versus host disease. The method can also be used to
 CC remove malignant cells from bone marrow transplants. AA225812-226825
 CC represent human polymorphic sites described in the method of the
 CC invention.
 XX
 SQ Sequence 21 BP; 15 A; 2 C; 0 G; 4 T; 0 other;
 Query Match 1.5%; Score 16.8; DB 1; Length 21;
 Best Local Similarity 90.0%; Pred. No. 2.4e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 1078 ACTATTAAAAA 1097
 Db 2 ACTTTCAAAAA 21
 RESULT 557
 AAH88803/c
 ID AAH88803 standard; DNA; 21 BP.
 XX
 AC AAH88803;
 XX
 DT 27-FEB-2002 (first entry)
 XX Human polymorphic oligonucleotide Y12855 fragment #5.
 XX Human; single nucleotide polymorphic; SNP; forensic science;
 XX paternity testing; phenotypic trait; genetic mapping; animal breeding;
 XX plant breeding; ds.
 XX Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH Variation replace(11,a)
 FT /*tag= a
 FT /standard_name= "single nucleotide polymorphism"
 XX
 XX WO200134840-A2.
 PN
 XX 17-MAY-2001.
 PD
 XX 10-NOV-2000; 2000WO-US30766.
 PF
 XX 10-NOV-1999; 99US-0164596.
 PR
 XX (GLAX) GLAXO GROUP LTD.
 PA

PA (AFFY-) AFFYMETRIX INC.
 XX Au K, Chen J, Patil N, Thomas D;
 XX WPI; 2001-335945/35.
 XX New polymorphic sites derived from the human genome are useful to
 PT determine sites correlating with phenotypic traits, particularly
 PT disease, and also in forensics and paternity testing.
 XX Claim 27; Page 7; 43pp; English.
 XX The present invention relates to human oligonucleotides comprising a
 CC single nucleotide polymorphic site (SNP: AAH89219). The present
 CC sequence is one such oligonucleotide. The oligonucleotides can be used in
 CC forensics, paternity testing, correlation of polymorphisms with
 CC phenotypic traits, genetic mapping of phenotypic traits and marker
 CC assisted breeding of animals and crop plants.
 XX Sequence 21 BP; 3 A; 9 C; 4 G; 5 T; 0 other;
 SQ
 Query Match 1.5%; Score 16.8; DB 1; Length 21;
 Best Local Similarity 90.0%; Pred. No. 2.4e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 956 GCTGGGCGAGGTGGCAGT 975
 DB 21 GCTGGGCGAGGTGGCAAAGT 2
 RESULT 558
 AAA64547/C
 ID AAA64547 standard; DNA; 23 BP.
 XX
 AC AAA64547;
 XX
 DT 02-JAN-2001 (first entry)
 XX
 DE Nucleotide sequence of a donor site of human FEZ1 gene.
 XX
 KW Human; FEZ1 gene; tumour suppressor gene; 8p22; cancer; tumour growth;
 KW tumour proliferation; tubulin; microtubule; protein EF1-gamma;
 KW tubulin polymerisation disorder; mitosis initiation; cell proliferation;
 KW cell growth; cell shape; cell rigidity; cell motility; DNA replication;
 KW tumorigenesis; tumour survival; metastasis; ss.
 OS Homo sapiens.
 XX
 PN WO2000050565-A2.
 XX
 PD 31-AUG-2000.
 XX
 PF 25-FEB-2000; 2000WO-US04950.
 XX
 PR 25-FEB-1999; 99US-0121537.
 XX
 PA (UYJE-) UNIV JEFFERSON THOMAS.
 XX
 PI Croce CM, Ishii H;
 XX
 DR WPI; 2000-558396/51.
 XX
 PT New polynucleotide homologous with a portion of one strand of the human
 PT FEZ1 gene, useful for alleviating abnormal cell proliferation such as
 PT cancer -
 XX
 PS Example 1; Page 103; 255pp; English.
 XX
 CC AAA64539-50 represent donor and acceptor sites of the human FEZ1 gene.
 CC FEZ1 is a tumour suppressor gene, located at chromosome location
 CC 8p22. Decreased or no expression of FEZ1 is detected in a variety
 CC of cancer cells. Expression of FEZ1 inhibits tumour growth and
 CC proliferation. FEZ1 also interacts with tubulin, with microtubules,

CC and with protein EF1-gamma. Post-translational phosphorylation and
 CC dephosphorylation modulates the effect of the FEZ1 protein.
 CC Inhibitors of FEZ1 gene expression are useful for inducing cells to
 CC proliferate. Compounds which modulate FEZ1 association with tubulin
 CC are useful for alleviating tubulin hyper- or hypo-polymerisation
 CC disorders, such as those associated with aberrant initiation of
 CC mitosis, modulation of the initiation and rate of cell proliferation
 CC and cell growth, modulation of cell shape, cell rigidity, cell
 CC motility, rate and stage of cellular DNA replication, intracellular
 CC distribution of organelles, metastatic potential of cell and cellular
 CC transformation from a non-cancerous to cancerous phenotype. Compounds
 CC which modulate FEZ1 binding and phosphorylation are also useful for
 CC alleviating a disorder, such as tumorigenesis, tumour survival, growth
 CC and metastasis.
 XX Sequence 23 BP; 6 A; 4 C; 10 G; 3 T; 0 other;
 SQ
 Query Match 1.5%; Score 16.8; DB 1; Length 23;
 Best Local Similarity 90.0%; Pred. No. 2.7e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 404 CCTGCTCCAGCAGCTCTCC 423
 DB 21 CCTGCTCCAGCAGCTTCACC 2
 RESULT 559
 AAV06320/C
 ID AAV06320 standard; DNA; 24 BP.
 XX
 AC AAV06320;
 XX
 DT 06-MAY-1998 (first entry)
 XX
 DE Human prolyl 4-hydroxylase alpha subunit amplifying 3' primer.
 XX
 KW Collagen; human; recombinant; post-translational enzyme; procollagen;
 KW prolyl 4-hydroxylase alpha subunit; PCR primer; ss.
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO9738710-A1.
 XX
 PD 23-OCT-1997.
 XX
 PF 11-APR-1997; 97WO-US07300.
 XX
 PR 12-APR-1996; 96US-0631336.
 XX
 PA (FIFT-) ACAD FINLAND.
 PA (FIB-) FIBROGEN INC.
 XX
 PI Kivirikki KI, Pihlajaniemi T;
 XX
 DR WPI; 1997-526203/48.
 XX
 PT Recombinant production of (pro)collagen having correct folding -
 PT using vectors encoding collagen subunit and collagen
 PT post-translational enzyme respectively
 XX
 PS Example 10; Page 57; 90pp; English.
 XX
 CC This primer is used to mutate a plasmid pBS(SK-) by PCR by introducing a
 CC NotI site upstream of the initiation codon for human prolyl 4-hydroxylase
 CC alpha subunit. This is used in the construction of recombinant vectors
 CC containing collagen modifying enzymes. A novel method for producing a
 CC (pro)collagen polypeptide comprises culturing a host cell, where the host
 CC cell has been infected, transfected or transformed with a first
 CC expression vector comprising a polynucleotide molecule having a nucleic
 CC acid sequence which encodes a (pro)collagen subunit and a second
 CC expression vector comprising a polynucleotide molecule having a nucleic
 CC acid sequence which encodes at least one (pro)collagen post-translational

CC enzyme or enzyme subunit. The (pro)collagen polypeptide is then purified
 CC from the cultured cell. The (pro)collagen polypeptide is selected from
 CC collagen types IV, V, VI, VII, VIII, IX, X, XI, XII, XIII, XIV, XV, XVI,
 CC XVII, XVIII, and XIX. The methods can be used for the production of
 CC collagens such as human collagens which can be used in therapeutic
 CC applications. The method provides for the synthesis of correctly folded
 CC proteins so that they exhibit the normal triple-helical conformation
 CC characteristic of procollagens and collagens. Purification of the
 CC collagens is greatly facilitated.

XX Sequence 24 BP; 7 A; 6 C; 4 G; 7 T; 0 other;

Query Match 1.5%; Score 16.8; DB 1; Length 24;
 Best Local Similarity 90.0%; Pred. No. 2.8e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 748 TGGTCTCTTAAGGAGATGGCA 767

DB 20 TGGTCTCTTAAGGATATGCA 1

RESULT 560

ABN85224/c

ID ABN85224 standard; DNA; 24 BP.

AC ABN85224;

DT 24-SEP-2002 (first entry)

DE Human translation initiation factor eIF4E binding protein 17.27 primer#2.

KW Human; translation initiation factor subunit eIF4E binding protein 17.27;

KW embryo development malformation; tumour; diabetes; menoxenia;

KW peptic ulcer; translation initiation factor; eIF4E; binding protein;

KW PCR; primer; ss.

OS Homo sapiens.

PN CN1339492-A.

PD 13-MAR-2002.

PF 23-AUG-2000; 2000CN-0119722.

PR 23-AUG-2000; 2000CN-0119722.

PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.

PI Mao Y, Xie Y;

DR WPI; 2002-464075/50.

PT New polypeptide-human translation initiation factor subunit eIF4E

PT binding protein 17.27 for treating embryo development malformation,

PT tumors, diabetes, menoxenia, and peptic ulcer -

PS Example 3; Page 20 (Disclosure); 33pp; Chinese.

CC The present invention relates to human translation initiation factor

CC subunit eIF4E binding protein 17.27 (see ABN83427). The protein and

CC its coding sequence are useful for treating various diseases, such as

CC embryo development malformation, tumours, diabetes, menoxenia, peptic

CC ulcer, etc. The present sequence is a PCR primer, which was used in an

CC example from the invention.

XX Sequence 24 BP; 3 A; 0 C; 3 G; 18 T; 0 other;

QY 1081 ATTAAAAA

Query Match 1.5%; Score 16.8; DB 1; Length 24;

Best Local Similarity 90.0%; Pred. No. 2.8e+02;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

DB 20 TGGTCTCTTAAGGATATGCA 1

QY 1081 ATTAAAAA

Query Match 1.5%; Score 16.4; DB 1; Length 18;

Best Local Similarity 94.4%; Pred. No. 2.4e+02;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

DB 20 TGGTCTCTTAAGGATATGCA 1

QY 1081 ATTAAAAA

Query Match 1.5%; Score 16.4; DB 1; Length 18;

Best Local Similarity 94.4%; Pred. No. 2.4e+02;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

DB 20 TGGTCTCTTAAGGATATGCA 1

QY 1081 ATTAAAAA

Query Match 1.5%; Score 16.4; DB 1; Length 18;

Best Local Similarity 94.4%; Pred. No. 2.4e+02;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

DB 20 TGGTCTCTTAAGGATATGCA 1

QY 1081 ATTAAAAA

DB 21 ATTCAAAAAA

RESULT 561

AAQ30446/c

ID AAQ30446 standard; DNA; 18 BP.

AC AAQ30446;

DT 25-MAR-2003 (updated)

DE 07-DEC-1992 (first entry)

DE Oligomer TNR941 for forming triplex with HUMNFR target duplex.

KW Human tumour necrosis factor receptor mRNA; AIDS; modified; HIV;

KW RSV; HPV; malignancy; hepatitis; inflammation; ss.

OS Synthetic.

PH Key

FT modified_base 5

FT /tag= a

FT /mod_base= m5c

FT modified_base 18

FT /tag= b

FT /mod_base= OTHER

FT /note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"

PN WO9209705-A1.

XX 11-JUN-1992.

XX 25-NOV-1991; 91WO-US08811.

PR 23-NOV-1990; 90US-0617907.

PR 18-JAN-1991; 91US-0643382.

PR 08-APR-1991; 91US-0683420.

PR 17-APR-1991; 91US-0686544.

PR 17-APR-1991; 91US-0686546.

PR 17-APR-1991; 91US-0686547.

PR 27-SEP-1991; 91US-0766733.

XX (GILE-) GILEAD SCI INC.

XX Froehner B, Krawczyk S, Matteucci MD, Milligan J;

XX WPI; 1992-217083/26.

XX New oligomers contg. modified bases - which form a triplex with

XX G-C doublet in a DNA duplex, for treating and diagnosing HIV,

XX hepatitis, herpes, malignancy and inflammation

XX Claim 12; Page 72; 77pp; English.

CC The synthetic oligomer is capable of forming a triplex at

CC physiological pH with a purine rich target sequence by coupling

CC into the major groove of the duplex. The specific target sequence

CC of this oligomer is the human tumour necrosis factor receptor mRNA

CC beginning at nucleotide 2354 contg. a purine rich sequence concd. on

CC one strand of the duplex. The oligomer, and others like it are useful

CC in diagnosis and therapy of diseases characterised by specific DNA

CC duplex targets, e.g. HPV, HER, HIV, hepatitis B, herpes, malignant

CC tumours and inflammation. The triple helices form under mild conditions

CC thus assays may be carried out without subjecting the test specimen to

CC harsh conditions.

CC See also AAQ25452-25501 and AAQ30226-448.

CC (Updated on 25-MAR-2003 to correct PN field.)

CC (Updated on 25-MAR-2003 to correct PD field.)

XX Sequence 18 BP; 1 A; 1 C; 0 G; 16 T; 0 other;

QY Query Match 1.5%; Score 16.4; DB 1; Length 18;

Best Local Similarity 94.4%; Pred. No. 2.4e+02;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

DB 20 TGGTCTCTTAAGGATATGCA 1

QY 1081 ATTAAAAA

Query Match 1.5%; Score 16.4; DB 1; Length 18;

Best Local Similarity 94.4%; Pred. No. 2.4e+02;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

DB 20 TGGTCTCTTAAGGATATGCA 1

QY 1081 ATTAAAAA

```

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1083 TAAAAAAAAAAAAAAAAA 1100
DB 18 TAAAAAAAAAAAAAAAAA 1

RESULT 562
AAF75598/c
ID AAF75598 standard; DNA; 18 BP.
AC AAF75598;
XX
DT 10-MAY-2001 (first entry)
DE
XX
XX Binary encoded sequence tag method anchored primer #3.
XX
XX Binary encoded sequence tag; BEST; nucleic acid analysis;
KW gene expression; adaptor; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO200112855-A2.
XX
XX
PD 22-FEB-2001.
XX
XX 11-AUG-2000; 2000WO-US22164.
XX
XX 13-AUG-1999; 99US-0148870.
XX
XX 06-APR-2000; 2000US-0544713.
XX
XX (UYA ) UNIV YALE.
XX
XX Kaufman JC, Roth ME, Lizardi PM, Feng L, Latimer DR;
XX WPI; 2001-202878/20.
XX
XX
XX Producing binary sequence tags, useful for analyzing nucleic acid
XX sequence tags, gene expression or gene-expression patterns, involves
XX generating nucleic acid fragments, which are mixed with offset adaptors
XX and adaptor-indexers -
XX
XX Disclosure; Page 101; 101pp; English.
XX
XX The present invention describes a method of producing binary sequence
XX tags from nucleic acid fragments in a sample, involving incubating the
XX sample with cleaving reagents, mixing offset adaptors with the sample,
XX incubating with more cleaving reagents and mixing the sample with
XX adaptor-indexers where the adaptors are coupled to binary sequence tags.
XX The method is useful in sequence analysis, including analysis and
XX comparison of gene expression, nucleic acid samples and genomes.
XX
SQ Sequence 18 BP; 1 A; 1 C; 0 G; 16 T; 0 other;
Query Match 1.5%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 2.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1082 TTAATAAAAAAAAAAAAAA 1099
DB 18 TGAATAAAAAAAAAAAAAA 1

RESULT 563
AAS05715/c
ID AAS05715 standard; DNA; 20 BP.
XX
AC AAS05715;
XX
XX 07-SEP-2001 (first entry)
DT
XX
DE 8-aminopurine substituted region of an RP-TFO.
XX

```

```

KW reverse phase triplex forming oligonucleotide; RP-TFO;
KW protected nucleic acid sequence; PNAS; single nucleotide polymorphism;
KW SNP; short tandem repeat; cancer; Factor V Leiden SNP; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX modified_base 17
XX /tag= a
XX /label= "OTHER"
XX /note= "Other= Hypoxanthine or Inosine"
XX
XX WO200132929-A1.
XX
XX 10-MAY-2001.
XX
XX 03-NOV-2000; 2000WO-US30534.
XX
XX 03-NOV-1999; 99US-0163356.
XX
XX 03-NOV-1999; 99US-0163416.
XX
XX 21-DEC-1999; 99US-0171348.
XX
XX 07-JUL-2000; 2000US-0216579.
XX
XX (CYGE-) CYGENE INC.
XX
XX (OSTE/) OSTE C C.
XX
XX Oste CC, Ramberg ER;
XX
XX WPI; 2001-343488/36.
XX
XX
XX Analysing target nucleic acid sequences, useful for population
XX genetics, drug development and diagnosing cancer, comprises hybridizing
XX triple forming oligonucleotide and probe to target sequence -
XX
XX Example 2; Page 66; 141pp; English.
XX
XX The sequence is a second reverse phase triplex forming oligonucleotide,
XX RP-TFO (3' to the SNP) used to analyse Factor V Leiden SNP using the
XX method of the invention. The invention relates to analysing target
XX nucleic acid sequences comprising restricting isolated DNA, hybridising
XX at least one triplex forming oligonucleotide (TFO), adding a 3' to 5'
XX exonuclease to form a protected nucleic acid sequence (PNAS) tail
XX structure, hybridising the captured structure with a single nucleotide
XX polymorphisms (SNP) identification probe and determining the SNP score.
XX The methods can be used for analysing target nucleic acid sequences, or
XX especially genomic DNA sequences, to determine if they contain SNPs or
XX short tandem repeats (STRs). The methods can be used to detect SNPs for
XX use in population genetics, drug development, forensics, cancer, genetic
XX disease research, genomic analysis, diagnostics and therapeutics in
XX humans, plants and animals.
XX
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 19 T; 1 other;
Query Match 1.5%; Score 16.4; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 2.7e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1081 ATTAATAAAAAAAAAAAAAA 1099
DB 19 AANAATAAAAAAAAAAAAAA 1

RESULT 564
AAF99943
ID AAF99943 standard; DNA; 20 BP.
XX
AC AAF99943;
XX
XX 12-JUL-2001 (first entry)
DT
XX
DE Synthetic oligonucleotide #9.
XX
XX Oligonucleotide purification; liquid chromatography;
KW

```

KW hydrophobic protective group; deprotection; ds.

XX Synthetic.

XX JP2000342265-A.

XX 12-DEC-2000.

XX 02-JUN-1999; 99JP-0154374.

XX 02-JUN-1999; 99JP-0154974.

XX (TOAG) TOA GOSSEI CHEM IND LTD.

XX WPI; 2001-268251/28.

XX A process for purification of oligonucleotides using liquid chromatography -

XX Example 1; Page 4; 13pp; Japanese.

XX The present sequence is an oligonucleotide provided in a specification relating to the simplified purification of oligonucleotides by liquid chromatography. The process comprises:

XX (a) pouring oligonucleotides protected with a hydrophobic group and oligonucleotide with no protective group into a liquid chromatography column packed with an acid and alkali resistant packing agent, such as polystyrene resin;

XX (b) pouring a mixed developing solvent composed of a buffer made from a volatile salt and a water soluble organic solvent at a suitable concentration gradient into the column;

XX (c) pouring an acid, particularly 6-16 v/v% acetic acid, into the column to deprotect the oligonucleotides protected with the hydrophobic group;

XX (d) pouring a mixed developing solvent composed of a buffer made from a volatile salt, particularly 0.05-0.5 N aqueous ammonium hydrogencarbonate solution adjusted at pH 8-10, and a water soluble organic solvent at a suitable concentration gradient to elute the deprotected oligonucleotides; and

XX (e) removal of the solvent and the salt from the eluted oligonucleotides.

XX Sequence 20 BP; 17 A; 1 C; 1 G; 1 T; 0 other;

XX Query Match 1.5%; Score 16.4; DB 1; Length 20;

XX Best Local Similarity 94.4%; Pred. No. 2.7e+02;

XX Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1083 TAAAAAAGAAAAA 1100

DB 1 TAAAAAAGAAAAA 18

RESULT 565

ABA05916/c

ID ABA05916 standard; DNA; 20 BP.

XX ABA05916;

XX 05-MAR-2002 (first entry)

XX Hepatitis B virus diagnostic PCR primer SEQ ID NO 6.

XX Hepatitis B virus; HBV; infection; hepatocellular carcinoma; diagnosis;

XX PCR primer; ss.

XX Hepatitis B virus.

XX Ep1152063-A1.

XX 07-NOV-2001.

XX 03-MAY-2000; 2000EP-0109436.

XX

PR

XX

PA

XX

PI

XX

DR

XX

XX

PT

XX

PT

XX

PS

XX

XX

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

03-MAY-2000; 2000EP-0109436.

(DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.

Schroeder KH, Koike K;

WPI; 2002-068256/10.

Diagnosing hepatitis B virus (HBV) infection stages and determining the risk for hepatocellular carcinoma, comprises identifying full length HBV transcripts and truncated HBV transcripts in a serum sample -

Example 1; Page 6; 25pp; English.

The invention relates to diagnosis of hepatitis B virus (HBV) infection stages comprising identification of full length HBV transcripts (I) and truncated HBV transcripts (II) in a serum sample, where the ratio of I:II is indicative of a particular infection stage. The method is useful for diagnosing HBV infection stages and determining the risk for developing hepatocellular carcinoma. The present sequence is that of a HBV diagnostic PCR primer, useful for the invention.

Sequence 20 BP; 2 A; 1 C; 2 G; 15 T; 0 other;

Query Match 1.5%; Score 16.4; DB 1; Length 20;

Best Local Similarity 94.4%; Pred. No. 2.7e+02;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1082 TTAATAAAAAAAAAAAAA 1099

DB 18 TTAATAAAAAAAAAAAAA 1

RESULT 566

AA23577/c

ID AAX23577 standard; DNA; 23 BP.

XX AAX23577;

XX 18-JUN-1999 (first entry)

XX Deletion sequence oligonucleotide 30.

XX Deletion sequence oligonucleotide; sensor array; eukaryotic pathogen; probe; cellular adhesion modulator; cellular proliferation modulator; human retrovirus; human immunodeficiency virus; non-human retrovirus; HIV; primer; ss.

XX Synthetic.

XX WO9911820-A1.

XX 11-MAR-1999.

XX 01-SEP-1998; 98WO-US18084.

XX 02-SEP-1997; 97US-0923771.

XX (ISIS-) ISIS PHARM INC.

XX Chen D, Srivatsa GS;

XX WPI; 1999-205198/17.

New compositions comprising sensor arrays made up of unique probe oligonucleotides - useful for characterizing a sample of target deletion oligonucleotides

Example 9; Page 99; 163pp; English.

This invention describes a novel composition comprising a number of sensor arrays, where each array comprises a unique probe oligonucleotide, which is the reverse complement of part of a unique

CC target oligonucleotide present in a mixture of target deletion sequence
CC oligonucleotides. The compositions form a method for characterizing a
CC sample of target deletion oligonucleotides which are labelled and
CC hybridize with the probe oligonucleotides of the sensor arrays. Such
CC oligonucleotides and their targets are represented in AAX33548-X23709.
CC Oligonucleotides characterized by the method form pharmaceutical
CC compositions that are useful for modulating cellular adhesion or
CC proliferation, and being active against a eukaryotic pathogen, a human
CC retrovirus, a human immunodeficiency virus (HIV), or a non-human
CC retrovirus, including influenza virus, Epstein-Barr virus, Respiratory
CC Syncytial Virus or cytomegalovirus (CMV). The compositions enable
CC characterization of deletion sequence oligonucleotides having related,
CC but different nucleobase sequences, and quantification of different
CC species of deletion sequence ("target") oligonucleotides in a mixture.
CC Also, if the specificity of the oligonucleotide's nucleobase sequence
CC for its reverse complement is not modified, the method may be performed
CC using oligodeoxynucleotides.

SQ Sequence 23 BP; 4 A; 1 C; 3 G; 15 T; 0 other;
Query Match 1.5%; Score 16.4; DB 1; Length 23;
Best Local Similarity 94.4%; Pred. No. 3.1e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1082 TTAATAAAAAAAAAAAAA 1099
DB 18 TTAATAAAAAAAAAAAAA 1

RESULT 567
AA29753/c
ID AAA29753 standard; DNA; 23 BP.
XX
AC AAA29753;
XX
DT 15-AUG-2000 (first entry)
XX
DE Synthetic oligonucleotide #1.
XX
XW Primer; destabilise non-specific duplex formation; PCR; detection;
KW purification; sequencing; genetic marker; RACE; DNA synthesis; ss.
XX
OS Synthetic.

Key Location/Qualifiers
FT modified_base 8 /*tag= a
FT /*mod_base= i
FT /*note= "inosine"
FT modified_base 18 /*tag= b
FT /*mod_base= i
FT /*note= "inosine"
XX WO200020630-A1.
XX
XX
PD 13-APR-2000.
XX
PF 06-OCT-1999; 99WO-CA00933.
XX
PR 07-OCT-1998; 98CA-2246623.
XX (UYMC-) UNIV MCGILL.
XX
PI Pelletier J, Das M;
XX
XX
DR WPI; 2000-328943/28.
XX

PT Novel method of stabilizing duplex formation, or destabilizing
PT non-specific duplex formation using primer containing modified
PT nucleotide analogs, useful for preventing mispriming during PCR, RACE,
PT DNA synthesis or sequencing -
XX

PS Example 1; Page 25; 46pp; English.

XX The present invention describes a method for destabilising non-specific
CC duplex formation, between an oligonucleotide and a target nucleic acid
CC (NA), comprising incubating the target NA with a modified
CC oligonucleotide (I) comprising a homopolymeric sequence having a
CC modification which decreases or abrogates H-bonding between the
CC modified oligonucleotide and the non-specific target NA. The modified
CC oligonucleotide is used to improve discrimination between the targeted
CC homopolymeric sequence and a non-homopolymeric target sequence. It is
CC used to increase the proportion of full length cDNA clones for a library,
CC to reduce mispriming during sequencing, 5' or 3' RACE (rapid
CC amplification of cDNA ends) or DNA synthesis or to generate bona fide
CC genetic markers. The present sequence represents an oligonucleotide
CC which is used in the exemplification of the present invention.

SQ Sequence 23 BP; 0 A; 0 C; 0 G; 21 T; 2 other;

Query Match 1.5%; Score 16.4; DB 1; Length 23;
Best Local Similarity 85.0%; Pred. No. 3.1e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1081 ATTAATAAAAAAAAAAAAA 1100
DB 20 AATAATAAAAAAAAAAAAA 1

RESULT 568
AAH30031/c
ID AAH30031 standard; DNA; 23 BP.
XX
AC AAH30031;
XX
DT 19-JUL-2001 (first entry)
XX
DE Human interleukin 8 antigen sequencing primer C.
XX
KW Human; antibody; immunoglobulin; interleukin 8; IL8; immunogen;
KW human antibody phage display library; immunisation; transgenic animal;
KW PCR primer; ss.
OS Homo sapiens.
OS Synthetic.
XX
XX WO200125492-A1.
XX
PD 12-APR-2001.
XX
PF 02-OCT-2000; 2000WO-US27237.
XX
PR 02-OCT-1999; 99US-0157415.
PR 01-DEC-1999; 99US-0453234.
XX
XX (BIOS-) BIOSITE DIAGNOSTICS INC.
XX (GENP-) GENPHARM INT SUBSIDIARY OF MEDAREX INC.
XX
XX Buechler J, Valkirs G, Gray J, Lonberg N;
XX
XX WPI; 2001-335567/35.
XX

PT Producing a human antibody phage display library comprises providing a
PT transgenic animal whose genome comprises human immunoglobulin genes and
PT isolating nucleic acids encoding antibody chains from lymphatic cells -
XX
PS Example 23; Page 102; 161pp; English.

XX The present invention describes a method (M1) for producing a human
CC antibody phage display library (I), comprising: (1) providing a nonhuman
CC transgenic animal (II) whose genome comprises human immunoglobulin genes;
CC (2) isolating nucleic acids encoding human antibody chains (III) from
CC lymphatic cells; and (3) forming a library of display packages whose
CC members comprise a nucleic acid encoding (III) which is displayed from
CC the package. The method is used for producing a human antibody display

CC library, e.g., a Fab phage display library. The display method may be
CC used to screen nucleic acids encoding antibody chains obtained from
CC immunised nonhuman transgenic animals, and from this a population of
CC antibodies may be prepared. Production of a human monoclonal antibodies
CC display library using this method means there is no need to immunise
CC humans with antigens, and the difficulties faced with immortalising B
CC cells are avoided. AAH29958 to AAH30066 and AAB74994 to AAB75056
CC represent sequences used in the exemplification of the present invention.

XX
SQ Sequence 23 BP; 6 A; 7 C; 5 G; 5 T; 0 other;
Query Match 1.5%; Score 16.4; DB 1; Length 23;
Best Local Similarity 94.4%; Pred. No. 3.1e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 997 GTCTGAGCGCTGGAGAATG 1014
|||||
Db 18 GTCTGAGCGCTGGAGAATG 1

RESULT 569
AAH30035/c
ID AAH30035 standard; DNA; 23 BP.

XX
AC AAH30035;
XX
DT 19-JUL-2001 (first entry)

XX Human myelin proteolipid protein (PLP) antigen sequencing primer C.

XX Human; antibody; immunoglobulin; interleukin 8; IL8; immunogen;
XX human antibody phage display library; immunisation; transgenic animal;
XX PCR primer; ss.

XX Homo sapiens.
XX Synthetic.

XX W0200125492-A1.

XX 12-APR-2001.

XX 02-OCT-2000; 2000WO-US7237.

XX 02-OCT-1999; 99US-0157415.

XX 01-DEC-1999; 99US-0453234.

XX (BIOS-) BIOSITE DIAGNOSTICS INC.

XX (GENP-) GENPHARM INT SUBSIDIARY OF MEDAREX INC.

XX Buechler J, Valkirs G, Gray J, Lonberg N;

XX WPI; 2001-335567/35.

XX Producing a human antibody phage display library comprises providing a
XX transgenic animal whose genome comprises human immunoglobulin genes and
XX isolating nucleic acids encoding antibody chains from lymphatic cells -
XX Example 24; Page 103; 161pp; English.

XX The present invention describes a method (M1) for producing a human
XX antibody phage display library (I), comprising: (1) providing a nonhuman
XX transgenic animal (II) whose genome comprises human immunoglobulin genes;
XX (2) isolating nucleic acids encoding human antibody chains (III) from
XX lymphatic cells; and (3) forming a library of display packages whose
XX members comprise a nucleic acid encoding (III) which is displayed from
XX the package. The method is used for producing a human antibody display
XX library, e.g., a Fab phage display library. The display method may be
XX used to screen nucleic acids encoding antibody chains obtained from
XX immunised nonhuman transgenic animals, and from this a population of
XX antibodies may be prepared. Production of a human monoclonal antibodies
XX display library using this method means there is no need to immunise
XX humans with antigens, and the difficulties faced with immortalising B
XX cells are avoided. AAH29958 to AAH30066 and AAB74994 to AAB75056

CC represent sequences used in the exemplification of the present invention.
XX
SQ Sequence 23 BP; 6 A; 7 C; 5 G; 5 T; 0 other;

Query Match 1.5%; Score 16.4; DB 1; Length 23;
Best Local Similarity 94.4%; Pred. No. 3.1e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 997 GTCTGAGCGCTGGAGAATG 1014
|||||
Db 18 GTCTGAGCGCTGGAGAATG 1

RESULT 570
AAH18389/c
ID AAH18389 standard; DNA; 18 BP.

XX
AC AAH18389;
XX
DT 11-MAY-1999 (first entry)

XX RT-PCR primer of the invention SEQ ID 30.

XX RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.

XX Synthetic.

XX JP11032765-A.

XX 09-FEB-1999.

XX 18-JUL-1997; 97JP-0208312.

XX 18-JUL-1997; 97JP-0208312.

XX (TAKI) TAKARA SHUZO CO LTD.

XX WPI; 1999-183822/16.

XX Peptides having at least two new nucleotides - useful as primers in
XX RT-PCR

XX Example 1; Page 12; 19pp; Japanese.

XX This sequence represents a primer of the invention. The invention relates
XX to sequences of at least two nucleotides of formula:

XX (X)MS'-(alpha)n-beta-N3'; or (X)MS'-(gamma)k-delta-N3'; where

XX X = a labelled compound and/or a nucleotide with voluntary sequence;

XX m = 0 or 1; alpha = thymine; n = natural number indicating the repetition

XX of alpha; beta, delta = V or N; V = adenine, guanine or cytosine;

XX N = adenine, guanine, cytosine or thymine; gamma = thymine;

XX k = natural number of 3 or over indicating the repetition of gamma, in

XX which thymine expressed by gamma is composed of 1/3 or less of adenine,

XX guanine and/or cytosine. The new nucleotides are useful as primers for

XX RT-PCR and determination of base sequences. The new sequences allow for

XX reproductive and highly efficient analysis of gene sequences.

XX
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 16 T; 2 other;

Query Match 1.5%; Score 16.2; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 2.7e+02;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1083 TAAAAAATAAAAAAAAAA 1099
:|||||
Db 17 BAAAAAATAAAAAAAAAA 1

RESULT 571

AAZ26563

ID AAZ26563 standard; DNA; 21 BP.

XX
AC AAZ26563;

| | |
|------------|--|
| XX | |
| DT | 30-NOV-1999 (first entry) |
| XX | |
| DE | Human polymorphic region 752. |
| XX | |
| KW | Polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH; |
| KW | cell viability; loss of heterozygosity; precancerous condition; ASI; |
| KW | allele specific inhibitor; somatic cell; diagnosis; prevention; |
| KW | atherosclerotic plaque; premalignant metaplastic lesion; endometriosis; |
| KW | dysplastic lesion; benign tumour; polycystic kidney disease; transplant; |
| KW | graft versus host disease; malignant cell removal; bone marrow; ss. |
| XX | |
| OS | Homo sapiens. |
| XX | |
| PN | WO9841648-A2. |
| XX | |
| PD | 24-SEP-1998. |
| XX | |
| PD | 19-MAR-1998; 98WO-US05419. |
| XX | |
| PF | 20-MAR-1997; 97US-0041057. |
| XX | |
| PR | (VARI-) VARIAGENICS INC. |
| PA | |
| PI | Housman D, Ledley FD, Stanton VP; |
| XX | |
| DR | WFI; 1998-521232/44. |
| XX | |
| PT | Identifying target genes for allele-specific drugs - used for |
| PT | diagnosis, prevention and treatment of, e.g. cancers, atherosclerotic |
| PT | plaque, dysplastic lesions, endometriosis or graft versus host disease |
| XX | |
| PS | Disclosure; Figure 7; 605pp; English. |
| XX | |
| CC | This invention describes a novel method for identifying an inhibitor |
| CC | potentially useful for treatment of cancer, where the inhibitor is |
| CC | active on a gene vital for cell growth or viability, and where the gene |
| CC | is subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is |
| CC | used for preventing the development of cancer in a patient having a |
| CC | precancerous condition, by administering to the patient a first allele |
| CC | specific inhibitor (ASI) targeted to an allele of a first essential gene |
| CC | present in cells of the precancerous condition, where the normal somatic |
| CC | cells of the patient are heterozygous for the first gene, the inhibitor |
| CC | is active on at least one but less than all allelic forms of the gene |
| CC | present in a population and targets only one allelic form present in the |
| CC | normal somatic cells, and the first gene. The products and methods can |
| CC | be used in the diagnosis, prevention and treatment of LOH disorders, |
| CC | e.g. cancers, atherosclerotic plaques, premalignant metaplastic or |
| CC | dysplastic lesions, benign tumours, endometriosis, polycystic kidney |
| CC | disease, and graft versus host disease. The method can also be used to |
| CC | remove malignant cells from bone marrow transplants. AA225812-Z26825 |
| CC | represent human polymorphic sites described in the method of the |
| CC | invention. |
| XX | |
| SQ | Sequence 21 BP; 19 A; 1 C; 1 G; 0 U; 0 other; |
| | |
| | Query Match 1.5%; Score 16.2; DB 1; Length 21; |
| | Best Local Similarity 85.7%; Pred.No.3.le+02; |
| | Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0; |
| | |
| QY | 1077 AACATTATTAATAAAAAAAAAA 1097 |
| | |
| Db | 1 AACAAAGAAAAAATAAAAAAAAAA 21 |
| | |
| RESULT 572 | |
| AAF93028 | |
| ID | AAF93028 standard; DNA; 22 BP. |
| XX | |
| AC | AAF93028; |
| XX | |
| DT | 17-MAY-2001 (first entry) |
| XX | |

| | | |
|------------|---|--|
| DE | Polymorphic sequence for ABC1 polymorphic site #38. | |
| XX | | |
| KW | High density lipoprotein-cholesterol; HDL-C; cardiovascular; ABC1; ds. | |
| XX | | |
| OS | Homo sapiens. | |
| XX | | |
| PN | W0200115676-A2. | |
| XX | | |
| PD | 08-MAR-2001. | |
| XX | | |
| PF | 01-SEP-2000; 2000WO-IB01492. | |
| XX | | |
| PR | 01-SEP-1999; 99US-0151977. | |
| PR | 15-MAR-2000; 2000US-0526193. | |
| PR | 23-JUN-2000; 2000US-0213958. | |
| XX | | |
| PA | (UYBR-) UNIV BRITISH COLUMBIA. | |
| PA | (XENO-) XENON GENETICS INC. | |
| XX | | |
| PI | Hayden MR, Brooks-Wilson AR, Pimstone SN, Clee SM; | |
| XX | | |
| DR | WPI; 2001-244356/25. | |
| XX | | |
| PT | Treating a lower than normal high density lipoprotein-cholesterol | |
| PT | (HDL-C) level, a higher than normal triglyceride level, or a | |
| PT | cardiovascular disease, by administering a compound that modulates LXR- | |
| PT | or RXR-mediated transcriptional activity - | |
| XX | | |
| PS | Disclosure; Fig 4; 317pp; English. | |
| XX | | |
| CC | The present invention relates to a method for treating a patient | |
| CC | diagnosed as having a lower than normal high density | |
| CC | lipoprotein-cholesterol (HDL-C) level, a higher than normal | |
| CC | triglyceride level, or a cardiovascular disease, involving | |
| CC | administering a compound that modulates LXR- or RXR-mediated | |
| CC | transcriptional activity or ABC1 expression or activity. | |
| CC | The LXR gene product may be used in an assay to identify | |
| CC | compounds useful for the treatment of a disease or condition selected a | |
| CC | lower than normal HDL cholesterol level, a higher than normal | |
| CC | triglyceride level, and a cardiovascular disease. | |
| XX | | |
| SQ | Sequence 22 BP; 6 A; 2 C; 10 G; 3 T; 1 other; | |
| | | |
| | Query Match 1.5%; Score 16.2; DB 1; Length 22; | |
| | Best Local Similarity 81.8%; Pred. No. 3.3e+02; | |
| | Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps | |
| | | |
| Qy | 991 TTGGAGCTCTGAGCTGGAGAA 1012 | |
| Db | 1 TTGGAGCGCTNAGGACGAGAA 22 | |
| | | |
| RESULT 573 | | |
| AAAX07568 | | |
| ID | AAAX07568 standard; cDNA; 16 BP. | |
| XX | | |
| AC | AAAX07568; | |
| XX | | |
| DT | 21-JUN-1999 (first entry) | |
| DE | | |
| XX | Homo sapiens fetal kidney clone AK647 secreted protein gene 3' end. | |
| XX | | |
| KW | Secreted protein; fetal kidney; ds. | |
| XX | | |
| OS | Homo sapiens. | |
| XX | | |
| PN | W09900405-A1. | |
| XX | | |
| PD | 07-JAN-1999. | |
| XX | | |
| XX | 29-JUN-1998; 98WO-US13530. | |
| PF | | |
| XX | | |
| PR | 30-JUN-1997; 97US-0885610. | |

XX (GEMV) GENETICS INST INC.
 PA Agostino MJ, Evans C, Jacobs K, Lavallie ER, McCooy JM;
 PI Merberg D, Racie LA, Treacy M;
 XX WPI; 1999-095671/08.
 DR
 XX New polynucleotides encoding secreted human proteins - are derived
 PT from foetal kidney or adult retina cDNA libraries, used as, e.g.
 PT potential vaccines
 XX
 XX Disclosure; Page 54; 76pp; English.
 XX
 CC The sequence is that of the 3' end of a sequence encoding
 CC a secreted protein from a human fetal kidney clone AK296.
 CC Such a sequence is predicted to have biological
 CC activities which would make them suitable for treating, preventing or
 CC ameliorating medical conditions in humans and animals, although no
 CC supporting data is given. Suggested activities include nutritional
 CC activity, cytokine and cell proliferation/differentiation activity,
 CC immune stimulating (e.g. as vaccines) or suppressing activity,
 CC haematopoiesis regulating activity, tissue growth activity,
 CC activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
 CC and thrombolytic activity, receptor/ligand activity, anti-inflammatory
 CC activity, cadherin/tumour invasion suppressor activity, and tumour
 CC inhibition activity. It is also stated to be useful for gene
 CC therapy.
 XX
 XX Sequence 16 BP; 16 A; 0 C; 0 G; 0 U; 0 other;
 SQ
 Query Match 1.5%; Score 16; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1084 AAAAAAAAAAAAAA 1099
 Db 1 AAAAAAAAAAAAAA 16
 RESULT 574
 AAC66068
 ID AAC66068 standard; DNA; 16 BP.
 AC AAC66068;
 XX
 DT 22-FEB-2001 (first entry)
 XX
 DE DNA chip primer #4.
 XX
 XX DNA chip; primer; nucleoside derivative; photolabile protecting group;
 KW photolithographic nucleic acid chip; ss.
 XX
 OS Synthetic.
 XX
 PN WO200061594-A2.
 XX
 PD 19-OCT-2000.
 XX
 PF 07-APR-2000; 2000WO-DE01148.
 XX
 PR 08-APR-1999; 99DE-1015867.
 PR 28-JAN-2000; 2000DE-1003631.
 XX
 PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
 XX
 PI Beier M, Hoheisel J;
 XX
 DR WPI; 2000-679457/66.
 XX
 XX New nucleoside derivatives with photolabile protecting groups, useful
 PT in oligonucleotide synthesis, particularly on solid phases, e.g. for
 PT hybridization testing -

XX Disclosure; Fig 9; 48pp; German.
 XX
 CC This invention describes nucleoside derivatives (I) with photolabile
 CC protecting groups. (I) are used to synthesize oligonucleotides using the
 CC photolithographic nucleic acid chip method, particularly where these
 CC are intended for performing enzymatic reactions initiated from a free
 CC 3'-hydroxy (especially solid-phase polymerase reactions or ligase
 CC reactions, but also reverse transcription, cDNA synthesis etc.), also
 CC for hybridization testing, sequencing and in DNA computing. (I) are
 CC produced with high selectivity by reaction with a mild acylating agent
 CC that has high specificity for the 3'-position, without significant
 CC side-reactions (cf. more reactive acylating agents such as
 CC chloroformates).
 XX
 SQ Sequence 16 BP; 16 A; 0 C; 0 G; 0 U; 0 other;
 Query Match 1.5%; Score 16; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1084 AAAAAAAAAAAAAA 1099
 Db 1 AAAAAAAAAAAAAA 16
 RESULT 575
 AAH42481/C
 ID AAH42481 standard; DNA; 16 BP.
 XX
 AC AAH42481;
 XX
 DT 01-OCT-2001 (first entry)
 XX
 DE Oligonucleotide used to produce branched chain compounds.
 XX
 KW Branched chain compound; nucleic acid synthesis; primer extension;
 KW reverse transcription; nucleic acid hybridization;
 KW nucleic acid amplification; ss.
 XX
 OS Synthetic.
 XX
 PH Key Location/Qualifiers
 FT modified_base 1 /tag= a
 FT /note= "COOH attached"
 FT modified_base 2 /tag= b
 FT /note= "COOH attached"
 FT misc_feature 2..3 /tag= c
 FT /note= "branch present"
 XX
 PN EP1111068-A1.
 XX
 PD 27-JUN-2001.
 XX
 PF 21-DEC-1999; 99EP-0125484.
 XX
 PR 21-DEC-1999; 99EP-0125484.
 XX
 PA (LION-) LION BIOSCIENCE AG.
 PA (VBOG-) VBC GENOMICS GMBH.
 XX
 PI Schmidt W, Hiller R, Huber M, Mueller M;
 XX
 DR WPI; 2001-466959/51.
 XX
 XX Branched compounds useful in e.g. nucleic acid synthesis reaction
 PT comprises nucleic acid moieties optionally extended by a polymerase
 XX
 PS Example 1; Page 10; 31pp; English.
 XX

CC The specification describes branched compounds containing nucleic
 CC acid moieties optionally extended by a polymerase. The branched chain
 CC compounds of the invention are used in nucleic acid synthesis reaction,
 CC primer extension reaction, reverse transcription reaction of RNA into
 CC DNA, nucleic acid hybridization experiment (for identifying sequence
 CC of a nucleic acid), and nucleic acid amplification experiment (for
 CC analysing the expression pattern of genes). The compounds are also used
 CC in solid-phase enzymatic reactions. The present sequence was used
 CC in the course of the invention to produce branched chain compounds.

SQ Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 other;
 Query Match 1.5%; Score 16; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1099
 DB 16 AAAAAAAAAAAAAA 1

RESULT 576
 AAF30880/c
 ID AAF30880 standard; DNA; 16 BP.

AC AAF30880;

DT 09-JUL-2001 (first entry)

XX Oligonucleotide portion of ODN-MGB-LF conjugate.

XX ODN-MGB-LF; oligonucleotide; minor groove binder;
 XX latent fluorophore; hybridisation; detection; fluorescence; probe;
 XX ss.

XX Synthetic.

XX WO200131063-A1.

XX 03-MAY-2001.

XX 26-OCT-2000; 2000WO-US29786.

XX 26-OCT-1999; 99US-0428236.

XX (EPOC-) EPOCH BIOSCIENCES INC.

XX Dempcy RO, Afonina IA, Vermeulen NMJ;

XX WPI; 2001-328656/34.

XX Conjugate of oligonucleotide, minor groove binder and latent
 XX fluorophore, useful for detecting specific nucleic acids, e.g. for
 XX single-nucleotide mismatch discrimination -

XX Disclosure; Page 58; 105pp; English.

XX The present sequence is that of the oligonucleotide (ODN) component
 CC of an ODN-MGB (minor groove binder)-LF (latent fluorophore)
 CC conjugate of the invention. MGBs bind in a non-intercalating
 CC manner to the minor groove of non-single-stranded DNA, RNA or their
 CC hybrids, while a LF binds similarly but in an intercalating manner,
 CC or lies in the minor groove, or is oriented in some other way to
 CC the DNA molecule by MGB, such that it becomes fluorescent (or its
 CC fluorescence properties change detectably). The conjugates are used
 CC as hybridisation probes and amplification primers for fluorescent
 CC detection of specifically hybridising sequences, for analysis or
 CC diagnosis, especially (real-time) PCR, for single-nucleotide
 CC mismatch discrimination, target or signal amplification,
 CC array-based assays and sequencing, including detection of
 CC double-stranded DNA by triplex formation. Many different targets
 CC can be detected a single reaction vessel. The present ODN-MGB-LF
 CC conjugate was used to demonstrate hybridisation-triggered

CC fluorescence. Upon hybridisation to the complementary target
 CC sequence there was an increase in fluorescence yield, measured as
 CC the ratio of the fluorescence emitted by the hybrid between the
 CC ODN-MGB-LF conjugate and its target sequence to the fluorescence
 CC emitted by unhybridised (i.e. single-stranded) ODN-MGB-LF, of 8.3.

SQ Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 other;

Query Match 1.5%; Score 16; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1099
 DB 16 AAAAAAAAAAAAAA 1

RESULT 577

AAF30895/c

ID AAF30895 standard; DNA; 16 BP.

AC AAF30895;

DT 09-JUL-2001 (first entry)

XX Oligonucleotide-minor groove binder complex.

XX ODN-MGB-LF; oligonucleotide; minor groove binder;
 XX latent fluorophore; hybridisation; detection; fluorescence; probe;
 XX ss.

XX Synthetic.

XX Key Location/Qualifiers

XX modified_base 1

XX /*tag= a

XX /note= "thymine modified by a minor groove binder
 XX (2-dimethylaminonaphthalene-6-
 XX sulfonamide"

XX WO200131063-A1.

XX 03-MAY-2001.

XX 26-OCT-2000; 2000WO-US29786.

XX 26-OCT-1999; 99US-0428236.

XX (EPOC-) EPOCH BIOSCIENCES INC.

XX Dempcy RO, Afonina IA, Vermeulen NMJ;

XX WPI; 2001-328656/34.

XX Conjugate of oligonucleotide, minor groove binder and latent
 XX fluorophore, useful for detecting specific nucleic acids, e.g. for
 XX single-nucleotide mismatch discrimination -

XX Disclosure; Page 101; 105pp; English.

XX The present sequence is that of an oligonucleotide (ODN)-minor
 CC groove binder (MGB) complex. MGBs bind in a non-intercalating
 CC manner to the minor groove of non-single-stranded DNA, RNA or their
 CC hybrids. ODN-MGB-LF conjugates of the invention also comprise a
 CC latent fluorophore (LF), which binds similarly to the MGB but in an
 CC intercalating manner, or lies in the minor groove, or is oriented
 CC in some other way to the DNA molecule by MGB, such that it becomes
 CC fluorescent (or its fluorescent properties change detectably). The
 CC conjugates are used as hybridisation probes and amplification
 CC primers for fluorescent detection of specifically hybridising
 CC sequences, for analysis or diagnosis, especially (real-time) PCR,
 CC for single-nucleotide mismatch discrimination, target or signal
 CC amplification, array-based assays and sequencing, including

XX DE Oligo-homodeoxyribonucleotide sequence, oligo dT.
 XX
 KW Detection; single-stranded sensor; detectable fluorescence emission;
 KW forensic testing; paternity testing; tissue typing; hereditary disorder;
 KW human population genetics; human evolutionary history; cystic fibrosis;
 KW human haplotype diversity; Tay-Sachs; sickle-cell anaemia; ss.
 XX
 OS Unidentified.
 XX
 XX WO200284271-A2.
 XX
 XX PD 24-OCT-2002.
 XX
 XX PF 16-APR-2002; 2002WO-US12176.
 XX
 XX PR 16-APR-2001; 2001US-0836579.
 XX
 XX PA (RBGC) UNIV CALIFORNIA.
 XX
 XX PA (CHAJ/) CHA J N.
 XX
 XX PI Cha JN, Morse DE, Stucky GD;
 XX
 XX DR WPI; 2003-103378/09.
 XX
 XX PT Detecting polynucleotides, for pharmacogenetic testing, comprises
 XX contacting a target polynucleotide with a complementary single-stranded
 XX sensor polynucleotide and an agent that allows the sensor to fluoresce
 XX upon excitation -
 XX
 XX PS Example 1; Page 25; 41pp; English.
 XX
 CC The invention relates to a novel assay for detecting a polynucleotide in
 CC a sample, which comprises: contacting a sample suspected of containing a
 CC target polynucleotide with a predetermined single-stranded sensor
 CC polynucleotide complementary to the target polynucleotide, in a solution
 CC comprising an agent that is a nonaqueous solvent that allows the sensor
 CC polynucleotide to produce a detectable fluorescence emission; exciting
 CC the sensor polynucleotide; and determining fluorescence emission. The
 CC assay is useful for detecting a single or double-stranded target
 CC polynucleotide, such as, DNA or RNA in a sample. The assay finds use in a
 CC wide variety of different applications including pharmacogenetic testing,
 CC forensic testing to identify the species or individual which was the
 CC source of a forensic specimen, in anthropological setting, paternity
 CC testing, testing for compatibility between prospective tissue or blood
 CC donors and patients and in screening for hereditary disorders. The method
 CC is also useful to study alterations of gene expression in response to a
 CC stimulus, disease, drug or medication, and other applications include
 CC human population genetics, analyses of human evolutionary history and
 CC characterisation of human haplotype diversity. The method is useful for
 CC detecting polynucleotide sequences from contaminants or pathogens
 CC including bacteria, yeast, and viruses to detect single nucleotide
 CC polymorphisms, which may be associated with particular alleles or subsets
 CC of alleles. The method is useful for detection of mutations and to detect
 CC nucleotide sequences associated with increased risk of diseases or
 CC disorders including cystic fibrosis, Tay-Sachs, and sickle-cell anaemia.
 CC This polynucleotide sequence represents an oligonucleotide sequence used
 CC in a fluorescence technique of the invention.
 XX
 SQ Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 other;
 Query Match 1.5%; Score 16; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1084 AAAAAAAAAAAAAA 1099
 Db 16 AAAAAAAAAAAAAA 1
 RESULT 581
 AAX69800/c
 ID AAX69800 standard; RNA; 17 BP.
 XX
 XX Query Match 1.5%; Score 16; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1084 AAAAAAAAAAAAAA 1099
 Db 17 AAAAAAAAAAAAAA 2
 RESULT 582
 AAX69801/c
 ID AAX69801 standard; RNA; 17 BP.
 XX
 XX AC AAX69801;
 XX
 XX DT 28-JUL-1999 (first entry)
 XX
 XX DE Human flt1 VEGF receptor hammerhead ribozyme substrate #1096.
 XX
 KW Vascular endothelial growth factor receptor; VEGF receptor; flt-1;
 KW flk-1; KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
 KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
 KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
 KW foetal liver kinase 1; ss.
 XX

XX AC AAX69800;
 XX
 XX DT 28-JUL-1999 (first entry)
 XX
 XX DE Human flt1 VEGF receptor hammerhead ribozyme substrate #1095.
 XX
 KW Vascular endothelial growth factor receptor; VEGF receptor; flt-1;
 KW flk-1; KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
 KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
 KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
 KW foetal liver kinase 1; ss.
 XX
 XX OS Homo sapiens.
 XX
 XX PN WO9715662-A2.
 XX
 XX PD 01-MAY-1997.
 XX
 XX PF 25-OCT-1996; 96WO-US17480.
 XX
 XX PR 11-JAN-1996; 96US-0584040.
 XX
 XX PR 26-OCT-1995; 95US-0005974.
 XX
 XX PA (CHIR) CHIRON CORP.
 XX
 XX PA (RIBO-) RIBOZYME PHARM INC.
 XX
 XX PI Escobedo J, McSwiggen J, Pavco P, Stinchcomb D;
 XX
 XX DR WPI; 1997-259017/23.
 XX
 XX PT Nucleic acid molecule modulating VEGF receptor(s) gene expression or
 XX mRNA stability - useful for treating e.g. tumour angiogenesis,
 XX psoriasis, rheumatoid arthritis, etc., in a human patient
 XX
 XX PS Claim 4; Page 79; 218pp; English.
 XX
 CC The present invention describes nucleic acid molecules which modulate
 CC the synthesis, expression and/or stability of a mRNA encoding 1 or more
 CC receptors of vascular endothelial growth factor (VEGF). A patient
 CC (preferably human) having a condition associated with the level of the
 CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
 CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
 CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can
 CC be treated by administering the nucleic acid molecule or the expression
 CC vector to the patient. AAX67275 to AAX75752 represent specific examples
 CC of nucleic acid molecules from the present invention.
 XX
 SQ Sequence 17 BP; 0 A; 1 C; 0 G; 16 U; 0 other;
 Query Match 1.5%; Score 16; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1084 AAAAAAAAAAAAAA 1099
 Db 17 AAAAAAAAAAAAAA 2
 RESULT 582
 AAX69801/c
 ID AAX69801 standard; RNA; 17 BP.
 XX
 XX AC AAX69801;
 XX
 XX DT 28-JUL-1999 (first entry)
 XX
 XX DE Human flt1 VEGF receptor hammerhead ribozyme substrate #1096.
 XX
 KW Vascular endothelial growth factor receptor; VEGF receptor; flt-1;
 KW flk-1; KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
 KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
 KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
 KW

KW foetal liver kinase 1; ss.
 XX Homo sapiens.
 OS WO9715662-A2.
 XX PN
 XX PD 01-MAY-1997.
 XX PF 25-OCT-1996; 96WO-US17480.
 XX PR 11-JAN-1996; 96US-0584040.
 XX PR 26-OCT-1995; 95US-0005974.
 XX (CHIR) CHIRON CORP.
 PA (RIBO-) RIBOZYME PHARM INC.
 XX Escobedo J, McSwiggen J, Pavco P, Stinchcomb D;
 XX WPI; 1997-259017/23.
 XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or
 PT mRNA stability - useful for treating e.g. tumour angiogenesis,
 PT psoriasis, rheumatoid arthritis, etc., in a human patient
 XX Claim 4; Page 79; 218pp; English.
 XX The present invention describes nucleic acid molecules which modulate
 CC the synthesis, expression and/or stability of a mRNA encoding 1 or more
 CC receptors of vascular endothelial growth factor (VEGF). A patient
 CC (preferably human) having a condition associated with the level of the
 CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
 CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
 CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can
 CC be treated by administering the nucleic acid molecule or the expression
 CC vector to the patient. AAX67275 to AAX75752 represent specific examples
 CC of nucleic acid molecules from the present invention.
 XX Sequence 17 BP; 0 A; 1 C; 0 G; 16 U; 0 other;
 SQ

Query Match 1.5%; Score 16; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1084 AAAAAAAAAAAAAA 1098
 DB ||||||||||||
 16 AAAAAAAAAAAAAA 1

RESULT 583
 AAV49503/C
 ID AAV49503 standard; cDNA to mRNA; 17 BP.
 XX AC AAV49503;
 XX 18-NOV-1998 (first entry)
 XX Human eosinophil cell activator HVC002 primer #1.
 XX Bosinophil cell activator; treatment; diagnosis; malignant tumour;
 KW parasitic infection; allergic inflammation; eosinophilic pneumonia;
 KW rapid onset eosinophilia; autoimmune disease; gene therapy; primer; ss.
 XX Synthetic.
 OS Homo sapiens.
 XX WO9824817-A1.
 XX 11-JUN-1998.
 XX 05-DEC-1997; 97WO-JP04470.
 XX 05-DEC-1996; 96JP-0325762.
 XX

(KYOW) KYOWA HAKKO KOGYO KK.
 PA Koike M, Kuga T, Nakagawa S, Nishi T, Saito A;
 PI Shinkai A, Yoshisue H;
 XX WPI; 1998-333261/29.
 XX DNA and encoded protein which activates eosinophil cells - for
 PT treatment of cancer, parasite infection, autoimmune disease and
 PT allergic inflammation
 XX Example 1; Page 64; 92pp; Japanese.
 XX AAV49503-V49507 are primers used in the isolation of a human eosinophil
 CC cell activator. This protein and antibodies generated from the protein
 CC can be used for treatment and diagnosis of malignant tumours, parasitic
 CC infections, allergic inflammation, eosinophilic pneumonia, rapid onset
 CC eosinophilia, and autoimmune diseases. DNA can be used for diagnosis,
 CC and the antisense DNA in gene therapy of these disorders. The protein
 CC can be used for screening of potential agonists or antagonists of its
 CC activity.
 XX Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 other;
 SQ

Query Match 1.5%; Score 16; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1083 TAAAAAAAAAAAAA 1098
 DB ||||||||||||
 17 TAAAAAAAAAAAAA 2

RESULT 584
 AAX18371/C
 ID AAX18371 standard; DNA; 17 BP.
 XX AC AAX18371;
 XX 11-MAY-1999 (first entry)
 XX RT-PCR primer of the invention SEQ ID 12.
 XX RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
 XX Synthetic.
 XX JP11032765-A.
 XX 09-FEB-1999.
 XX 18-JUL-1997; 97JP-0208312.
 XX 18-JUL-1997; 97JP-0208312.
 XX (TAKI) TAKARA SHUZO CO LTD.
 XX WPI; 1999-183822/16.
 XX Peptides having at least two new nucleotides - useful as primers in
 PT RT-PCR
 XX Disclosure; Page 11; 19pp; Japanese.
 XX This sequence represents a primer of the invention. The invention relates
 CC to sequences of at least two nucleotides of formula:
 CC (X)m5'-(alpha)n-beta-N3'; or (X)m5'-(gamma)k-delta-N3'; where
 CC X = a labelled compound and/or a nucleotide with voluntary sequence;
 CC m = 0 or 1; alpha = thymine; n = natural number indicating the repetition
 CC of alpha; beta, delta = V or N; V = adenine, guanine or cytosine;
 CC N = adenine, guanine, cytosine or thymine; gamma = thymine;
 CC k = natural number of 3 or over indicating the repetition of gamma, in
 CC which thymine expressed by gamma is composed of 1/3 or less of adenine,

Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 other;

Qy 1083 TAAAAAAAAAAAAA 1098
db 17 TAAAAAAAAAAAAA 2

Qy 1083 TAAAAAAAAAAAAA 1098
db 17 TAAAAAAAAAAAAA 2

```

RESULT 587
AAC64181/c
ID AAC64181 standard; DNA; 17 BP.
XX AC
XX AAC64181;
XX DT
XX 21-FEB-2001 (first entry)
XX DE
XX PCR anchor primer, SEQ ID NO:2, used in human gene 419 isolation.
XX KW
XX Human; pollinosis-associated gene 419; FAF-1 homologue;
XX KW Fas-associated factor-1; IGE; immunoglobulin E;
XX KW cedar pollen allergy; T-cell; reduced expression; detection;
XX KW diagnosis; drug screening; allergic disease; PCR primer; ss.
XX OS
XX Synthetic.
XX FN
XX WO200065045-A1.
XX PD
XX 02-NOV-2000.
XX PF
XX 26-APR-2000; 2000WO-JP02729.
XX PR
XX 27-APR-1999; 99JP-0120490.
XX PA
XX (GENO-) GENOX RES INC.
XX PI
XX Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
XX PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
XX DR
XX WPI; 2000-687338/67.
XX PT
XX Pollinosis-associated gene 419 undergoing significantly low expression
XX PT in subjects with high cedar pollen-specific IGE levels, useful in
XX PT diagnosis of allergic diseases and screening drug candidates -
XX PS
XX Example 6; Page 49; 77pp; Japanese.
XX CC
XX The invention relates to the human pollinosis-associated gene 419 which
XX CC exhibits reduced expression in the T-cells of individuals with high cedar
XX CC pollen-specific IGE (immunoglobulin E) levels. The gene was isolated
XX CC from T-cells from individuals allergic to cedar pollen using the
XX CC differential display method. Pollinosis-associated gene 419 has
XX CC homology with the gene encoding human Fas-associated factor-1 (FAF-1).
XX CC The invention also relates to the protein encoded by pollinosis gene
XX CC 419; expression constructs and host cells comprising pollinosis-
XX CC associated gene 419 nucleic acids; pollinosis-associated gene 419 primers
XX CC and probes; antibodies against the protein encoded by the gene; methods
XX CC of detection of pollinosis-associated gene 419 nucleic acids; and a
XX CC method of diagnosis of allergic diseases via the detection of pollinosis-
XX CC associated gene 419 nucleic acids. The invention additionally encompasses
XX CC methods of screening drug candidates for the treatment of allergic
XX CC disease by measuring the expression of pollinosis-associated gene 419 in
XX CC pollen antigen-stimulated T-cells in the presence of a test compound
XX CC relative to a control. Pollinosis-associated gene 419 is useful in the
XX CC diagnosis of allergic diseases and in the screening of drug candidates
XX CC for the treatment of such diseases. The present sequence represents
XX CC a PCR primer used in the isolation of human pollinosis-associated gene
XX CC 419 cDNA.
XX SQ
XX Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 other;
XX
Query Match 1.5%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1083 TAAAAAAAAAAAAA 1098
DB 17 TAAAAAAAAAAAAA 2
RESULT 588
AAC64213/c
ID AAC64213 standard; DNA; 17 BP.
XX AC
XX AAC64213;
XX DT
XX 21-FEB-2001 (first entry)
XX DE
XX PCR anchor primer, SEQ ID NO:3, used in human gene 373 isolation.
XX KW
XX Human; pollinosis-associated gene 373; IGE; immunoglobulin E;
XX KW cedar pollen allergy; T-cell; reduced expression; detection;
XX KW diagnosis; drug screening; allergic disease; PCR primer; ss.
XX OS
XX Synthetic.
XX FN
XX WO200065046-A1.
XX PD
XX 02-NOV-2000.
XX PF
XX 26-APR-2000; 2000WO-JP02730.
XX PR
XX 27-APR-1999; 99JP-0120489.
XX PA
XX (GENO-) GENOX RES INC.
XX PI
XX Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
XX PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
XX DR
XX WPI; 2000-687339/67.
XX PT
XX Pollinosis-associated gene 373 undergoing significantly low expression
XX PT in subjects with high cedar pollen-specific immunoglobulin-E levels,
XX PT useful in diagnosis of allergic diseases and screening drug candidates
XX PS
XX Example 6; Page 69; 80pp; Japanese.
XX CC
XX The invention relates to the human pollinosis-associated gene 373 which
XX CC exhibits significantly reduced expression in the T-cells of individuals
XX CC with high cedar pollen-specific IGE (immunoglobulin E) levels. The gene
XX CC was isolated from T-cells from individuals allergic to cedar pollen
XX CC using the differential display method. The invention also relates also
XX CC relates to the protein encoded by pollinosis gene 373; expression
XX CC constructs and host cells comprising pollinosis-associated gene 373
XX CC nucleic acids; pollinosis-associated gene 373 primers and probes;
XX CC antibodies against the protein encoded by the gene; methods of detection
XX CC of pollinosis-associated gene 373 nucleic acids; and a method of
XX CC diagnosis of allergic diseases via the detection of pollinosis-associated
XX CC gene 373 nucleic acids. The invention additionally encompasses methods of
XX CC screening drug candidates for the treatment of allergic disease by
XX CC measuring the expression of pollinosis-associated gene 373 in pollen
XX CC antigen-stimulated T-cells in the presence of a test compound relative to
XX CC a control. Pollinosis-associated gene 373 is useful in the diagnosis of
XX CC allergic diseases and in the screening of drug candidates for the
XX CC treatment of such diseases. The present sequence represents a PCR primer
XX CC used in the isolation of human pollinosis-associated gene 373 cDNA.
XX SQ
XX Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 other;
XX
Query Match 1.5%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1083 TAAAAAAAAAAAAA 1098
DB 17 TAAAAAAAAAAAAA 2
RESULT 589
AAC64213/c
ID AAC64213 standard; DNA; 17 BP.
XX AC
XX AAC64213;

```

```

XX DT 21-FEB-2001 (first entry)
XX XX PCR anchor primer, SEQ ID NO:2, used in human gene 627 isolation.
XX DE
XX XX
XX KW Human, pollinosis-associated gene 627; IgE; immunoglobulin E;
XX KW cedar pollen allergy; T-cell; reduced expression; detection;
XX KW diagnosis; drug screening; allergic disease; PCR primer; ss.
XX XX
XX OS Synthetic.
XX XX
XX PN WO200065051-A1.
XX XX
XX PD 02-NOV-2000.
XX PF 26-APR-2000; 2000WO-JP02735.
XX PR 27-APR-1999; 99JP-0120493.
XX XX
XX PA (GENO-) GENOX RES INC.
XX PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
XX PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
XX XX
XX DR WPI; 2000-687344/67.
XX XX
XX PT Pollinosis-associated gene 627 undergoing significantly low expression
XX PT in subjects with high cedar pollen-specific IgE levels, useful in
XX PT diagnosis of allergic diseases and screening drug candidates -
XX PS
XX PS Example 6; Page 41; 51pp; Japanese.
XX CC
XX CC The invention relates to the human pollinosis-associated gene 627 which
XX CC exhibits significantly reduced expression in the T-cells of individuals
XX CC with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene
XX CC was isolated from T-cells from individuals allergic to cedar pollen using
XX CC the differential display method. The invention also relates to methods of
XX CC detection of pollinosis-associated gene 627 nucleic acids; a method of
XX CC diagnosis of allergic diseases via the detection of pollinosis-associated
XX CC gene 627 nucleic acids; and a method of screening drug candidates for the
XX CC treatment of allergic disease by measuring the expression of pollinosis-
XX CC associated gene 627 in pollen antigen-stimulated T-cells in the presence
XX CC of a test compound relative to a control. Pollinosis-associated gene 627
XX CC is useful in the diagnosis of allergic diseases and in the screening of
XX CC drug candidates for the treatment of such diseases. The present sequence
XX CC represents a PCR primer used in the isolation of human pollinosis-
XX CC associated gene 627 cDNA.
XX SQ
XX Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 other;
XX Query Match 1.5%; Score 16; DB 1; Length 17;
XX Best Local Similarity 100.0%; Pred. No. 2.7e+02;
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 1083 TAAAAAATAAAAAA 1098
XX Db 17 TAAAAAATAAAAAA 2
XX
XX RESULT 590
XX AAC64230/c
XX ID AAC64230 standard; DNA; 17 BP.
XX XX
XX AC AAC64230;
XX XX
XX DT 21-FEB-2001 (first entry)
XX XX
XX DE PCR anchor primer, SEQ ID NO:2, used in human gene 795 isolation.
XX KW Human; pollinosis-associated gene 795; vimentin homologue;
XX KW IgE; immunoglobulin E; cedar pollen allergy; T-cell; reduced expression;
XX KW detection; diagnosis; drug screening; allergic disease; PCR primer; ss.
XX XX

```

```

OS Synthetic.
XX WO200065050-A1.
XX PD
XX PF 02-NOV-2000.
XX PF 26-APR-2000; 2000WO-JP02734.
XX PR
XX PR 27-APR-1999; 99JP-0120494.
XX PA (GENO-) GENOX RES INC.
XX PA (EISA) EISAI CO LTD.
XX PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
XX PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K, Takahashi E;
XX PI Yokoi A;
XX XX
XX DR WPI; 2000-687343/67.
XX XX
XX PT Pollinosis-associated gene 795 undergoing significantly low expression
XX PT in subjects with high cedar pollen-specific IgE levels, useful in
XX PT diagnosis of allergic diseases and screening drug candidates -
XX PS
XX PS Page 45; Example 6; 73pp; Japanese.
XX CC
XX CC The invention relates to the human pollinosis-associated gene 795 which
XX CC exhibits significantly reduced expression in the T-cells of individuals
XX CC with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene
XX CC was isolated from T-cells from individuals allergic to cedar pollen using
XX CC the differential display method. Pollinosis-associated gene 795 has
XX CC homology with the human vimentin gene. The invention also relates also
XX CC relates to the protein encoded by pollinosis gene 795; to expression
XX CC constructs and host cells comprising pollinosis-associated gene 795
XX CC nucleic acids; pollinosis-associated gene 795 primers and probes;
XX CC antibodies against the protein encoded by the gene; methods of detection
XX CC of pollinosis-associated gene 795 nucleic acids; and a method of
XX CC diagnosis of allergic diseases via the detection of pollinosis-associated
XX CC gene 795 nucleic acids. The invention additionally encompasses methods of
XX CC screening drug candidates for the treatment of allergic disease by
XX CC measuring the expression of pollinosis-associated gene 795 in pollen
XX CC antigen-stimulated T-cells in the presence of a test compound relative to
XX CC a control. Pollinosis-associated gene 795 is useful in the diagnosis of
XX CC allergic diseases and in the screening of drug candidates for the
XX CC treatment of such diseases. The present sequence represents a PCR primer
XX CC used in the isolation of human pollinosis-associated gene 795 cDNA.
XX SQ
XX Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 other;
XX Query Match 1.5%; Score 16; DB 1; Length 17;
XX Best Local Similarity 100.0%; Pred. No. 2.7e+02;
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 1083 TAAAAAATAAAAAA 1098
XX Db 17 TAAAAAATAAAAAA 2
XX
XX RESULT 591
XX AAX82720/c
XX ID AAX82720 standard; DNA; 17 BP.
XX XX
XX AC AAX82720;
XX XX
XX DT 10-NOV-2000 (first entry)
XX XX
XX DE Human IgA nephropathy-associated cDNA primer #51.
XX KW IgA nephropathy-associated protein; diagnosis; treatment; antisense;
XX KW human; primer; ss.
XX OS Homo sapiens.
XX XX
XX PN WO9963085-A1.

```

```

XX PD 09-DEC-1999.
XX PF 28-MAY-1999; 99WO-JP02855.
XX PR 02-JUN-1998; 98JP-0152603.
XX PA (KYOW ) KYOMA HAKKO KOGYO KK.
XX PI Ishiwata T, Sakurada M, Kawabata A, Nakagawa S, Nishi T, Kuga T;
XX PI Sawada S, Takei M, Shibata K, Furuya A;
XX DR WPI; 2000-097328/08.
XX PT DNA sequences preferentially expressed in IgA nephropathy patients,
XX PT proteins encoded by them, and antibodies to those proteins -
XX PS Claim 3; Page 169; 180pp; Japanese.
XX CC This invention describes novel DNA sequences preferentially expressed in
XX CC IgA nephropathy patients, and DNA sequences stringently hybridizing to
XX CC them. Independent claims cover diagnostic reagents for IgA nephropathy
XX CC incorporating the antisense sequences; the treatment of IgA nephropathy
XX CC using the antisense sequences for mRNA inhibition; proteins associated
XX CC with IgA nephropathy, containing sequences for mRNA inhibition; proteins associated
XX CC antibodies recognizing these proteins; the production of the DNA sequences;
XX CC by culture of host cells transformed with DNA encoding them; diagnostic
XX CC reagents for IgA nephropathy containing the antibodies; and compositions
XX CC for the treatment of IgA nephropathy which contain the antibodies. The
XX CC products of the invention can be used for the diagnosis and treatment of
XX CC IgA nephropathy. This sequence represents a primer used in the isolation
XX CC and identification of the human IgA nephropathy-associated proteins
XX CC described in the method of the invention.
XX SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 other;

Query Match 1.58; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1083 TAAAAAATAAAAAAAAAA 1098
Db 17 TAAAAAATAAAAAAAAAA 2

RESULT 592
AAA30179/c
ID AAA30179 standard; DNA; 17 BP.
AC AAA30179;
XX 16-AUG-2000 (first entry)
XX PCR primer GT15A used in pollenosis associated gene identification.
XX Pollenosis-associated protein; high pollen-specific immunoglobulin E;
XX IgE; diagnose; cedar pollenosis; treatment; human; PCR primer; ss.
XX Synthetic.
XX WO200020575-A1.
XX 13-APR-2000.
XX 06-OCT-1999; 99WO-JP05506.
XX 06-OCT-1998; 98JP-0284610.
XX (GENO-) GENOX RES INC.
XX Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
XX Obayashi I, Imai Y, Lu N, Ogawa K;

WPI; 2000-317712/27.
Gene highly expressed in patients with high cedar pollen-specific IgE
levels, useful for diagnosing pollenosis, and screening candidate
compounds for pollenosis treatment -
Example 6; Page 38; 44pp; Japanese.
This sequence represents a PCR primer used in the identification of a
human pollenosis associated gene. The gene is highly expressed in
individuals with high pollen-specific immunoglobulin E (IgE) levels. The
invention relates to the nucleotide sequence encoding the pollenosis
associated protein, diagnosing pollenosis and screening candidate
compounds for treating pollenosis. The gene can be used in diagnosing
pollenosis, particularly cedar pollenosis, and screening candidate
compounds for pollenosis treatment.
Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 other;

Query Match 1.58; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1083 TAAAAAATAAAAAAAAAA 1098
Db 17 TAAAAAATAAAAAAAAAA 2

RESULT 593
AAA25449/c
ID AAA25449 standard; DNA; 17 BP.
AC AAA25449;
XX 19-JUL-2000 (first entry)
XX Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1947.
XX Oestrogen receptor; c-raf, k-ras, bcl-2; ribozyme; cleavage;
XX hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
XX gene expression modification; cancer; phosphorothioate; endonuclease;
XX anticancer; breast cancer; endometrium cancer; ss.
XX Homo sapiens.
XX WO9954459-A2.
XX 28-OCT-1999.
XX 19-APR-1999; 99WO-US08547.
XX 20-APR-1998; 98US-0082404.
XX 23-JUN-1998; 98US-0103636.
XX (RIBO-) RIBOZYME PHARM INC.
XX Thompson JD, Beigelman L, McSwiggen JA, Karpeisky A, Bellon L;
XX Reynolds M, Zwick M, Jarvis T, Woolf T, Haeblerli P;
XX Matulic-Adamic J;
XX WPI; 2000-013248/01.
XX New nucleic acids that interact, and optionally cleave, target
XX sequences, used to treat cancer -
XX Claim 77; Page 79; 148pp; English.
XX The present invention describes nucleic acids (A) that interact stably
XX with a target sequence and contain at least one phosphorodithioate
XX link, having endonuclease activity. (A), and more generally any
XX catalytic nucleic acid (A') that modulates expression of the oestrogen
XX receptor gene, are used to treat cancer (particularly of breast or
XX endometrium), in vivo or by transforming cells ex vivo and implanting

```

CC treated cells, or for other conditions associated with levels of
 CC oestrogen receptor. Because of the high selectivity for targeted RNA, (A)
 CC can also be used to correlate inhibition of gene expression with
 CC alterations in phenotype, particularly for identification of therapeutic
 CC targets, and as research reagents (for RNA, in the same way that
 CC restriction endonucleases are used with DNA). The combination of
 CC and/or activity. AAA23503 to AAA24747 represent oestrogen receptor
 CC hammerhead ribozyme sequences, and AAA25993 to AAA26105 represent their
 CC corresponding target sequences. AAA25993 to AAA26105 represent oestrogen
 CC receptor hairpin ribozyme sequences, and AAA26107 to AAA26218 represent
 CC their corresponding target sequences. AAA26219 to AAA26271 represent
 CC other ribozyme sequences and antisense oligonucleotides used in the
 CC exemplification of the present invention.

XX
 XX Sequence 17 BP; 0 A; 0 C; 1 G; 16 T; 0 other;
 Query Match 1.5%; Score 16; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1099
 Db 17 AAAAAAAAAAAAAA 2

RESULT 594
 AAA25451/C
 ID AAA25451 standard; DNA; 17 BP.
 XX
 AC AAA25451;
 XX
 DT 19-JUL-2000 (first entry)
 XX
 DE Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1949.
 KW
 KW Oestrogen receptor; c-ras; k-ras; bcl-2; ribozyme; cleavage;
 KW hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
 KW gene expression modification; cancer; phosphorothioate; endonuclease;
 KW anticancer; breast cancer; endometrium cancer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO9954459-A2.
 XX
 PD 28-OCT-1999.
 XX
 PF 19-APR-1999; 99WO-US08547.
 XX
 PR 20-APR-1998; 98US-0082404.
 XX
 PR 23-JUN-1998; 98US-0101636.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 PI Thompson JD, Beigelman L, McSwiggen JA, Karpeisky A, Bellon L;
 PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haeblerl P;
 PI Matulic-Adamic J;
 XX
 DR WPI; 2000-013248/01.
 XX
 PT New nucleic acids that interact, and optionally cleave, target
 PT sequences, used to treat cancer -
 XX
 PS Claim 77; Page 79; 148pp; English.

CC The present invention describes nucleic acids (A) that interact stably
 CC with a target sequence and contain at least one phosphorodithioate
 CC link, having endonuclease activity. (A), and more generally any
 CC catalytic nucleic acid (A') that modulates expression of the oestrogen
 CC receptor gene, are used to treat cancer (particularly of breast or
 CC endometrium), in vivo or by transforming cells ex vivo and implanting
 CC treated cells, or for other conditions associated with levels of
 CC oestrogen receptor. Because of the high selectivity for targeted RNA, (A)

CC can also be used to correlate inhibition of gene expression with
 CC alterations in phenotype, particularly for identification of therapeutic
 CC targets, and as research reagents (for RNA, in the same way that
 CC restriction endonucleases are used with DNA). The combination of
 CC modifications in (A) improves resistance to nucleases, binding affinity
 CC and/or activity. AAA23503 to AAA24747 represent oestrogen receptor
 CC hammerhead ribozyme sequences, and AAA24748 to AAA25992 represent their
 CC corresponding target sequences. AAA25993 to AAA26105 represent oestrogen
 CC receptor hairpin ribozyme sequences, and AAA26107 to AAA26218 represent
 CC their corresponding target sequences. AAA26219 to AAA26271 represent
 CC other ribozyme sequences and antisense oligonucleotides used in the
 CC exemplification of the present invention.

XX
 XX Sequence 17 BP; 0 A; 0 C; 1 G; 16 T; 0 other;
 Query Match 1.5%; Score 16; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1099
 Db 16 AAAAAAAAAAAAAA 1

RESULT 595
 AAZ36739/C
 ID AAZ36739 standard; DNA; 17 BP.
 XX
 AC AAZ36739;
 XX
 DT 13-MAR-2000 (first entry)
 XX
 DE Anchored oligo(dT) primer AT15A used for modified differential display.
 XX
 KW Stimulus-regulated nucleic acid; sequence profile; nucleic acid level;
 KW differentially expressed nucleic acid; disease state; cancer;
 KW autoimmune disease; infectious disease; aging; developmental disorder;
 KW proliferative disorder; neurological disorder; toxicity; primer;
 KW treatment resistance; differential expression; drug discovery;
 KW growth factor; epidermal growth factor; radiation; stress; pathogen; ss.
 XX
 OS Synthetic.
 XX
 PN WO9955913-A2.
 XX
 PD 04-NOV-1999.
 XX
 PF 27-APR-1999; 99WO-US09119.
 XX
 PR 27-APR-1998; 98US-0083331.
 XX
 PR 27-AUG-1998; 98US-0098070.
 XX
 PR 04-FEB-1999; 99US-0118624.
 XX
 PA (KIMM-) KIMMEL CANCER CENT SIDNEY.
 XX
 PI McClelland M, Welsh J, Trenkle T;
 XX
 DR WPI; 2000-086388/07.
 XX
 PT Measuring expression of low abundance reduced complexity target nucleic
 PT acid molecules -
 XX
 PS Example 3; Page 91; 187pp; English.

CC AAZ36739-41 represent oligo(dT) primers used for modified differential
 CC display, in the method of the invention. The specification describes a
 CC method for measuring the level of two or more nucleic acid molecules in
 CC a target. The method comprises contacting a probe with an arbitrarily or
 CC statistically sampled target and detecting the amount of specific
 CC binding of the target to the probe. The methods can be used to identify
 CC differentially expressed nucleic acid molecules associated with disease
 CC states, such as cancer, autoimmune disease, infectious disease, aging,
 CC developmental disorder, proliferative disorder or neurological disorder.

CC Alternatively the methods can be used to assess the efficacy or toxicity
CC of or a resistance to a treatment. Also the methods can be used to
CC determine differential expression of nucleic acid molecules in response
CC to a stimulus, e.g. a chemical, drug or growth factor (especially
CC epidermal growth factor), radiation, stress or a pathogen. The methods
CC can also be used to determine co-regulated genes that can be potential
CC targets for drug discovery.

XX Sequence 17 BP; 2 A; 0 C; 0 G; 15 T; 0 other;

Query Match 1.5%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAATAAAAAAAAAA 1098
DB 17 TAAAAAATAAAAAAAAAA 2

RESULT 596
AAC82874/c
ID AAC82874 standard; DNA; 17 BP.

XX AC AAC82874;

XX DT 20-MAR-2001 (first entry)

XX DE Human pollinosis-associated gene 441 primer #1.

XX KW Pollinosis; pollinosis-associated gene 441; allergy; T cell;

XX KW pollen scattering; antigen; primer; ss.

XX OS Homo sapiens.

XX PN WO200073435-A1.

XX PD 07-DEC-2000.

XX PF 18-MAY-2000; 2000WO-JP03190.

XX PR 27-MAY-1999; 99JP-0148783.

XX PA (GENO-) GENOX RES INC.

XX PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;

XX PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;

XX WPI; 2001-061526/07.

XX PT Pollinosis-associated gene 441 which undergoes lower expression in
PT subjects after pollen scattering, useful in diagnosis of allergic
PT diseases and screening candidate compounds to regulate response of T
PT cells to antigen stimulus

XX Example 6; Page 35; 42pp; Japanese.

XX This invention describes a novel nucleic acid molecule comprising a
CC sequence (I) which undergoes significantly low expression in subjects
CC after pollen scattering, and is useful in diagnosis of allergic diseases
CC and screening candidate compounds for remedies capable of regulating the
CC response of T cells to the stimulus by an antigen.

XX Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 other;

Query Match 1.5%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAATAAAAAAAAAA 1098
DB 17 TAAAAAATAAAAAAAAAA 2

RESULT 597
AAC91719/c
ID AAC91719 standard; DNA; 17 BP.

XX AC AAC91719;

XX DT 27-MAR-2001 (first entry)

XX DE PCR anchor primer, SEQ ID NO:2, used in human gene 787 isolation.

XX KW Human; pollinosis-associated gene 787; pollen allergy; T-cell;

XX KW reduced expression; detection; diagnosis; drug screening;

XX KW allergic disease; PCR primer; ss.

XX OS Synthetic.

XX PN WO200073440-A1.

XX PD 07-DEC-2000.

XX PF 18-MAY-2000; 2000WO-JP03192.

XX PR 27-MAY-1999; 99JP-0148785.

XX PA (GENO-) GENOX RES INC.

XX PA (EISA) EISAI CO LTD.

XX PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;

XX PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K, Takahashi E;

XX PI Yokoi A;

XX WPI; 2001-032159/04.

XX PT Pollinosis-associated gene 787 undergoing significantly low expression
PT in subjects after pollen scattering, useful in diagnosis of allergic
PT diseases and screening candidate compounds to regulate response of T
PT cells to antigen stimulus

XX Example 6; Page 40; 54pp; Japanese.

XX The invention relates to the human pollinosis-associated gene 787 which
CC exhibits significantly reduced expression in the T-cells of individuals
CC after the pollen-scattering season, relative to expression levels in
CC T-cells before the pollen-scattering season. The gene was isolated from
CC T-cells from individuals allergic to pollen using the differential
CC display method. The invention also relates to pollinosis-associated gene
CC 787 primers and probes; methods of detection of pollinosis-associated
CC gene 787 nucleic acids; and a method of diagnosis of allergic diseases
CC via the detection of pollinosis-associated gene 787 nucleic acids. The
CC invention additionally encompasses a method of screening drug candidates
CC for the treatment of allergic disease by measuring the expression of
CC pollinosis-associated gene 787 in pollen antigen-stimulated T-cells in
CC the presence of a test compound relative to a control. Pollinosis-
CC associated gene 787 is useful in the diagnosis of allergic diseases and
CC in the screening of drug candidates for the treatment of such diseases.
CC The present sequence represents a PCR primer used in the isolation of
CC human pollinosis-associated gene 787 cDNA.

XX Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 other;

Query Match 1.5%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAATAAAAAAAAAA 1098
DB 17 TAAAAAATAAAAAAAAAA 2

RESULT 598
AAC92292/c
ID AAC92292 standard; DNA; 17 BP.

XX

```

AC AAC92292;
XX
XX 22-MAR-2001 (first entry)
XX
XX Human pollinosis-associated gene 465 related PCR primer SEQ ID NO:2.
XX
XX Human; pollinosis-associated gene 465; pollen scattering; allergy;
XX
XX allergic disease; PCR primer; ss.
XX
XX Homo sapiens.
XX
XX WO200073439-A1.
XX
XX 07-DEC-2000.
XX
XX 18-MAY-2000; 2000WO-JP03191.
XX
XX 27-MAY-1999; 99JP-0148784.
XX
XX (GENO-) GENOX RES INC.
XX
XX (EISA) EISAI CO LTD.
XX
XX Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
XX
XX Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K, Takahashi E;
XX
XX Yokoi A;
XX
XX WPI; 2001-061528/07.
XX
XX Pollinosis-associated gene 465 undergoing significantly low expression
XX
XX in subjects after pollen scattering, useful in diagnosis of allergic
XX
XX diseases and screening candidate compounds to regulate response of T
XX
XX cells to antigen stimulus -
XX
XX Example 6; Page 43; 61pp; Japanese.
XX
XX The present invention describes the human pollinosis-associated gene 465
XX
XX which has a nucleic acid sequence of 3442 base pairs (bp), given in
XX
XX (AAC92291), that undergoes significantly low expression in subjects
XX
XX after pollen scattering, and is useful in the diagnosis of allergic
XX
XX diseases and screening candidate compounds for remedies capable of
XX
XX regulating the response of T cells to the stimulus by an antigen. The
XX
XX gene is useful in the diagnosis of allergic diseases and screening
XX
XX candidate compounds for remedies capable of regulating the response of T
XX
XX cells to the stimulus by an antigen. The present sequence represents a
XX
XX PCR primer which is used in an example from the present invention.
XX
XX Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 other;
XX
XX Query Match 1.5%; Score 16; DB 1; Length 17;
XX
XX Best Local Similarity 100.0%; Pred. No. 2.7e+02;
XX
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1083 TAAAAA 1098
XX
XX Db 17 TAAAAA 2
XX
XX RESULT 599
XX
XX AAH47126/C
XX
XX ID AAH47126 standard; DNA; 17 BP.
XX
XX AC AAH47126;
XX
XX 30-NOV-2001 (first entry)
XX
XX Nucleotide sequence of primer GT15A.
XX
XX B1001; B1466; B1072; B1151; T-cell; allergy; atopic dermatitis;
XX
XX human; PCR primer; ss.
XX
XX Homo sapiens.
XX
XX WO200165259-A1.

```

```

XX 07-SEP-2001.
XX
XX 23-FEB-2001; 2001WO-JP01372.
XX
XX 02-MAR-2000; 2000JP-0061832.
XX
XX (GENO-) GENOX RES INC.
XX
XX (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
XX
XX Nagasu T, Oshida T, Obayashi I, Matsui K, Saito H;
XX
XX WPI; 2001-557789/62.
XX
XX Diagnosis of allergies including atopic dermatitis -
XX
XX Example 6; Page 65; 83pp; Japanese.
XX
XX The invention provides a method of diagnosis of allergies that involves:
XX
XX assaying the levels of expression of genes B1001, B1466, B1072 or B1151
XX
XX in T-cells; and comparing them with the level of expression in healthy
XX
XX T-cells. The method is useful for diagnosing allergies, particularly
XX
XX atopic dermatitis. The present sequence represents a PCR primer used
XX
XX for analysis of the expression of the above genes.
XX
XX Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 other;
XX
XX Query Match 1.5%; Score 16; DB 1; Length 17;
XX
XX Best Local Similarity 100.0%; Pred. No. 2.7e+02;
XX
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1083 TAAAAA 1098
XX
XX Db 17 TAAAAA 2
XX
XX RESULT 600
XX
XX AAL49948/C
XX
XX ID AAL49948 standard; DNA; 17 BP.
XX
XX AC AAL49948;
XX
XX 10-DEC-2002 (first entry)
XX
XX Human B1153 expression in allergic disease related PCR primer GT15A.
XX
XX Human; allergy; B1153; differential expression; anti-allergic; asthma;
XX
XX antiasthmatic; antiinflammatory; atopic skin inflammation; PCR;
XX
XX primer; ss.
XX
XX Unidentified.
XX
XX WO200250269-A1.
XX
XX 27-JUN-2002.
XX
XX 21-DEC-2001; 2001WO-JP11286.
XX
XX 21-DEC-2000; 2000JP-0389476.
XX
XX (GENO-) GENOX RES INC.
XX
XX (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
XX
XX Matsumoto Y, Imai Y, Oshida T, Sugita Y, Nagasu T, Tsujimoto G;
XX
XX WPI; 2002-713252/77.
XX
XX Examination of allergic diseases comprises detecting gene B1153
XX
XX over-expressed in T cells of allergy patients for diagnosis treatment
XX
XX and investigation of atopic skin inflammation and asthma -
XX
XX Example 6; Page 81; 102pp; Japanese.

```

CC The present invention relates to a method of examining allergic diseases
CC which comprises comparing the expression level of gene B1153 in allergy
CC patients with the expression level in healthy subjects. The method is
CC useful for the treatment, prevention, diagnosis and study of allergic
CC diseases including atopic skin inflammation and asthma. The present
CC sequence is a PCR primer described in the exemplification of the
CC invention.
XX
SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 other;

Query Match 1.5%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1083 TAAAAA 1098
Db 17 TAAAAA 2

RESULT 601
AAL47234/C
ID AAL47234 standard; DNA; 17 BP.
XX
AC AAL47234;
XX
DT 22-AUG-2002 (first entry)
XX
DE Allergic disease examination method related anchor primer SEQ ID NO: 2.
XX
DE Allergic disease; allergy; antiallergic; intersectin 2; eosinophil;
XX
KW atopic dermatitis; human; PCR; primer; ss.
XX
OS Unidentified.
XX
PN WO200233122-A1.
XX
PD 25-APR-2002.
XX
PF 11-OCT-2001; 2001WO-JP08937.
XX
PR 13-OCT-2000; 2000JP-0314093.
XX
PA (GENO-) GENOX RES INC.
PA (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
PA (EISA) EISAI CO LTD.
XX
PI Sugita Y, Hashida R, Ogawa K, Obayashi M, Nagasu T, Saito H;
PI Takahashi E;
XX
DR WPI; 2002-372313/40.
XX
PT Method for examining allergic diseases by differential display of
PT intersectin 2 gene showing different expression particularly
PT significant increase in eosinophils in patients -
XX
PS Example 1; Page 52; 90pp; Japanese.
XX
CC The present invention relates to a method for examining allergic diseases
CC with intersectin 2 gene or a gene with equivalent function of intersectin
CC 2 as an indicator gene, which comprises determining the expression level
CC of the gene in the eosinophils in a patient, and comparing the expression
CC level with that in the eosinophils of a healthy individual. The method is
CC for examining allergic diseases, particularly atopic dermatitis, which is
CC also applicable in screening candidate compounds for remedies. The
CC present sequence is an anchor primer described in the exemplification
CC of the invention.
XX
SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 other;

Query Match 1.5%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1083 TAAAAA 1098
Db 17 TAAAAA 2

RESULT 603
ABN99829/C
ID ABN99829 standard; DNA; 17 BP.
XX
AC ABN99829;
XX
DT 15-AUG-2002 (first entry)
XX
DE Human allergic disease related PCR primer SEQ ID NO: 18.
XX
KW Human; allergy; atopic dermatitis; eosinophil; anti-allergic; PCR;
KW primer; ss.
XX
OS Homo sapiens.
XX
PN WO200233069-A1.
XX

Qy 1083 TAAAAA 1098
Db 17 TAAAAA 2

RESULT 602
ABL59038/C
ID ABL59038 standard; DNA; 17 BP.
XX
AC ABL59038;
XX
DT 20-AUG-2002 (first entry)
XX
DE Nucleotide sequence of PCR primer GT15A.
XX
KW Human; allergosis; eosinophil; PCR; primer; ss.
XX
OS Homo sapiens.
XX
PN JP2002095500-A.
XX
PD 02-APR-2002.
XX
PF 25-SEP-2000; 2000JP-0291316.
XX
PR 25-SEP-2000; 2000JP-0291316.
XX
PA (GENO-) GENOX SOYAKU KENKYUSHO KK.
PA (KOKU-) KOKURITSU SHONI BYOIN INCHO.
XX
DR WPI; 2002-439993/47.
XX
PT Examining allergosis, involves measuring the expression levels of a
PT specific gene, and comparing it to the levels in the eosinophils of a
PT healthy control -
XX
PS Example 1; Page 17; 20pp; Japanese.
XX
CC The specification describes a method for examining allergosis. The
CC method comprises measuring the expression level of the gene given
CC in ABL59037, and comparing it with the expression level of the gene
CC in the eosinophils of a healthy person. The method is used for the
CC examination of allergosis. The present sequence represents a PCR
CC primer, which is used in the course of the invention.
XX
SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 other;

Query Match 1.5%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1083 TAAAAA 1098
Db 17 TAAAAA 2

RESULT 603
ABN99829/C
ID ABN99829 standard; DNA; 17 BP.
XX
AC ABN99829;
XX
DT 15-AUG-2002 (first entry)
XX
DE Human allergic disease related PCR primer SEQ ID NO: 18.
XX
KW Human; allergy; atopic dermatitis; eosinophil; anti-allergic; PCR;
KW primer; ss.
XX
OS Homo sapiens.
XX
PN WO200233069-A1.
XX

```

PD 25-APR-2002.
XX
XX
XX 28-SEP-2001; 2001WO-JP08574.
XX
XX 13-OCT-2000; 2000JP-0314093.
XX
XX (GENO-) GENOX RES INC.
XX (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
XX
XX Sugita Y, Hashida R, Ogawa K, Obayashi M, Nagasu T, Saito H;
XX WPI; 2002-372311/40.
XX
XX Method for examining allergic diseases by differential display of
XX seventeen genes showing different expression particularly significant
XX increase in eosinophils in patients with mild atopic dermatitis, also
XX applicable in screening compounds -
XX
XX Example 1; Page 109; 165pp; Japanese.
XX
XX The present invention relates to a method for examining allergic diseases
XX which involves determining the expression level of a gene, having one of
XX the 17 nucleotide sequences shown in ABN99812-ABN99828, in the
XX eosinophils in a patient and comparing the expression level with that in
XX eosinophils of a healthy individual. The method can be used to
XX examine allergic diseases, particularly atopic dermatitis, and its early
XX diagnosis, which is also applicable in screening candidate compounds for
XX remedies. The present sequence is a PCR primer described in the
XX exemplification of the invention.
XX
XX Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 other;

Query Match      1.5%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAATAAAAAAAAAA 1098
Db 17 TAAAAAATAAAAAAAAAA 2

RESULT 604
ABK49634/C
ID ABK49634 standard; DNA; 17 BP.
XX
XX AC ABK49634;
XX
XX 15-JUL-2002 (first entry)
XX
XX Human Acetyltransferase-like protein 20-90-05 PCR primer GT15A.
XX
XX Human; ss; PCR; acetyltransferase; 20-90-05; allergic disease; primer;
XX differential display; eosinophil; antiallergic; atopic dermatitis;
XX GT15A.
XX
XX OS Homo sapiens.
XX
XX PN WO200224903-A1.
XX
XX PD 28-MAR-2002.
XX
XX PF 21-SEP-2001; 2001WO-JP08246.
XX
XX PR 25-SEP-2000; 2000JP-0291318.
XX
XX PA (GENO-) GENOX RES INC.
XX PA (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
XX PA (EISA) EISAI CO LTD.
XX
XX PI Sugita Y, Hashida R, Ogawa K, Fujishima T, Nagasu T, Tsujimoto G;
XX PI Takahashi E;
XX WPI; 2002-315738/35.
XX

```

```

XX
XX Examining allergic diseases by differential display of gene showing
XX different expression particularly increased expression in remission
XX stage in eosinophils of patients, also applicable in screening
XX candidate compounds for remedies -
XX
XX Example 1; Page 56; 72pp; Japanese.
XX
XX The invention relates to a method for examining allergic diseases
XX comprising determining the expression level of a gene containing,
XX the human cDNA appearing as ABK49633 which has homology with
XX acetyltransferases in the eosinophils of a patient and comparing the
XX expression level with that in the eosinophils of a healthy individual
XX (i.e. differential display). Also included are methods of screening
XX for candidate compounds which affect the expression level of the gene or
XX the activity of the protein encoded by the gene (including related
XX proteins and mutants), the use of probes based on the gene sequence
XX in the examination of allergic diseases, the use of reporter
XX constructs in the screening of candidate compounds, a vector containing a
XX the transcription-controlling region of the gene, cells transformed a
XX with the vector, an antibody against the protein and a model animal for
XX allergic diseases which is a transgenic non-human vertebrate with
XX lowering of expression intensity of the gene in eosinophils.
XX The method is examining allergic diseases particularly atopic
XX dermatitis which is also applicable in screening candidate
XX compounds for remedies. Such method can be performed in high throughput,
XX at low cost. The present sequence is a differential display PCR primer
XX for the cDNA encoding the human acetyltransferase-like protein 20-90-05.
XX
XX Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 other;

Query Match      1.5%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAATAAAAAAAAAA 1098
Db 17 TAAAAAATAAAAAAAAAA 2

RESULT 605
ABK49756/C
ID ABK49756 standard; DNA; 17 BP.
XX
XX AC ABK49756;
XX
XX 15-JUL-2002 (first entry)
XX
XX Human atopic dermatitis cDNA related PCR primer GT15a.
XX
XX Atopic dermatitis; ss; differential display; primer; PCR;
XX eosinophil; allergic disease; antiallergic; dermatological; GT15a.
XX
XX OS Synthetic.
XX
XX PN WO200226962-A1.
XX
XX PD 04-APR-2002.
XX
XX PF 21-SEP-2001; 2001WO-JP08247.
XX
XX PR 26-SEP-2000; 2000JP-0293021.
XX
XX PA (GENO-) GENOX RES INC.
XX PA (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
XX
XX PI Sugita Y, Hashida R, Ogawa K, Fujishima T, Nagasu T, Saito H;
XX WPI; 2002-330097/36.
XX
XX Examining allergic diseases by differential display of genes showing
XX different expression particularly increase in remission stage in
XX eosinophils in patients -
XX

```

XX PS Example 1; Page 54; 74pp; Japanese.

XX CC This invention relates to gene sequences that are differentially

CC expressed in eosinophils from patients with atopic dermatitis in the

CC increment stage as compared with those in the remission stage. These

CC sequences are used in a novel method for examining allergic diseases

CC comprising determining the expression levels of these genes and

CC comparing the expression level with that in the eosinophils of a

CC healthy individual. The method of the invention may have anti-allergic

CC or dermatological activities. The method can be used to diagnose

CC allergic diseases particularly atopic dermatitis, and may also

CC be used to screen candidate compounds for remedies. The method of the

CC invention can be performed in high throughput, at low cost. The

CC present sequence represents the G715a PCR primer used to amplify

CC the differentially amplified atopic dermatitis related cDNA sequences

CC of the invention.

XX CC Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 other;

SQ Query Match 1.5%; Score 16; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 2.7e+02;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAATAAAAAA 1098

DB 17 TAAAAAATAAAAAA 2

RESULT 606

ABK13941/C

ID ABK13941 standard; DNA; 17 BP.

XX AC ABK13941;

XX CC

DT 21-MAY-2002 (first entry)

XX DE

DE 5'-PCR primer used to produce single pattern characteristic by FokI.

XX KW Identification of transcribed gene; mRNA profile; gene expression;

KW cellular process; fingerprinting; susceptibility to external factor;

KW development; disease; PCR; primer; ss.

XX OS Synthetic.

XX PN WO200208461-A2.

XX PD 31-JAN-2002.

XX PF 23-JUL-2001; 2001WO-IB01539.

XX PR 21-JUL-2000; 2000GB-0018016.

XX PR 21-JUL-2000; 2000US-219925P.

XX PA (GLOB-) GLOBAL GENOMICS AB.

XX PI Linnarsson S, Ernfors P, Bauren G;

XX DR WPI; 2002-217065/27.

XX CC Providing mRNA profile, by generating two independent patterns

PT characteristic of sample mRNA population, analysing patterns, comparing

PT gene expression by cell types under varied conditions, and identifying

PT genes -

XX PS Disclosure; Fig 2; 67pp; English.

XX CC The present invention relates to a method for providing a profile of

CC mRNA molecules present in a sample. The method comprises generating

CC two independent patterns characteristic of the population of mRNA

CC molecules expressed in the sample and analysing the patterns using a

CC combinatorial algorithm, comparing gene expression by different or

CC same cell types under different conditions, and identifying genes

CC having a role in various cellular processes. The method is useful

CC for the analysis and identification of transcribed genes, and

CC fingerprinting. The method can be used to identify genes which play a

CC role in determining various cellular processes, including susceptibility

CC to external factors, development, and disease. The present sequence for

CC a PCR primer is used in the production of a single pattern

CC characteristic of a sample, employing a Type IIS restriction enzyme

CC (i.e. FokI) in the methods of the present invention.

XX SQ Sequence 17 BP; 0 A; 1 C; 0 G; 16 T; 0 other;

Query Match 1.5%; Score 16; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 2.7e+02;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAATAAAAAA 1099

DB 16 AAAAAAATAAAAAA 1

RESULT 607

ABZ70578/C

ID ABZ70578 standard; DNA; 17 BP.

XX AC ABZ70578;

XX CC

DT 23-MAY-2003 (first entry)

XX DE Primer.

XX KW Aspergillus phenolics; oxalate decarboxylase; APOXD;

KW transgenic plant; crop protection; primer; ss.

XX OS Synthetic.

XX PN CA2350328-A1.

XX PD 26-DEC-2002.

XX PF 26-JUN-2001; 2001CA-2350328.

XX PR 26-JUN-2001; 2001CA-2350328.

XX PA (PION-) PIONEER HI-BRED INT INC.

XX PI Scelonge C, Bidney D;

XX DR WPI; 2003-240188/25.

XX CC New isolated nucleic acid encoding oxalate decarboxylase from

PT Aspergillus phenolics, for degrading oxalic acid, identifying

PT transformed plant cells, and preventing pathogenic disease in plants -

XX PS Disclosure; Page 50; 60pp; English.

XX CC The present sequence is that of a primer used in the invention.

CC The invention relates to a novel nucleic acid (see ABZ70560)

CC encoding Aspergillus phenolics oxalate decarboxylase (APOXD)

CC (see ABZ72475). The gene and its encoded protein are useful in

CC degrading oxalate, in diagnostic assays, for protecting plants

CC against disease, and as a selectable marker.

XX SQ Sequence 17 BP; 0 A; 0 C; 0 G; 16 T; 1 other;

Query Match 1.5%; Score 16; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 2.7e+02;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAATAAAAAA 1099

DB 17 AAAAAAATAAAAAA 2

```

RESULT 608
AAN30173
ID AAN30173 standard; DNA; 18 BP.
XX
AC AAN30173;
XX
DT 05-APR-1992 (first entry)
XX
DE Sequence derived from the L1 region of the bovine papillomavirus (bpv)
DE type 1a genome.
XX
KW Diagnostic reagent; vaccine; medicine; wart; tumour; ss.
XX
OS Bovine papillomavirus.
XX
FH Key Location/Qualifiers
CDS 1..18
FT /*tag= a
FT
XX
XX EP2456-A.
XX
XX 26-OCT-1983.
XX
XX 01-APR-1983; 83EP-0901081.
XX
XX 05-APR-1982; 82FR-0005887.
XX
XX (INSP ) INST PASTEUR.
XX
XX (DANO/) DANOS O.
XX
XX Danos O, Katinka M, Yaniv M;
XX
XX WPI; 1983-802979/44.
XX
XX P-PSDB; AAP30313.
XX
DNA fragment coding for Papillomavirus antigenic proteins - and
PT derived immunogen, vaccine and antibody
XX
XX Claim 6; Page 16; 25pp; French.
XX
XX The inventors claim DNA fragments capable of expressing, in a host,
XX a prod. contg. at least one antigenic determinant of papillomavirus
XX (PV), (see AAN30170-N30173). Also claimed are immunogens consisting
XX of at least one peptide sequence coded for by the DNA fragments (see
XX AAP3010-P30313), vaccines contg. the immunogens and antibodies raised
XX from them. The vaccines are useful in human and veterinary medicine
XX and the antibodies are useful as diagnostic reagents. The DNA
XX fragments are most esp. derived from the L1 region of human PV type
XX 1a.
XX
XX Sequence 18 BP; 16 A; 1 C; 1 G; 0 U; 0 other;
Query Match 1.5%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1099
Db 3 AAAAAAAAAAAAAA 18

RESULT 609
AAV54167/c
ID AAV54167 standard; cDNA; 18 BP.
XX
AC AAV54167;
XX
XX 21-DEC-1998 (first entry)
XX
XX Nucleotide sequence PCR primer 4.
DE
XX PCR; primer; amplification; apoptosis; antibody; inhibition; ss;
KW immunohistological staining.

```

```

XX Synthetic.
XX
XX WO9839437-A1.
XX
XX 11-SEP-1998.
XX
XX 05-MAR-1998; 98WO-JP00905.
XX
XX 05-MAR-1997; 97JP-0050302.
XX
XX (KYOW ) KYOWA HAKKO KOGYO KK.
XX
XX Sakaki Y;
XX
XX WPI; 1998-495844/42.
XX
XX Novel apoptosis-related DNAs and proteins - for diagnosis,
XX preventing or treating diseases associated with apoptosis
XX
XX Example 1; Page 48; 70pp; Japanese.
XX
XX This is the nucleotide sequence of a PCR primer used in the method
XX of the invention, involving the use of novel apoptosis-related DNAs
XX and proteins. The inventions can be used as diagnostic reagents for
XX apoptosis e.g. (monoclonal) antibodies for the protein, as a reagent
XX in immunohistological staining, as apoptosis inhibitors. It can also
XX be used for treatment of apoptosis-related diseases.
XX
XX Sequence 18 BP; 1 A; 0 C; 1 G; 16 T; 0 other;
Query Match 1.5%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAAAAAAAAA 1098
Db 17 TAAAAAAAAAAAAA 2

RESULT 610
AAV54170/c
ID AAV54170 standard; cDNA; 18 BP.
XX
AC AAV54170;
XX
XX 21-DEC-1998 (first entry)
XX
XX Nucleotide sequence PCR primer 7.
XX
XX PCR; primer; amplification; apoptosis; antibody; inhibition; ss;
KW immunohistological staining.
XX
XX Synthetic.
XX
XX WO9839437-A1.
XX
XX 11-SEP-1998.
XX
XX 05-MAR-1998; 98WO-JP00905.
XX
XX 05-MAR-1997; 97JP-0050302.
XX
XX (KYOW ) KYOWA HAKKO KOGYO KK.
XX
XX Sakaki Y;
XX
XX WPI; 1998-495844/42.
XX
XX Novel apoptosis-related DNAs and proteins - for diagnosis,
XX preventing or treating diseases associated with apoptosis
XX
XX Example 1; Page 49; 70pp; Japanese.

```

```

XX CC This is the nucleotide sequence of a PCR primer used in the method
CC of the invention, involving the use of novel apoptosis-related DNAs
CC and proteins. The inventions can be used as diagnostic reagents for
CC apoptosis e.g. (monoclonal) antibodies for the protein, as a reagent
CC in immunohistological staining, as apoptosis inhibitors. It can also
CC be used for treatment of apoptosis-related diseases.
XX SQ Sequence 18 BP; 1 A; 0 C; 2 G; 15 T; 0 other;

Query Match 1.5%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAAAAAAAAA 1098
Db 17 TAAAAAAAAAAAAA 2

RESULT 611
AAV54173/c
ID AAV54173 standard; cDNA; 18 BP.
XX AC AAV54173;
XX DT 21-DEC-1998 (first entry)
XX DE Nucleotide sequence PCR primer 10.
XX KW PCR; primer; amplification; apoptosis; antibody; inhibition; ss;
XX KW immunohistological staining.
XX OS Synthetic.
XX PN WO9839437-A1.
XX PD 11-SEP-1998.
XX PF 05-MAR-1998; 98WO-JP00905.
XX PR 05-MAR-1997; 97JP-0050302.
XX PA (KYOW ) KYOWA HAKKO KOGYO KK.
XX PI Sakaki Y;
XX DR WPI; 1998-495844/42.
XX PT Novel apoptosis-related DNAs and proteins - for diagnosis,
XX PT preventing or treating diseases associated with apoptosis
XX PS Example 1; Page 50; 70pp; Japanese.
XX CC This is the nucleotide sequence of a PCR primer used in the method
CC of the invention, involving the use of novel apoptosis-related DNAs
CC and proteins. The inventions can be used as diagnostic reagents for
CC apoptosis e.g. (monoclonal) antibodies for the protein, as a reagent
CC in immunohistological staining, as apoptosis inhibitors. It can also
CC be used for treatment of apoptosis-related diseases.
XX SQ Sequence 18 BP; 1 A; 1 C; 1 G; 15 T; 0 other;

Query Match 1.5%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAAAAAAAAA 1098
Db 17 TAAAAAAAAAAAAA 2

RESULT 612
AAZ90640/c

```

```

ID XX AAZ90640 standard; DNA; 18 BP.
XX AC AAZ90640;
XX DT 13-JUN-2000 (first entry)
XX DE Human adipose tissue gene amplifying primer #1.
XX KW Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;
XX KW arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.
XX OS Homo sapiens.
XX PN JP2000037190-A.
XX PD 08-FEB-2000.
XX PF 23-JUL-1998; 98JP-0225228.
XX PR 23-JUL-1998; 98JP-0225228.
XX PA (NISE ) JAPAN TOBACCO INC.
XX DR WPI; 2000-306578/27.
XX PT A physiologically active protein specifically derived from mammal
XX PT tissue -
XX PS Example 2; Page 18; 50pp; Japanese.
XX CC The invention relates to identification of genes and proteins of adipose
XX CC tissue relating to obesity, particularly complications of visceral
XX CC obesity including diabetes, hyperlipemia, hypertension,
XX CC arteriosclerosis, hyperuricemia and sleep apnea syndrome. The genes
XX CC (AAZ90631-633) and the proteins (AAZ90631-633) are used in the genetic
XX CC diagnosis, prevention and treatment of adipose tissue related diseases.
XX CC Sequences AAZ90640-51 represent PCR primers amplifying the human adipose
XX CC tissue genes.
XX SQ Sequence 18 BP; 1 A; 0 C; 2 G; 15 T; 0 other;

Query Match 1.5%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAAAAAAAAA 1098
Db 17 TAAAAAAAAAAAAA 2

RESULT 613
AAZ90643/c
ID XX AAZ90643 standard; DNA; 18 BP.
XX AC AAZ90643;
XX DT 13-JUN-2000 (first entry)
XX DE Human adipose tissue gene amplifying primer #4.
XX KW Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;
XX KW arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.
XX OS Homo sapiens.
XX PN JP2000037190-A.
XX PD 08-FEB-2000.
XX PF 23-JUL-1998; 98JP-0225228.
XX PR 23-JUL-1998; 98JP-0225228.
XX XX

```

```
PA (NISB ) JAPAN TOBACCO INC.
XX WPI; 2000-306578/27.
XX A physiologically active protein specifically derived from mammal
XX tissue -
XX
XX Example 2; Page 18; 50pp; Japanese.
XX The invention relates to identification of genes and proteins of adipose
XX tissue relating to obesity, particularly complications of visceral
XX obesity including diabetes, hyperlipemia, hypertension,
XX arteriosclerosis, hyperuricemia and sleep apnea syndrome. The genes
XX (AAZ90631-633) and the proteins (AAV67598-Y67600) are used in the genetic
XX diagnosis, prevention and treatment of adipose tissue related diseases.
XX Sequences AAZ90640-51 represent PCR primers amplifying the human adipose
XX tissue genes.
XX
XX Sequence 18 BP; 1 A; 0 C; 1 G; 16 T; 0 other;
XX
XX Query Match 1.5%; Score 16; DB 1; Length 18;
XX Best Local Similarity 100.0%; Pred. No. 2.9e+02;
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1083 TAAAAA 1098
XX |||||
XX DB 17 TAAAAA 2
XX
XX RESULT 614
XX AAZ90649/C
XX ID AAZ90649 standard; DNA; 18 BP.
XX AC AAZ90649;
XX XX
XX DT 13-JUN-2000 (first entry)
XX DE Human adipose tissue gene amplifying primer #10.
XX
XX KW Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;
XX KW arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.
XX OS Homo sapiens.
XX XX
XX EN JPZ000037190-A.
XX
XX PD 08-FEB-2000.
XX XX
XX PF 23-JUL-1998; 98JP-0225228.
XX XX
XX PR 23-JUL-1998; 98JP-0225228.
XX XX
XX PA (NISB ) JAPAN TOBACCO INC.
XX XX
XX DR WPI; 2000-306578/27.
XX XX
XX PT A physiologically active protein specifically derived from mammal
XX PT tissue -
XX XX
XX PS Example 2; Page 18; 50pp; Japanese.
XX XX
XX CC The invention relates to identification of genes and proteins of adipose
XX CC tissue relating to obesity, particularly complications of visceral
XX CC obesity including diabetes, hyperlipemia, hypertension,
XX CC arteriosclerosis, hyperuricemia and sleep apnea syndrome. The genes
XX CC (AAZ90631-633) and the proteins (AAV67598-Y67600) are used in the genetic
XX CC diagnosis, prevention and treatment of adipose tissue related diseases.
XX CC Sequences AAZ90640-51 represent PCR primers amplifying the human adipose
XX CC tissue genes.
XX XX
XX SQ Sequence 18 BP; 1 A; 1 C; 1 G; 15 T; 0 other;
XX
XX Query Match 1.5%; Score 16; DB 1; Length 18;
XX Best Local Similarity 100.0%; Pred. No. 2.9e+02;
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1083 TAAAAA 1098
XX |||||
XX DB 17 TAAAAA 2
XX
XX RESULT 614
XX AAZ90649/C
XX ID AAZ90649 standard; DNA; 18 BP.
XX AC AAZ90649;
XX XX
XX DT 13-JUN-2000 (first entry)
XX DE Human adipose tissue gene amplifying primer #10.
XX
XX KW Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;
XX KW arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.
XX OS Homo sapiens.
XX XX
XX EN JPZ000037190-A.
XX
XX PD 08-FEB-2000.
XX XX
XX PF 23-JUL-1998; 98JP-0225228.
XX XX
XX PR 23-JUL-1998; 98JP-0225228.
XX XX
XX PA (NISB ) JAPAN TOBACCO INC.
XX XX
XX DR WPI; 2000-306578/27.
XX XX
XX PT A physiologically active protein specifically derived from mammal
XX PT tissue -
XX XX
XX PS Example 2; Page 18; 50pp; Japanese.
XX XX
XX CC The invention relates to identification of genes and proteins of adipose
XX CC tissue relating to obesity, particularly complications of visceral
XX CC obesity including diabetes, hyperlipemia, hypertension,
XX CC arteriosclerosis, hyperuricemia and sleep apnea syndrome. The genes
XX CC (AAZ90631-633) and the proteins (AAV67598-Y67600) are used in the genetic
XX CC diagnosis, prevention and treatment of adipose tissue related diseases.
XX CC Sequences AAZ90640-51 represent PCR primers amplifying the human adipose
XX CC tissue genes.
XX XX
XX SQ Sequence 18 BP; 1 A; 1 C; 1 G; 15 T; 0 other;
XX
XX Query Match 1.5%; Score 16; DB 1; Length 18;
XX Best Local Similarity 100.0%; Pred. No. 2.9e+02;
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1083 TAAAAA 1098
XX |||||
XX DB 17 TAAAAA 2
XX
XX RESULT 614
XX AAF75597/C
XX ID AAF75597 standard; DNA; 18 BP.
XX AC AAF75597;
XX XX
XX DT 10-MAY-2001 (first entry)
XX DE Binary encoded sequence tag method anchored primer #2.
XX
XX Query Match 1.5%; Score 16; DB 1; Length 18;
XX Best Local Similarity 100.0%; Pred. No. 2.9e+02;
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1084 AAAAAA 1099
XX |||||
XX DB 16 AAAAAA 1
XX
XX RESULT 616
XX AAF75597/C
XX ID AAF75597 standard; DNA; 18 BP.
XX AC AAF75597;
XX XX
XX DT 10-MAY-2001 (first entry)
XX DE Binary encoded sequence tag method anchored primer #2.
```



```

XX KW Binary encoded sequence tag; BEST; nucleic acid analysis;
XX KW gene expression; adaptor; PCR primer; ss.
XX OS Synthetic.
XX PN WO200112855-A2.
XX PD 22-FEB-2001.
XX PF 11-AUG-2000; 2000WO-US22164.
XX PR 13-AUG-1999; 99US-0148870.
XX PR 06-APR-2000; 2000US-0544713.
XX PA (UYUA ) UNIV YALE.
XX PI Kaufman JC, Roth ME, Lizardi PM, Feng L, Latimer DR;
XX WPI; 2001-202878/20.
XX PT Producing binary sequence tags, useful for analyzing nucleic acid
XX PT sequence tags, gene expression or gene-expression patterns, involves
XX PT generating nucleic acid fragments, which are mixed with offset adaptors
XX PT and adaptor-indexers -
XX PS Disclosure; Page 100; 101pp; English.
XX CC The present invention describes a method of producing binary sequence
XX CC tags from nucleic acid fragments in a sample, involving incubating the
XX CC sample with cleaving reagents, mixing offset adaptors with the sample,
XX CC incubating with more cleaving reagents and mixing the sample with
XX CC adaptor-indexers where the adaptors are coupled to binary sequence tags.
XX CC The method is useful in sequence analysis, including analysis and
XX CC comparison of gene expression, nucleic acid samples and genomes.
XX SQ Sequence 18 BP; 0 A; 0 C; 1 G; 17 T; 0 other;

Query Match 1.5%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1099
Db 16 AAAAAAAAAAAAAA 1

RESULT 617
ABK51158/c
ID ABK51158 standard; DNA; 18 BP.
AC ABK51158;
XX 30-JUL-2002 (first entry)
XX Human cytomegalovirus (HCMV) RT-PCR primer TXN.
XX Human cytomegalovirus; HCMV; virucide; cytomegalovirus infection; CMV;
XX cellular kinase; RICK; RIP; Nck-Interacting kinase; MKK3; SRPK-2;
XX reverse transcriptase PCR; RT-PCR; primer; ss.
XX Human cytomegalovirus.
XX OS
XX Key Location/Qualifiers
XX misc_difference 17 /*tag= a
XX FT /label= n
XX FT /note= "n= dATP, dCTP or dGTP"
XX PN EP1201765-A2.
XX PD 02-MAY-2002.
XX PT

15-OCT-2001; 2001EP-0124604.
16-OCT-2000; 2000US-240750P.
(AXXI-) AXIMA PHARM AG.
Schubart D, Habenberger P, Stein-Gerlach M, Bevec D;
WPI; 2002-373930/41.
Identifying agents for treatment or prevention of cytomegalovirus
infection, comprises contacting test compound with cellular kinase and
detecting change in cellular kinase activity -
Example 1; Page 13; 49pp; English.
The present invention relates to a new method for identifying compounds
for treating and/or preventing cytomegalovirus (CMV) infection and/or
related diseases. The method of the invention comprises contacting a
test compound with at least one of the cellular kinases RICK, RIP,
Nck-interacting kinase, MKK3 and SRPK-2 and detecting any change in
kinase activity. The method of the invention can be used to treat and/or
prevent CMV infections and related diseases. Oligonucleotides that can
detect the specified kinases can also be used for diagnosis of infection.
The present nucleic acid sequence represents human CMV reverse
transcriptase (RT)-PCR primer TXN that was used in the methods of the
invention for preparation of radioactively labelled cDNA probes.
Sequence 18 BP; 0 A; 0 C; 0 G; 16 T; 2 other;

Query Match 1.5%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1099
Db 16 AAAAAAAAAAAAAA 1

RESULT 618
ABK13935/c
ID ABK13935 standard; DNA; 18 BP.
AC ABK13935;
XX 21-MAY-2002 (first entry)
XX 5'-PCR primer used to produce single pattern characteristic by HaeII.
XX Identification of transcribed gene; mRNA profile; gene expression;
XX cellular process; fingerprinting; susceptibility to external factor;
XX development; disease; PCR; primer; ss.
XX Synthetic.
XX WO200208461-A2.
XX 31-JAN-2002.
XX 23-JUL-2001; 2001WO-IB01539.
XX 21-JUL-2000; 2000GB-0018016.
XX 21-JUL-2000; 2000US-219925P.
XX (GLOB-) GLOBAL GENOMICS AB.
XX Linnarsson S, Ernfrors P, Bauren G;
XX WPI; 2002-217065/27.
XX Providing mRNA profile, by generating two independent patterns
XX characteristic of sample mRNA population, analysing patterns, comparing
XX gene expression by cell types under varied conditions, and identifying

```

```

PT genes -
XX
PS Disclosure; Fig 1; 67pp; English.
XX
CC The present invention relates to a method for providing a profile of
CC mRNA molecules present in a sample. The method comprises generating
CC two independent patterns characteristic of the population of mRNA
CC molecules expressed in the sample and analysing the patterns using a
CC combinatorial algorithm, comparing gene expression by different or
CC same cell types under different conditions, and identifying genes
CC having a role in various cellular processes. The method is useful
CC for the analysis and identification of transcribed genes, and
CC fingerprinting. The method can be used to identify genes which play a
CC role in determining various cellular processes, including susceptibility
CC to external factors, development, and disease. The present sequence for
CC a PCR primer is used in the production of a single pattern
CC characteristic of a sample, employing a Type II restriction enzyme
CC (i.e. HaeII) in the methods of the present invention.
XX
SQ Sequence 18 BP; 0 A; 1 C; 1 G; 16 T; 0 other;

Query Match 1.5%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1099
Db 16 AAAAAAAAAAAAAA 1

RESULT 619
AADS2799/c
ID AADS2799 standard; DNA; 18 BP.
XX
AC AADS2799;
XX
DT 14-MAY-2003 (first entry)
XX
DE Primer used to prepare radioactively labelled cDNA probes from RNA.
XX
KW Human; pyridylpyrimidine derivative; cellular protein kinase; Scrapie;
KW cellular protein phosphatase; cellular signal transduction; prophylaxis;
KW prion infection; chronic wasting disease; CWD; Creutzfeldt-Jacob disease;
KW CJD; transmissible mink encephalopathy; bovine spongiform encephalopathy;
KW TSE; BSE; Gerstmann-Strausler-Scheinker syndrome; GSS; Alpers syndrome;
KW fatal familial insomnia; FFI; Kuru and Alpers syndrome, especially BSE, CJD,
KW Alzheimer's disease; primer; ss.
XX
OS Homo sapiens.
XX
FN WO200293164-A2.
XX
PD 21-NOV-2002.
XX
PF 16-MAY-2002; 2002WO-EP05420.
XX
PR 16-MAY-2001; 2001EP-0111859.
PR 29-MAY-2001; 2001US-293528P.
PR 13-JUL-2001; 2001EP-0117113.
PR 18-JUL-2001; 2001US-305898P.
XX
PA (AXXI-) AXXIMA PHARM AG.
XX
PI Stein-Gerlach M, Salassidis K, Bacher G, Mueller S;
XX
DR WPI; 2003-120714/11.
XX
CC New pyridylpyrimidine derivatives useful in the treatment or prevention
CC of infectious disease e.g. Kuru syndrome and Creutzfeldt-Jacob disease
CC (CJD) -
XX
PS Example; Page 38; 96pp; English.
XX

```

The invention relates to novel pyridylpyrimidine derivatives and methods of detecting prion infections and/or prion disease in an individual or in cells, cell cultures and/or cell lysates. The method involves adding at least one monoclonal antibody, oligonucleotide or pyridylpyrimidine derivative to the sample or in cells, cell cultures and/or cell lysates and detecting the activity of at least one human cellular protein kinases (e.g., GGF-R1 (also known as fig, Fl-1, Flt-2, B-FGFR), Tkt (also known as CCK-2, DDR-2 or EDDR; EC number 2.7.1.112), Abl (also known as c-abl), ctki, MKK7 (also known as SAPK1a, SAPKalpha), CDC2 (also known as CDK1), PRK), human cellular protein phosphatases such as ppp-SL (also known as MCP83) and ptp-zeta, the cellular signal transduction molecules HSP90 and GPR-1. The invention is useful for regulating the production of prions in cells and in the manufacture of pharmaceutical composition for prophylaxis and/or treatment of infectious disease (e.g. Scrapie, chronic wasting disease (CWD), transmissible mink encephalopathy (TME), Creutzfeldt-Jacob disease (CJD), bovine spongiform encephalopathy (BSE), variant CJD, Gerstmann-Strausler-Scheinker syndrome (GSS), fatal familial insomnia (FFI), Kuru and Alpers syndrome, especially BSE, CJD, vCJD) or neurodegenerative diseases (e.g., Alzheimer's disease) in humans or ruminants. The present DNA sequence is a primer used to prepare radioactively labelled cDNA probes from RNA. This sequence is used in the exemplification of the invention.

Sequence 18 BP; 0 A; 0 C; 0 G; 16 T; 2 other;

Query Match 1.5%; Score 16; DB 1; Length 18; Best Local Similarity 100.0%; Pred. No. 2.9e+02; Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1099
Db 16 AAAAAAAAAAAAAA 1

RESULT 620
AAS05714
ID AAS05714 standard; DNA; 20 BP.
XX
AC AAS05714;
XX
DT 07-SEP-2001 (first entry)
XX
DE Aminopurine substituted region of an RP-TFO.
XX
KW reverse phase triplex forming oligonucleotide; RP-TFO;
KW protected nucleic acid sequence; PNAS; single nucleotide polymorphism;
KW SNP; short tandem repeat; cancer; Factor V Leiden SNP; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1 /*tag= a
FT /label= "OTHER"
FT /note= "A is aminopurine substituted"
FT modified_base 3 /*tag= b
FT /label= "OTHER"
FT /note= "A is aminopurine substituted"
FT modified_base 5 /*tag= c
FT /label= "OTHER"
FT /note= "A is aminopurine substituted"
FT modified_base 7 /*tag= d
FT /label= OTHER
FT /note= "A is aminopurine substituted"
FT modified_base 9 /*tag= f
FT /label= "OTHER"
FT /note= "A is aminopurine substituted"
FT modified_base 11 /*tag= g

```
FT /label= "OTHER"  
FT /note= "A is aminopurine substituted"  
FT 13  
FT /*tag= g  
FT /label= "OTHER"  
FT /note= "A is aminopurine substituted"  
FT 15  
FT /*tag= h  
FT /label= "OTHER"  
FT /note= "A is aminopurine substituted"  
FT 16  
FT /*tag= i  
FT /label= "OTHER"  
FT /note= "A is aminopurine substituted"  
FT 17  
FT /*tag= j  
FT /label= "OTHER"  
FT /note= "Other= Hypoxanthine or Inosine"  
FT 18  
FT /*tag= k  
FT /label= "OTHER"  
FT /note= "A is aminopurine substituted"  
FT 20  
FT /*tag= l  
FT /label= "OTHER"  
FT /note= "A is aminopurine substituted"  
FT  
PN W0200132929-A1.  
XX  
XX  
XX 10-MAY-2001.  
XX  
XX 03-NOV-2000; 2000WO-US30534.  
XX  
XX 03-NOV-1999; 99US-0163356.  
PR 03-NOV-1999; 99US-0163416.  
PR 21-DEC-1999; 99US-0171348.  
PR 07-JUL-2000; 2000US-0216579.  
XX  
XX (CYGE-) CYGENE INC.  
PA (OSTE/) OSTE C C.  
XX  
XX Oste CC, Ramberg ER;  
XX WPI; 2001-343488/36.  
XX  
XX Analysing target nucleic acid sequences, useful for population  
PT genetic, drug development and diagnosing cancer, comprises hybridizing  
PT triple forming oligonucleotide and probe to target sequence -  
XX  
XX Example 2; Page 66; 14lp; English.  
XX  
XX The sequence is a second reverse phase triplex forming oligonucleotide,  
CC RP-TFO (3' to the SNP) used to analyse Factor V Leiden SNP using the  
CC method of the invention. The invention relates to analysing target  
CC nucleic acid sequences comprising restricting isolated DNA, hybridising  
CC at least one triplex forming oligonucleotide (TFO), adding a 3' to 5',  
CC exonuclease to form a protected nucleic acid sequence (PNAS) tail  
CC structure, hybridising the captured structure with a single nucleotide  
CC polymorphisms (SNP) identification probe and determining the SNP score.  
CC The methods can be used for analysing target nucleic acid sequences,  
CC especially genomic DNA sequences, to determine if they contain SNPs or  
CC short tandem repeats (STRs). The methods can be used to detect SNPs for  
CC use in population genetics, drug development, forensics, cancer, genetic  
CC disease research, genomic analysis, diagnostics and therapeutics in  
CC humans, plants and animals.  
XX  
XX Sequence 20 BP; 19 A; 0 C; 0 G; 0 U; 1 other;
```

```
Query Match 1.5%; Score 16; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.2e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1084 AAAAAAAAAAAAAA 1099
```

```
Db 1 AAAAAAAAAAAAAA 16
```

```
RESULT 621  
AAC82923/C  
ID AAC82923 standard; DNA; 20 BP.
```

```
XX AAC82923;
```

```
XX 21-MAR-2001 (first entry)
```

```
XX Human S-9 derived oligonucleotide #7.
```

```
XX Recognition system; screening; identification; pharmaceutical; toxin;  
XX plant protection agent; toxin; venom; carcinogen; venom; teratogen;  
XX herbicide; fungicide; pesticide; beta-actin; human; ss.
```

```
XX Homo sapiens.
```

```
XX DE19923966-A1.
```

```
XX 30-NOV-2000.
```

```
XX 25-MAY-1999; 99DE-1023966.
```

```
XX 25-MAY-1999; 99DE-1023966.
```

```
XX (AVET ) AVENTIS RES & TECHNOLOGIES GMBH & CO KG.
```

```
XX Boekenkamp D, Hoppe H, Burgstaller P;
```

```
XX WPI; 2001-050938/07.
```

```
XX Recognition system, e.g. for identifying nucleic acids, comprises at  
XX least one recognition unit comprising a region with a defined structure  
XX adjacent to a region with a randomized structure -  
XX Examples; Fig 1; 8pp; German.
```

```
XX This invention describes a novel recognition system comprising at least  
XX 1 recognition unit bound to a support, each recognition unit comprising a  
XX region A with a defined structure adjacent to a region B with a  
XX randomized structure. The recognition system is useful for screening,  
XX identifying, or characterizing at least 1 component of a sample,  
XX especially nucleic acids and/or proteins, and for screening for and/or  
XX identifying cellular or synthetic binding partners, preferably proteins,  
XX peptides, nucleic acids, chemical agents, preferably organic compounds,  
XX pharmaceuticals, plant protection agents, toxins, venoms, carcinogens,  
XX teratogens, herbicides, fungicides or pesticides.
```

```
XX Sequence 20 BP; 2 A; 2 C; 2 G; 14 T; 0 other;
```

```
Query Match 1.5%; Score 16; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.2e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1081 AAAAAAAAAAAAAA 1096
```

```
Db 16 AAAAAAAAAAAAAA 1
```

```
RESULT 622  
AAD33499
```

```
XX AAD33499 standard; DNA; 20 BP.
```

```
XX AAD33499;
```

```
XX 01-JUL-2002 (first entry)
```

```
XX T7T18Apad_PS27-20-0003 probe for calibration of molecular array data.
```

```
XX Molecular array; probe; ss.
```

```

XX OS Unidentified.
XX PN BP1186673-A2.
XX PD 13-MAR-2002.
XX PF 10-SEP-2001; 2001EP-0307665.
XX PR 11-SEP-2000; 2000US-0659173.
XX PA (AGIL-) AGILENT TECHNOLOGIES INC.
XX PI Wobler PK, Delenstarr GC;
XX DR WPI; 2002-282886/33.
XX PT Calibration of molecular array data by employing calibration probes
PT that generate signals proportional to total concentrations of labeled
PT target molecules, and molecular arrays incorporating sets of
XX calibration probes -
XX PS Disclosure; Page 14; 32pp; English.
XX CC The invention relates to a method for calibrating data scanned from a
XX molecular array. The method involves employing calibrations probes that
XX generate signals proportional to the total concentrations of labelled
XX target molecules to which the molecular array probes are directed over
XX an entire range of sample solutions and molecular arrays incorporating
XX sets of calibration probes. Method is useful for calibrating different
XX types of signals scanned from a molecular array, or calibrating signals
XX scanned from different molecular arrays. The present sequence is poly
XX (A) normalisation probe used in calibration of molecular array data.
XX SQ Sequence 20 BP; 16 A; 2 C; 0 G; 2 T; 0 other;

Query Match 1-5%; Score 16; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1099
Db 1 AAAAAAAAAAAAAA 16

RESULT 623
ABA05917/c
ID ABA05917 standard; DNA; 20 BP.
XX AC ABA05917;
XX DT 05-MAR-2002 (first entry)
XX DE Hepatitis B virus diagnostic PCR primer SEQ ID NO 7.
XX KW Hepatitis B virus; HBV; infection; hepatocellular carcinoma; diagnosis;
XX PCR primer; ss.
XX OS Hepatitis B virus.
XX PN EP1152063-A1.
XX PD 07-NOV-2001.
XX PF 03-MAY-2000; 2000EP-0109436.
XX PR 03-MAY-2000; 2000EP-0109436.
XX PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
XX PI Schroeder KH, Koike K;
XX DR WPI; 2002-068256/10.

XX PT Diagnosing hepatitis B virus (HBV) infection stages and determining the
XX risk for hepatocellular carcinoma, comprises identifying full length
XX HBV transcripts and truncated HBV transcripts in a serum sample -
XX PS Example 1; Page 6; 25pp; English.
XX CC The invention relates to diagnosis of hepatitis B virus (HBV) infection
XX stages comprising identification of full length HBV transcripts (I) and
XX truncated HBV transcripts (II) in a serum sample, where the ratio of
XX I:II is indicative of a particular infection stage. The method is useful
XX for diagnosing HBV infection stages and determining the risk for
XX developing hepatocellular carcinoma. The present sequence is that of a
XX HBV diagnostic PCR primer, useful for the invention.
XX SQ Sequence 20 BP; 1 A; 2 C; 1 G; 16 T; 0 other;

Query Match 1-5%; Score 16; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAAAAAAAAA 1098
Db 16 TAAAAAAAAAAAAA 1

RESULT 624
BAZ09196/c
ID AAZ09196 standard; DNA; 21 BP.
XX AC AAZ09196;
XX DT 19-OCT-1999 (first entry)
XX DE Oligonucleotide 8 for DNA analysis.
XX KW Primer; DNA analysis; amplification; hybridisation; ss.
XX OS Synthetic.
XX PN JP11196874-A.
XX PD 27-JUL-1999.
XX PF 14-JAN-1998; 98JP-0005399.
XX PR 14-JAN-1998; 98JP-0005399.
XX PA (HITA) HITACHI LTD.
XX DR WPI; 1999-496652/42.
XX PT Analysis of DNA fragment - comprises addition of known common
XX oligonucleotide, amplification of resultant DNA fragment and
XX analysis and labelling of amplified DNA
XX PS Example 1; Page 12; 17pp; Japanese.
XX CC This invention describes a novel method for the analysis of a DNA
XX fragment which comprises: (i) addition of a known common oligonucleotide
XX sequence to at least one terminal of each DNA fragment, (ii)
XX amplification of the resultant DNA fragment as a primer using a first
XX common primer containing a complementary nucleotide sequence to the above
XX mentioned known common oligonucleotide sequence, a second common primer
XX containing a complementary nucleotide sequence to the prepared known
XX common oligonucleotide sequence optionally having been introduced with
XX complementary nucleotide sequence at a terminal, and a specific primer
XX capable of hybridisation with a DNA fragment containing whole or
XX part of the gene having known sequence, to give amplified DNA, (iii)
XX analysis of the amplified DNA to find the information of the DNA
XX fragment, in which the specific primer is designed to prepare fragments
XX of the common first and second primers and to give short fragment of
XX amplified DNA and (iv) labelling them to make their differentiation.

```

CC Differentiation of informations of known and unknown genes readily
CC provides information of unknown gene and simultaneous monitoring of
CC signals derived from minor genes. Furthermore, labelling of DNAs
CC according to functions of known genes can be performed. AZ09189-209201
CC represent oligonucleotide primers used to illustrate the method
CC of the invention.
XX
SQ Sequence 21 BP; 0 A; 0 C; 3 G; 18 T; 0 other;

Query Match 1.5%; Score 16; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1099
| | | | | | | | | | | | | | | | | | | | |
DB 21 AAAAAAAAAAAAAA 6

RESULT 625
AAD33500
ID AAD33500 standard; DNA; 21 BP.
XX
AC AAD33500;
XX
DT 01-JUL-2002 (first entry)
XX
DE T7T18Apad_PS26-21-0003 probe for calibration of molecular array data.
XX
KW Molecular array; probe; ss.
XX
OS Unidentified.
XX
PN EP1186673-A2.
XX
PD 13-MAR-2002.
XX
PF 10-SEP-2001; 2001EP-0307665.
XX
PR 11-SEP-2000; 2000US-0659173.
XX
PA (AGIL-) AGILENT TECHNOLOGIES INC.
XX
PI Wohler PK, Delenstarr GC;
XX
WPI; 2002-282886/33.
XX
Calibration of molecular array data by employing calibration probes
that generate signals proportional to total concentrations of labeled
target molecules, and molecular arrays incorporating sets of
calibration probes -
XX
Disclosure; Page 14; 32pp; English.

The invention relates to a method for calibrating data scanned from a
molecular array. The method involves employing calibration probes that
generate signals proportional to the total concentrations of labeled
target molecules to which the molecular array probes are directed over
an entire range of sample solutions and molecular arrays incorporating
sets of calibration probes. Method is useful for calibrating different
types of signals scanned from a molecular array, or calibrating signals
scanned from different molecular arrays. The present sequence is poly
(A) normalisation probe used in calibration of molecular array data.
XX
SQ Sequence 21 BP; 0 A; 0 C; 3 G; 18 T; 0 other;
XX
Query Match 1.5%; Score 16; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1099
| | | | | | | | | | | | | | | | | | | | |
DB 1 AAAAAAAAAAAAAA 16

RESULT 627
AAD33500
ID AAD33500 standard; DNA; 21 BP.
XX
AC AAD33500;
XX
DT 01-JUL-2002 (first entry)
XX
DE T7T18Apad_PS25-22-0003 probe for calibration of molecular array data.
XX
KW Molecular array; probe; ss.
XX
OS Unidentified.
XX
PN EP1186673-A2.
XX
PD 13-MAR-2002.
XX
PF 10-SEP-2001; 2001EP-0307665.
XX
PR 11-SEP-2000; 2000US-0659173.
XX
PA (AGIL-) AGILENT TECHNOLOGIES INC.
XX
PI Wohler PK, Delenstarr GC;
XX
WPI; 2002-282886/33.
XX
Calibration of molecular array data by employing calibration probes
that generate signals proportional to total concentrations of labeled
target molecules, and molecular arrays incorporating sets of
calibration probes -
XX
Disclosure; Page 14; 32pp; English.

The invention relates to a method for calibrating data scanned from a
molecular array. The method involves employing calibration probes that
generate signals proportional to the total concentrations of labeled
target molecules to which the molecular array probes are directed over
an entire range of sample solutions and molecular arrays incorporating
sets of calibration probes. Method is useful for calibrating different
types of signals scanned from a molecular array, or calibrating signals
scanned from different molecular arrays. The present sequence is poly
(A) normalisation probe used in calibration of molecular array data.
XX
SQ Sequence 21 BP; 0 A; 0 C; 3 G; 18 T; 0 other;

Query Match 1.5%; Score 16; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1099
| | | | | | | | | | | | | | | | | | | | |
DB 1 AAAAAAAAAAAAAA 16

RESULT 626
AAD33501
ID AAD33501 standard; DNA; 22 BP.
XX
AC AAD33501;
XX
DT 01-JUL-2002 (first entry)
XX
DE T7T18Apad_PS25-22-0003 probe for calibration of molecular array data.
XX
KW Molecular array; probe; ss.
XX
OS Unidentified.
XX
PN EP1186673-A2.
XX
PD 13-MAR-2002.
XX
PF 10-SEP-2001; 2001EP-0307665.
XX
PR 11-SEP-2000; 2000US-0659173.
XX
PA (AGIL-) AGILENT TECHNOLOGIES INC.
XX
PI Wohler PK, Delenstarr GC;
XX
WPI; 2002-282886/33.
XX
Calibration of molecular array data by employing calibration probes
that generate signals proportional to total concentrations of labeled
target molecules, and molecular arrays incorporating sets of
calibration probes -
XX
Disclosure; Page 14; 32pp; English.

The invention relates to a method for calibrating data scanned from a
molecular array. The method involves employing calibration probes that
generate signals proportional to the total concentrations of labeled
target molecules to which the molecular array probes are directed over
an entire range of sample solutions and molecular arrays incorporating
sets of calibration probes. Method is useful for calibrating different
types of signals scanned from a molecular array, or calibrating signals
scanned from different molecular arrays. The present sequence is poly
(A) normalisation probe used in calibration of molecular array data.
XX
SQ Sequence 22 BP; 16 A; 4 C; 0 G; 2 T; 0 other;
XX
Query Match 1.5%; Score 16; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1099
| | | | | | | | | | | | | | | | | | | | |
DB 1 AAAAAAAAAAAAAA 16

RESULT 627
AAD33501
ID AAD33501 standard; DNA; 19 BP.
XX
AC AAD33501;
XX
DT 02-DEC-1996 (first entry)
XX
DE Primer for tyrosinase gene fragment.
XX
KW p53; mutant; mutation; cleavage; nuclease; cleavase; Theirmus;
XX
KW Escherichia; Saccharomyces; Campylobacter; Mycobacterium; Shigella;
XX
OS Staphylococcus; identification; detection; ss.
XX
Synthetic.

PN WO9615267-A1.
 PD 23-MAY-1996.
 XX
 XX
 PF 09-NOV-1995; 95WO-US14673.
 XX
 PR 30-AUG-1995; 95US-0520945.
 PR 09-NOV-1994; 94US-0337164.
 PR 09-MAR-1995; 95US-0402601.
 PR 07-JUN-1995; 95US-0484956.
 XX
 XX
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
 XX
 XX
 PI Brow MAD, Dahlberg JE, Fors L, Heisler LM, Lyamichev VI;
 PI Oldenburg MC, Olive DM;
 XX
 XX
 DR WPI; 1996-259862/26.
 XX
 XX
 PT Cleavage of nucleic acids to detect mutation(s) - allows detection
 PT esp. in human p53 gene, to identify strains of microorganisms and
 PT viruses
 XX
 PS Example 10; Page 119; 433pp; English.
 XX
 CC Cleavage of nucleic acids using an enzyme, especially a nuclease
 CC selected from the group consisting of Cleavase (RTM) BN enzyme,
 CC Thermus aquaticus DNA polymerase, Thermus thermophilus DNA
 CC polymerase, Escherichia coli ExoIII and the Saccharomyces cerevisiae
 CC Radi/Rad10 complex. The nucleic acid substrate is preferably an
 CC oligonucleotide containing a human p53 gene sequence or
 CC alternatively, microbial gene sequences. Cleavage products are
 CC compared to the cleavage products of reference gene sequences. The
 CC method is used for detecting mutation in the human p53 gene; for
 CC identifying strains of microorganisms, especially bacteria selected
 CC from the group of members of the genera Campylobacter,
 CC Escherichia, Mycobacterium, Salmonella, Shigella and Staphylococcus.
 CC The method may also be used for the identification of viruses,
 CC especially hepatitis C virus and simian immunodeficiency virus. The
 CC human tyrosinase gene (both wild type and mutant gene fragments) was
 CC used as a test sequence for the method. Three primers (AAT29080-82)
 CC were used alongside other primers (AAT27699-90) and in combination, to
 CC amplify fragments of wild type and mutant tyrosinase genes.
 XX
 XX
 SQ Sequence 19 BP; 3 A; 2 C; 7 G; 7 T; 0 other;
 Query Match 1.4%; Score 15.8; DB 1; Length 19;
 Best Local Similarity 89.5%; Pred. No. 3.3e+02;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 510 GCACGTTTGGCATTTGGGA 528
 Db |||||||
 1 GCAAGTTTGGCTTTGGGA 19
 RESULT 628
 AAV01125/c
 ID AAV01125 standard; DNA; 19 BP.
 XX
 XX
 AC AAV01125;
 XX
 XX
 DT 23-MAR-1998 (first entry)
 XX
 DE Elastin PCR primer for universal mammalian STS's.
 XX
 KW PCR primer; polymerase chain reaction; amplification; UM-STS;
 KW universal mammalian sequence tagged site; genomic map; clone; ss.
 XX
 OS Synthetic.
 XX
 XX
 PN WO9731012-A1.
 XX
 PD 28-AUG-1997.
 XX

PF 18-FEB-1997; 97WO-US02403.
 XX
 PR 22-FEB-1996; 96US-0012061.
 XX
 PA (UNMI) UNIV MICHIGAN.
 PA (UNMS) UNIV MICHIGAN STATE.
 XX
 PI Brewer GJ, Venta PJ, Yuzbasiyan-Gurkan V;
 XX
 DR WPI; 1997-435083/40.
 XX
 XX
 PT New oligonucleotide primers amplifying gene regions conserved among
 PT mammals - useful for developing genomic maps, isolating clones and
 PT making cross-species comparisons
 XX
 PS Claim 1; Page 9; 26pp; English.
 XX
 CC The present sequence represents a specifically claimed oligonucleotide
 CC PCR primer. The oligonucleotide can be used for polymerase chain
 CC reaction (PCR) amplification of DNA, specifically regions of specific
 CC genes that are conserved among mammalian species, i.e. pairs of
 CC oligonucleotides from the present specification represent universal
 CC mammalian sequence-tagged site (UM-STs) primers. The primers are used
 CC to develop genomic maps, to isolate clones from libraries, to make
 CC cross-species comparisons and to develop additional genetic markers.
 CC UM-STs allow genomic comparisons to be made between more species.
 XX
 SQ Sequence 19 BP; 5 A; 6 C; 6 G; 2 T; 0 other;
 Query Match 1.4%; Score 15.8; DB 1; Length 19;
 Best Local Similarity 89.5%; Pred. No. 3.3e+02;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 136 CTGCTTTGGGGCTGCAGC 154
 Db |||||||
 19 CTGCTTTAGCGCTGCAGC 1
 RESULT 629
 ABTL3587/c
 ID ABTL3587 standard; DNA; 19 BP.
 XX
 AC ABTL3587;
 XX
 DT 07-FEB-2003 (first entry)
 XX
 DE Liver regeneration-related gene panel PCR primer #115.
 XX
 KW PCR; primer; ss; liver regeneration; gene panel; expression profile;
 KW drug screening; drug development; hepatitis; liver transplantation.
 XX
 OS Unidentified.
 XX
 PN WO200277222-A1.
 XX
 PD 03-OCT-2002.
 XX
 PF 13-MAR-2002; 2002WO-JP02372.
 XX
 PR 13-MAR-2001; 2001JP-0070940.
 XX
 PA (AJIN) AJINOMOTO CO INC.
 XX
 PI Yokoya F, Okutsu T, Mori M, Takahara Y, Fukuda H, Aburatani H;
 PI Sonaka I;
 XX
 DR WPI; 2003-018922/01.
 XX
 XX
 PT Gene panel participating in liver regeneration, applicable in providing
 PT expression data, diagnosis and development of drugs for promoting liver
 PT regeneration e.g. after transplantation or removal of liver during
 PT cancer -
 XX

KW SNP; short tandem repeat; cancer; Factor V Leiden SNP; ss.
 XX Synthetic.
 OS WO200132929-A1.
 PN 10-MAY-2001.
 PD 03-NOV-2000; 2000WO-US30534.
 XX 03-NOV-1999; 99US-0163356.
 XX 03-NOV-1999; 99US-0163416.
 PR 21-DEC-1999; 99US-0171348.
 PR 07-JUL-2000; 2000US-0216579.
 XX (CYGE-) CYGENE INC.
 PA (OSTE/) OSTE C C.
 PA Oste CC, Ramberg ER;
 XX WPI; 2001-343488/36.
 DR Analysing target nucleic acid sequences, useful for population
 PT genetics, drug development and diagnosing cancer, comprises hybridizing
 PT triple forming oligonucleotide and probe to target sequence -
 XX Example 2; Page 66; 141pp; English.
 XX The sequence is a polypyrimidine oligonucleotide for binding a second
 CC reverse phase triplex forming oligonucleotide, pp-TFO, (3' to the SNP) to
 CC the target SNP used to analyse Factor V Leiden SNP using the
 CC method of the invention. The invention relates to analysing target
 CC nucleic acid sequences comprising restricting isolated DNA, hybridising
 CC at least one triplex forming oligonucleotide (TFO), adding a 3' to 5',
 CC exonuclease to form a protected nucleic acid sequence (pNAs) tail
 CC structure, hybridising the captured structure with a single nucleotide
 CC polymorphisms (SNP) identification probe and determining the SNP score.
 CC The methods can be used for analysing target nucleic acid sequences,
 CC especially genomic DNA sequences, to determine if they contain SNPs or
 CC short tandem repeats (STRs). The methods can be used to detect SNPs for
 CC use in population genetics, drug development, forensics, cancer, genetic
 CC disease research, genomic analysis, diagnostics and therapeutics in
 CC humans, plants and animals.
 XX Sequence 20 BP; 1 A; 1 C; 0 G; 18 T; 0 other;
 SQ Query Match 1.4%; Score 15.8; DB 1; Length 20;
 Best Local Similarity 89.5%; Pred. No. 3.5e+02;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 1081 ATTAAAAAATAAAAAAAAAA 1099
 DB 19 AATAAGAAAAAATAAAAAA 1
 RESULT 633
 AAT48469/c
 ID AAT48469 standard; DNA; 21 BP.
 XX AAT48469;
 AC AAT48469;
 DT 12-APR-1997 (first entry)
 XX Human polymorphic region 821.
 DE Polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH;
 XX cell viability; loss of heterozygosity; precancerous condition; AS1;
 KW allele specific inhibitor; somatic cell; diagnosis; prevention;
 KW atherosclerotic plaque; premalignant metaplastic lesion; endometriosis;
 KW dysplastic lesion; benign tumour; polycystic kidney disease; transplant;
 KW graft versus host disease; malignant cell removal; bone marrow; ss.
 OS Homo sapiens.
 XX WO9841648-A2.
 PN 24-SEP-1998.
 PD 19-MAR-1998; 98WO-US05419.
 XX 20-MAR-1997; 97US-0041057.
 PR (VARI-) VARIAGENICS INC.
 PA

FT /*tag= a
 FT /note= "psoralen attachment site"
 XX WO9640271-A1.
 PN 19-DEC-1996.
 PD 06-JUN-1996; 96WO-US09430.
 XX 07-JUN-1995; 95US-0473845.
 PR (UYXA) UNIV YALE.
 PA Glazer PM;
 PI WPI; 1997-099895/09.
 DR Repairing mutation(s) in haemoglobin by targetted mutagenesis or
 XX homologous recombination - mediated by a triplex forming
 PT oligonucleotide, opt. carrying a mutagen, partic. for treatment of
 PT sickle cell anaemia or thalassemia
 XX Claim 35; Page 47; 70pp; English.
 PS Third-strand oligonucleotides (AAT48467-70) bind to a purine-rich
 CC region (see also AAT48455) located at position 2655 in the beta-globin
 CC gene (see also AAT48454). They can be utilised in a targetted DNA
 CC replacement (TDR) method to correct a mutation that leads to sickle
 CC cell anaemia. In TDR, a third-strand oligonucleotide is targetted
 CC to a binding region in the gene, where it induces DNA damage. This
 CC stimulates homologous recombination with an introduced donor nucleic
 CC acid strand. TDR is highly specific and, since the corrected gene
 CC is in its native chromosome, the cure is permanent.
 XX Sequence 21 BP; 0 A; 7 C; 0 G; 14 T; 0 other;
 SQ Query Match 1.4%; Score 15.8; DB 1; Length 21;
 Best Local Similarity 89.5%; Pred. No. 3.6e+02;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 114 AGAAACGGGAGAAAGGA 132
 DB 19 AGAAAGGGGAGAAAGGA 1
 RESULT 634
 AAZ26632
 ID AAZ26632 standard; DNA; 21 BP.
 XX AAZ26632;
 AC AAZ26632;
 DT 30-NOV-1999 (first entry)
 XX Human polymorphic region 821.
 DE Polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH;
 XX cell viability; loss of heterozygosity; precancerous condition; AS1;
 KW allele specific inhibitor; somatic cell; diagnosis; prevention;
 KW atherosclerotic plaque; premalignant metaplastic lesion; endometriosis;
 KW dysplastic lesion; benign tumour; polycystic kidney disease; transplant;
 KW graft versus host disease; malignant cell removal; bone marrow; ss.
 OS Homo sapiens.
 XX WO9841648-A2.
 PN 24-SEP-1998.
 PD 19-MAR-1998; 98WO-US05419.
 XX 20-MAR-1997; 97US-0041057.
 PR (VARI-) VARIAGENICS INC.
 PA


```

XX
PI Houseman D, Ledley FD, Stanton VP;
XX WPI; 1998-521232/44.
XX
XX Identifying target genes for allele-specific drugs - used for
PT diagnosis, prevention and treatment of, e.g. cancers, atherosclerotic
PT plaque, dysplastic lesions, endometriosis or graft versus host disease
XX
XX Disclosure; Figure 7; 605pp; English.
XX
XX This invention describes a novel method for identifying an inhibitor
CC potentially useful for treatment of cancer, where the inhibitor is
CC active on a gene vital for cell growth or viability, and where the gene
CC is subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is
CC used for preventing the development of cancer in a patient having a
CC precancerous condition, by administering to an allele of a first allele
CC specific inhibitor (ASI) targeted to an allele of a first essential gene
CC present in cells of the precancerous condition, where the normal somatic
CC cells of the patient are heterozygous for the first gene, the inhibitor
CC is active on at least one but less than all allelic forms of the gene
CC present in a population and targets only one allelic form present in the
CC normal somatic cells, and the first gene. The products and methods can
CC be used in the diagnosis, prevention and treatment of LOH disorders,
CC e.g. cancers, atherosclerotic plaques, premalignant metaplastic or
CC dysplastic lesions, benign tumours, endometriosis, polycystic kidney
CC disease, and graft versus host disease. The method can also be used to
CC remove malignant cells from bone marrow transplants. AAZ25812-226825
CC represent human polymorphic sites described in the method of the
CC invention.
XX
XX Sequence 21 BP; 15 A; 2 C; 1 G; 3 T; 0 other;
SQ
Query Match 1.4%; Score 15.8; DB 1; Length 21;
Best Local Similarity 89.5%; Pred. NO. 3.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1081 ATTAAAAAATAAAAAA 1099
DB 3 ATTAACATAAAAAA 21
RESULT 635
AAAX14729/c
ID AAAX14729 standard; DNA; 21 BP.
AC AAAX14729;
XX
XX 24-MAR-1999 (first entry)
XX
XX Triple helix third strand of Beta-globin gene nucleotides 742-762.
XX
XX Triplex formation; DNA detection; triple helix; identification;
XX bacteria; oncogene; virus; ss.
XX
XX Synthetic.
XX Homo sapiens.
XX
XX US5861244-A.
XX
XX 19-JAN-1999.
XX
XX 22-DEC-1993; 93US-0173489.
XX
XX 22-DEC-1993; 93US-0173489.
XX 29-OCT-1992; 92US-0968436.
XX
XX (PROF-) PROFILE DIAGNOSTIC SCI INC.
XX
XX Hepburn AG, Wang C;
XX
XX WPI; 1999-130384/11.
XX
XX
XX Assay of genetic sequences based on triplex formation from double
PT stranded analyte - and hybrid of anchor and reporter sequences, with
PT reporter released if triplex formation occurs, used e.g. to identify
PT bacteria
XX
XX Disclosure; Columns 17-18; 168pp; English.
XX
XX The present sequence represents a polynucleotide that is able to
CC form a triple helix with a double stranded sequence. Cytosine bases
CC in the present can be replaced with 5-methylcytosine for increased
CC triplex stability. The present sequence is used in the assay of the
CC invention, where it can be part of the anchor DNA or reporter DNA
CC sequence. The assay comprises adding a sample containing double-stranded
CC DNA test sequences to an aqueous medium containing at least one complex
CC of anchor DNA, attached to a solid support, and reporter DNA, where
CC either a part of the anchor DNA or reporter DNA is designed to form
CC a triple-strand structure with part of the test sequence. Triplex
CC formation results in displacement of the reporter DNA which is
CC detected as an indication of the presence of the DNA test sequence.
CC The method is used to detect DNA sequences, particularly for
CC identification of bacteria (by detecting genes for ribosomal RNA) in
CC clinical samples, but also detection of oncogenes and Hepatitis B virus.
XX
XX Sequence 21 BP; 0 A; 7 C; 0 G; 14 T; 0 other;
SQ
Query Match 1.4%; Score 15.8; DB 1; Length 21;
Best Local Similarity 89.5%; Pred. NO. 3.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 114 AAGAAACGGGAAGGA 132
DB 19 AAGAAACGGGAAGGA 1
RESULT 636
AAAZ27844/c
ID AAZ27844 standard; DNA; 22 BP.
XX
XX AAZ27844;
XX
XX 23-DEC-1999 (first entry)
XX
XX PCR primer for human DNA marker clone S103.
XX
XX Tandem repeat sequence; DNA isolation; intermediate tandem repeat;
XX ITR sequence; pentanucleotide tandem repeat; stutter artifact;
XX DNA typing; DNA profiling; linkage analysis; criminal justice;
XX paternity testing; animal lineage analysis; microsatellite loci;
XX polymorphism detection; PCR primer; ss.
XX
XX Synthetic.
XX OS
XX Homo sapiens.
XX
XX WO9940194-A1.
XX
XX 12-AUG-1999.
XX
XX 04-FEB-1999; 99WO-US02345.
XX
XX 04-FEB-1998; 98US-0018584.
XX
XX (PROM-) PROMEGA CORP.
XX
XX Schumm JW, Bacher JW;
XX
XX WPI; 1999-590696/50.
XX
XX Isolating DNA containing intermediate tandem repeat sequences, useful
PT in DNA profiling
XX
XX Claim 30; Page 22; 111pp; English.
XX
XX This sequence is a PCR primer for a human DNA marker clone used in the
XX

```

method of the invention. The method is for isolating a fragment of DNA containing an intermediate tandem repeat (ITR) sequence using hybridization selection, and comprises: (a) providing several DNA fragments, at least one of which contains an ITR sequence, a region of the DNA fragment which contains at least one repeat unit consisting of a sequence of five, six or seven bases repeated in tandem at least two times; (b) providing a stationary support having at least one oligonucleotide associated with it, where the oligonucleotide includes a sequence of nucleotides which is complementary to a portion of the ITR sequence; and (c) combining the DNA fragments with the support under conditions where the DNA fragments including the DNA fragment containing the ITR sequence hybridize to the support. The method is particularly used to isolate DNA containing pentanucleotide tandem repeat sequences as well as to detect target ITR DNA sequences having a low incidence of stutter artifacts (no more than 2.4%). The method is useful in DNA profiling for linkage analysis, criminal justice, paternity testing and other forensic and medical uses. DNA typing is also useful for confirming the lineage of horses, dogs and other prize animals. The invention overcomes problems related to the use of microsatellite loci in DNA profiling. The method can detect polymorphisms with a low incidence of stutter artifacts, which has previously been a problem in interpreting allelic content of loci. The development of markers based on larger repeat units, enables easier separation of the fragments on larger electrophoretic gels. This allows the simultaneous analysis of more loci.

Sequence 22 BP; 2 A; 12 C; 2 G; 6 T; 0 other;

Query Match 1.4%; Score 15.8; DB 1; Length 22;
Best Local Similarity 89.5%; Pred. No. 3.8e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1001 GAGGCTGGAGATGGGAAG 1019

DB 20 GAGGCTGGGGAATGGCAG 2

RESULT 637

AA563416
ID AA563416 standard; DNA; 22 BP.

AC AA563416;

DT 29-JAN-2002 (first entry)

DE Oligonucleotide-nanoparticle probe #40.

KW Oligonucleotide-nanoparticle probe; diagnostic; forensic analysis;
KW nucleic acid detection; nanostructure; biochip; biofilter;
KW drug delivery; ss.

OS Synthetic.

PN WO200173123-A2.

PD 04-OCT-2001.

PF 28-MAR-2001; 2001WO-US10071.

PR 28-MAR-2000; 2000US-192699P.

PR 26-APR-2000; 2000US-200161P.

PR 26-JUN-2000; 2000US-213906P.

PR 26-JUN-2000; 2000US-0603830.

PR 08-DEC-2000; 2000US-254392P.

PR 11-DEC-2000; 2000US-255235P.

PR 12-JAN-2001; 2001US-0760500.

PR 28-MAR-2001; 2001US-0820279.

PA (NANO-) NANOSPHERE INC.

PI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;

PI Taton TA, Park S, Li Z;

XX WPI; 2001-656926/75.

XX

PT Detecting and separating nucleic acid, useful e.g. for diagnosis,
PT comprises reaction with nanoparticles that carry oligonucleotides
PT complementary to parts of the target

PS Example 16; Page 139; 404pp; English.

XX The invention relates to a method for detection of nucleic acid (I)
CC having at least 2 portions, comprising treatment with nanoparticles that
CC carry oligonucleotides complementary to at least 2 parts of (I), where
CC detectable change caused by hybridisation of the oligonucleotide to (I)
CC is observed. The method is used to detect (or to separate) specific (I),
CC e.g. for diagnosing a wide variety of diseases, sequencing, in forensic
CC analysis etc., and generally to detect analytes other than (I). The
CC oligonucleotide-derivatised nanoparticles are also useful for preparing
CC nanostructures useful, for example, as biochips, biofilters, mechanical
CC devices, separation membranes, chemical sensors, in computers, and for
CC drug delivery. Very stable nanoparticle-oligonucleotide conjugates
CC can be produced, allowing their direct use (as probes) in polymerase
CC chain reaction, i.e. they survive multiple heating/cooling cycles so do
CC not need to be added after amplification. (I) are detected by simple
CC colour change, without the need for special equipment, making possible
CC rapid field testing for e.g. pathogens. AA563374-AA563448 represent
CC oligonucleotide-nanoparticle probes, and related sequences, used in the
CC method of the invention.

Sequence 22 BP; 13 A; 4 C; 1 G; 4 T; 0 other;

Query Match 1.4%; Score 15.8; DB 1; Length 22;
Best Local Similarity 89.5%; Pred. No. 3.8e+02;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1076 CAACCTATTAAAAA 1094

DB 4 CAACCTCGTAAAAA 22

RESULT 638

AA563419

ID AA563419 standard; DNA; 22 BP.

AC AA563419;

DT 29-JAN-2002 (first entry)

DE Oligonucleotide-nanoparticle probe #43.

KW Oligonucleotide-nanoparticle probe; diagnostic; forensic analysis;
KW nucleic acid detection; nanostructure; biochip; biofilter;
KW drug delivery; ss.

OS Synthetic.

PN WO200173123-A2.

PD 04-OCT-2001.

PF 28-MAR-2001; 2001WO-US10071.

PR 28-MAR-2000; 2000US-192699P.

PR 26-APR-2000; 2000US-200161P.

PR 26-JUN-2000; 2000US-213906P.

PR 26-JUN-2000; 2000US-0603830.

PR 08-DEC-2000; 2000US-254392P.

PR 11-DEC-2000; 2000US-255235P.

PR 12-JAN-2001; 2001US-0760500.

PR 28-MAR-2001; 2001US-0820279.

PA (NANO-) NANOSPHERE INC.

PI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;

PI Taton TA, Park S, Li Z;

XX

```

DR WPI; 2001-656926/75.
XX Detecting and separating nucleic acid, useful e.g. for diagnosis,
PT comprises reaction with nanoparticles that carry oligonucleotides
XX complementary to parts of the target
XX Example 17; Figure 26B; 404pp; English.
XX
CC The invention relates to a method for detection of nucleic acid (I)
CC having at least 2 portions, comprising treatment with nanoparticles that
CC carry oligonucleotides complementary to at least 2 parts of (I), where
CC detectable change caused by hybridisation of the oligonucleotide to (I)
CC is observed. The method is used to detect (or to separate) specific (I),
CC e.g. for diagnosing a wide variety of diseases, sequencing, in forensic
CC analysis etc., and generally to detect analytes other than (I). The
CC oligonucleotide-derived nanoparticles are also useful for preparing
CC nanostructures useful, for example, as biochips, biofilters, mechanical
CC devices, separation membranes, chemical sensors, in computers, and for
CC drug delivery. Very stable nanoparticle-oligonucleotide conjugates
CC can be produced, allowing their direct use (as probes) in polymerase
CC chain reaction, i.e. they survive multiple heating/cooling cycles so do
CC not need to be added after amplification. (I) are detected by simple
CC colour change, without the need for special equipment, making possible
CC rapid field testing for e.g. pathogens. AAS63374-AAS63448 represent
CC oligonucleotide-nanoparticle probes, and related sequences, used in the
XX method of the invention.
XX
SQ Sequence 22 BP; 13 A; 4 C; 1 G; 4 T; 0 other;
Query Match 1.4%; Score 15.8; DB 1; Length 22;
Best Local Similarity 89.5%; Pred. No. 3.8e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1076 CAACTATTAAAAA 1094
DB 4 CAACTCGTAAAAA 22
RESULT 639
AAS10359
ID AAS10359 standard; DNA; 22 BP.
XX
AC AAS10359;
XX
AC AAS10359;
XX
DT 24-OCT-2001 (first entry)
XX
DE Oligonucleotide-gold conjugate, capture oligonucleotide.
XX
KW Nanoparticle; oligonucleotide; DNA detection; DNA isolation;
KW genetic disease; bacterial disease; viral disease; forensic science;
KW paternity testing; gene therapy; ss.
XX
OS Synthetic.
XX
XX Key Location/Qualifiers
FH misc_binding 11..22
FT /tag= a
FT /bound_moiety= "Nucleotides 12-1 of the sequence
FT appearing as AAS010360"
FT misc_feature 22
FT /tag= b
FT /note= "C is covalently linked to a colloidal gold
FT particle via a HS(CH2)3 moiety"
XX
PN WO200151665-A2.
XX
PD 19-JUL-2001.
XX
PF 12-JAN-2001; 2001WO-US011190.
XX
PR 13-JAN-2000; 2000US-0176409.
PR 26-APR-2000; 2000US-0200161.
PR 26-JUN-2000; 2000US-0603830.

```

```

PR 12-JAN-2001; 2001US-0760500.
XX (NANO-) NANOSPHERE INC.
XX
PI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JU, Elghanian R;
PI Taton TA, Li Z;
XX
DR WPI; 2001-451868/48.
XX
XX Detecting a nucleic acid useful in e.g. diagnosing genetic, bacterial
XX or viral diseases, by contacting the nucleic acid with oligonucleotides
XX attached to nanoparticles and having sequences complementary a portion
XX of the nucleic acid
XX Example 16; Page 110; 323pp; English.
XX
CC The sequence represents an oligonucleotide which is linked by its 3' end
CC to a nanoparticle. The sequence is complementary to a target
CC oligonucleotide. The nanoparticle may be linked to several
CC oligonucleotides. The sequence is used to demonstrate the method of the
CC invention. The invention relates to isolating or detecting a nucleic acid
CC of interest, in a mixture of nucleic acids, by binding it to 2 or more
CC complementary nucleotides which have a nanoparticle attached to their 5'
CC ends. The nanoparticles (e.g. colloidal gold) are used to both isolate
CC and detect (e.g. by linking the particle to a fluorescent probe) the
CC resultant complex. The methods are useful for detecting nucleic acids, be
CC natural or synthetic, and modified or unmodified. The methods may also be
CC applied in the diagnosis of genetic, bacterial and viral diseases, in
CC forensics, in DNA sequencing, for paternity testing, for cell line
CC authentication, and for monitoring gene therapy. The methods are
CC further useful in research and analytical laboratories in DNA
CC sequencing, in the field to detect the presence of specific pathogens,
CC for quick identification of an infection to assist in drug
CC prescription, and in homes and health centres for inexpensive
CC first-line screening. The methods, which are based on observing
CC colour change with the naked eye, are cheap, fast, simple, robust
CC (reagents are stable), do not require specialised or expensive equipment,
CC and little or no instrumentation is required.
XX
SQ Sequence 22 BP; 13 A; 4 C; 1 G; 4 T; 0 other;
Query Match 1.4%; Score 15.8; DB 1; Length 22;
Best Local Similarity 89.5%; Pred. No. 3.8e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1076 CAACTATTAAAAA 1094
DB 4 CAACTCGTAAAAA 22
RESULT 640
AAS10362
ID AAS10362 standard; DNA; 22 BP.
XX
AC AAS10362;
XX
AC AAS10362;
XX
DT 24-OCT-2001 (first entry)
XX
DE Oligonucleotide-gold conjugate, capture oligonucleotide #2.
XX
KW Nanoparticle; oligonucleotide; DNA detection; DNA isolation;
KW genetic disease; bacterial disease; viral disease; forensic science;
KW paternity testing; gene therapy; ss.
XX
OS Synthetic.
XX
XX Key Location/Qualifiers
FH misc_binding 11..22
FT /tag= a
FT /bound_moiety= "Nucleotides 12-1 of the sequence
FT appearing as AAS010364"
FT misc_feature 22
FT /tag= b

```

FT /note= "A is covalently linked to a colloidal gold
XX particle"
PN WO200151665-A2.
XX
PD 19-JUL-2001.
XX
PF 12-JAN-2001; 2001WO-US01190.
XX
PR 13-JAN-2000; 2000US-0176409.
XX
PR 26-APR-2000; 2000US-0200161.
XX
PR 26-JUN-2000; 2000US-0603830.
XX
PR 12-JAN-2001; 2001US-0760500.
XX
PA (NANO-) NANOSPHERE INC.
XX
XX Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;
PI Taton TA, Li Z;
XX
XX WPI; 2001-451868/48.
XX
XX Detecting a nucleic acid useful in e.g. diagnosing genetic, bacterial
PT or viral diseases, by contacting the nucleic acid with oligonucleotides
PT attached to nanoparticles and having sequences complementary a portion
PT of the nucleic acid -
XX
XX Example 17; Fig 23; 323pp; English.
XX
XX The sequence represents an oligonucleotide which is linked by its 3' end
CC to a nanoparticle. The sequence is complementary to a target
CC oligonucleotide. The nanoparticle may be linked to several
CC oligonucleotides. The sequence is used to demonstrate the method of the
CC invention. The invention relates to isolating or detecting a nucleic acid
CC of interest, in a mixture of nucleic acids, by binding it to 2 or more
CC complementary nucleotides which have a nanoparticle attached to their 5'
CC ends. The nanoparticles (e.g. colloidal gold) are used to both isolate
CC and detect (e.g. by linking the particle to a fluorescent probe) the
CC resultant complex. The methods are useful for detecting nucleic acids,
CC natural or synthetic, and modified or unmodified. The methods may also be
CC applied in the diagnosis of genetic, bacterial and viral diseases, in
CC forensics, in DNA sequencing, for paternity testing, for cell line
CC authentication, and for monitoring gene therapy. The methods are
CC further useful in research and analytical laboratories in DNA
CC sequencing, in the field to detect the presence of specific pathogens,
CC for quick identification of an infection to assist in drug
CC prescription, and in homes and health centres for inexpensive
CC first-line screening. The methods, which are based on observing
CC colour change with the naked eye, are cheap, fast, simple, robust
CC (reagents are stable), do not require specialised or expensive equipment,
CC and little or no instrumentation is required.
XX
SQ Sequence 22 BP; 13 A; 4 C; 1 G; 4 T; 0 other;
Query Match 1.4%; Score 15.8; DB 1; Length 22;
Best Local Similarity 89.5%; Pred. No. 3.8e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1076 CAACTATTAAAAA 1094
DB |||||
4 CAACTCGTAAAAA 22
RESULT 641
AAF28471
ID AAF28471 standard; DNA; 22 BP.
XX
XX AAF28471;
XX
XX
DT 03-APR-2001 (first entry)
XX
XX Random oligonucleotide, SEQ ID NO: 43.
DE
XX Nucleic acid detection; nanoparticle-oligonucleotide conjugate;
KW

KW disease diagnosis; forensic analysis; DNA sequencing; paternity testing;
XX cell line authentication; gene therapy; ss.
OS Synthetic.
XX
XX WO200100876-A1.
XX
XX PD 04-JAN-2001.
XX
XX 26-JUN-2000; 2000WO-US17507.
XX
XX 25-JUN-1999; 99US-0344667.
XX
XX 26-APR-2000; 2000US-0200161.
XX
XX (MIRK/) MIRKIN C A.
PA (LETS/) LETSINGER R L.
PA (MUCI/) MUCIC R C.
PA (STOR/) STORHOFF J J.
PA (ELGH/) ELGHANIAN R.
PA (TATO/) TATON T A.
XX
XX Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;
PI Taton TA;
XX
XX WPI; 2001-061976/07.
XX
XX Detecting nucleic acid, useful for e.g. diagnosis of diseases,
PT forensics and DNA sequencing, comprises observing detectable change
PT brought about by hybridization of nucleic acid with substrate or
PT particle bound oligonucleotides -
XX
XX Example 16; Page 85; 205pp; English.
XX
XX The present sequence is an oligonucleotide used in a method for detecting
CC a nucleic acid having at least 2 portions. The method comprises
CC hybridising the nucleic acid with oligonucleotides, such as the present
CC sequence, attached to a substrate and/or particle and detecting a change
CC in colour, conductivity or optical density. The method is useful for the
CC diagnosis and/or monitoring of diseases in forensics, in DNA sequencing,
CC for paternity testing, for cell line authentication and for monitoring
CC gene therapy. Detecting nucleic acids based upon observing a colour
CC change is cheap, fast, simple, and does not require specialised or
CC expensive equipment. The nanoparticle oligonucleotide conjugates remain
CC stable for at least 6 months. A single base mismatch and as little as 20
CC femtomoles (fm) of target can be detected using the conjugates.
XX
SQ Sequence 22 BP; 13 A; 4 C; 1 G; 4 T; 0 other;
Query Match 1.4%; Score 15.8; DB 1; Length 22;
Best Local Similarity 89.5%; Pred. No. 3.8e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1076 CAACTATTAAAAA 1094
DB |||||
4 CAACTCGTAAAAA 22
RESULT 642
AAF28474
ID AAF28474 standard; DNA; 22 BP.
XX
XX AAF28474;
XX
XX 03-APR-2001 (first entry)
XX
XX Random oligonucleotide, SEQ ID NO: 46.
DE
XX Nucleic acid detection; nanoparticle-oligonucleotide conjugate;
KW disease diagnosis; forensic analysis; DNA sequencing; paternity testing;
XX cell line authentication; gene therapy; ss.
OS Synthetic.
XX

```

PN WO200100876-A1.
XX
PD 04-JAN-2001.
XX
PF 26-JUN-2000; 2000WO-US17507.
XX
PR 25-JUN-1999; 99US-0344667.
XX
PR 26-APR-2000; 2000US-0200161.
XX
PA (MIRK/) MIRKIN C A.
PA (LETS/) LETSINGER R L.
PA (MUCI/) MUCIC R C.
PA (STOR/) STORHOFF J J.
PA (ELGH/) ELGHANIAN R.
PA (TATON/) TATON T A.
XX
PI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;
PI Taton TA;
XX
XX WPI; 2001-061976/07.
XX
XX Detecting nucleic acid, useful for e.g. diagnosis of diseases,
XX forensics and DNA sequencing, comprises observing detectable change
XX brought about by hybridization of nucleic acid with substrate or
XX particle bound oligonucleotides -
XX
XX Example 17; Fig 26; 205pp; English.
XX
CC The present sequence is an oligonucleotide used in a method for detecting
CC a nucleic acid having at least 2 portions. The method comprises
CC hybridising the nucleic acid with oligonucleotides, such as the present
CC sequence, attached to a substrate and/or particle and detecting a change
CC in colour, conductivity or optical density. The method is useful for the
CC diagnosis and/or monitoring of diseases, in forensics, in DNA sequencing,
CC for paternity testing, for cell line authentication and for monitoring
CC gene therapy. Detecting nucleic acids based upon observing a colour
CC change is cheap, fast, simple, and does not require specialised or
CC expensive equipment. The nanoparticle oligonucleotide conjugates remain
CC stable for at least 6 months. A single base mismatch and as little as 20
CC femtomoles (fM) of target can be detected using the conjugates.
XX
SQ Sequence 22 BP; 13 A; 4 C; 1 G; 4 T; 0 other;

Query Match 1.4%; Score 15.8; DB 1; Length 22;
Best Local Similarity 89.5%; Pred. No. 3.8e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1076 CAACTATTAAAAA 1094
Db 4 CAACTCGTAAAAA 22

RESULT 643
ABS54436
ID ABS54436 standard; DNA; 22 BP.
XX
AC ABS54436;
XX
DT 28-NOV-2002 (first entry)
XX
DE Silver staining method capture oligonucleotide.
XX
XX Silver staining; capture oligonucleotide; ss; DNA detection chip;
XX gold nanoparticle; cyanide etching; ultrasound wave; sonication; probe;
XX three component sandwich assay; glass substrate; signal; detection;
XX target-complementary DNA; tree; re-cycled; re-used.
XX
OS Synthetic.
XX
XX Key Location/Qualifiers
XX misc_binding 1..12
XX /*tag= a
XX /bound_moiety= "Target oligonucleotide bases 12-1"

FT FT /note= "Forms a double-stranded region with bases 12-1 of
FT modified_base 22 sequence ABS54437"
FT /*tag= b
FT /mod_base= "OTHER"
XX /note= "3' labelled with HS(CH2)3"
XX
PN WO200246483-A2.
XX
XX 13-JUN-2002.
XX
XX 30-NOV-2001; 2001WO-US45039.
XX
XX 06-DEC-2000; 2000US-251715P.
XX
XX (NOUN ) UNIV NORTHWESTERN.
XX
XX Mirkin CA, Park S, Jin R;
XX
XX WPI; 2002-698435/75.
XX
XX Removing silver from used DNA detection chips using cyanide etching
XX solutions and ultrasound, allows chips to be re-cycled -
XX
XX Example 1; Page 5; 10pp; English.
XX
CC The invention discloses methods for removing silver from a silver stained
CC DNA detection chip having bound gold nanoparticles, which comprises using
CC a cyanide etching solution or ultrasound waves. The chip based DNA
CC detection method employs gold nanoparticle probes, modified with
CC oligonucleotides, to indicate the presence of a particular DNA sequence
CC hybridised on a transparent substrate in a three component sandwich assay
CC format. Initially the capture oligonucleotide is immobilised onto a glass
CC substrate. The target oligonucleotide is then hybridised to the capture
CC oligonucleotide and then rinsed in a solution containing gold
CC nanoparticle probes functionalised with target-complementary DNA. The
CC signal can be enhanced, creating trees of nanoparticles, which can be
CC visualised with the naked eye. The silver staining method is preferred to
CC fluorescent methods as it is more simplified, selective and sensitive,
CC but the re-use of the chips depended on the complete removal of the stain
CC without damaging the chip. The advantage of these removal methods is that
CC the DNA detection chips from which the silver has been removed may be
CC re-cycled and re-used. The sequence presented is the capture
CC oligonucleotide.
XX
SQ Sequence 22 BP; 13 A; 4 C; 1 G; 4 T; 0 other;

Query Match 1.4%; Score 15.8; DB 1; Length 22;
Best Local Similarity 89.5%; Pred. No. 3.8e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1076 CAACTATTAAAAA 1094
Db 4 CAACTCGTAAAAA 22

RESULT 644
ABS64661
ID ABS64661 standard; DNA; 22 BP.
XX
AC ABS64661;
XX
XX 15-NOV-2002 (first entry)
XX
DT Nucleic acid detection method associated polynucleotide #43.
XX
DE Nucleic acid detection method; nanoparticle-oligonucleotide conjugate;
XX nanoparticle; viral RNA detection; bacterial DNA detection;
XX fungal DNA detection; nanoprobe conjugate; ss.
XX
OS Synthetic.
XX
XX WO200246472-A2.

```

```

XX PD 13-JUN-2002.
XX PF 07-DEC-2001; 2001WO-US46418.
XX PP 08-DEC-2000; 2000US-254392P.
XX PR 08-DEC-2000; 2000US-254418P.
XX PR 11-DEC-2000; 2000US-255233P.
XX PR 11-DEC-2000; 2000US-255233P.
XX PR 12-JAN-2001; 2001US-0760500.
XX PR 28-MAR-2001; 2001US-0820279.
XX PR 09-APR-2001; 2001US-282640P.
XX PR 10-AUG-2001; 2001US-0927777.
XX PA (NANO-) NANOSPHERE INC.
XX PI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;
XX PI Taton TA, Garimella V, Li Z, Park S;
XX DR WPI; 2002-608256/65.
XX PT Detecting nucleic acid having two portions, by providing nanoparticles
XX PT having oligonucleotides attached to it, contacting nucleic acid and
XX PT nanoparticles to allow hybridization, and observing detectable change
XX PT
XX PS Example 16; Page 151; 442pp; English.
XX CC The invention describes a method of detecting (M1) a nucleic acid having
XX CC two portions, involving providing nanoparticles having oligonucleotides
XX CC attached to it, which has a sequence complementary to sequence of two
XX CC portions of nucleic acid, contacting nucleic acid and nanoparticles, to
XX CC allow hybridization of oligonucleotides with two or more portions of
XX CC nucleic acid, and observing a detectable change brought about by
XX CC hybridization. (M1), nanoparticles (I), nanoparticle-oligonucleotide
XX CC conjugates (II) and the aggregate probe are useful for detecting two or
XX CC more nucleic acids (from a biological source) having at least two
XX CC portions, such as viral RNA, bacterial or fungal DNA, a gene associated
XX CC with a disease, synthetic, or structurally-modified natural or synthetic
XX CC RNA or DNA, or a product of a polymerase chain reaction amplification.
XX CC (II) is useful for preparing a nanoprobe conjugate for detecting an
XX CC analyte, and for detecting a nucleic acid bound to an electrode surface.
XX CC Nucleic acid having two portions from other nucleic acids. (I), (II) and
XX CC the aggregate probe are useful for detecting an analyte (especially
XX CC polyvalent analyte) in a sample. This sequence represents a
XX CC polynucleotide used to demonstrate the method of the invention.
XX SQ Sequence 22 BP; 13 A; 4 C; 1 G; 4 T; 0 other;

Query Match 1.4%; Score 15.8; DB 1; Length 22;
Best Local Similarity 89.5%; Pred. NO. 3.8e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1076 CAACTATTAAAAA 1094
Db ||||| ||||| ||||| |||||
4 CAACTCGTAAAAA 22

RESULT 645
ABS64664
ID ABS64664 standard; DNA; 22 BP.
XX AC ABS64664;
XX AC ABS64664;
XX DT 15-NOV-2002 (first entry)
XX DE Nucleic acid detection method associated polynucleotide #46.
XX KW Nucleic acid detection method; nanoparticle-oligonucleotide conjugate;
XX KW nanoparticle; viral RNA detection; bacterial DNA detection;
XX KW fungal DNA detection; nanoprobe conjugate; ss.

```

```

OS Synthetic.
XX WO200246472-A2.
XX PN 13-JUN-2002.
XX PD 07-DEC-2001; 2001WO-US46418.
XX PF 08-DEC-2000; 2000US-254392P.
XX PR 08-DEC-2000; 2000US-254418P.
XX PR 11-DEC-2000; 2000US-255233P.
XX PR 11-DEC-2000; 2000US-255233P.
XX PR 12-JAN-2001; 2001US-0760500.
XX PR 28-MAR-2001; 2001US-0820279.
XX PR 09-APR-2001; 2001US-282640P.
XX PR 10-AUG-2001; 2001US-0927777.
XX PA (NANO-) NANOSPHERE INC.
XX PI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;
XX PI Taton TA, Garimella V, Li Z, Park S;
XX DR WPI; 2002-608256/65.
XX PT Detecting nucleic acid having two portions, by providing nanoparticles
XX PT having oligonucleotides attached to it, contacting nucleic acid and
XX PT nanoparticles to allow hybridization, and observing detectable change
XX PT
XX PS Example 17; Fig 26B; 442pp; English.
XX CC The invention describes a method of detecting (M1) a nucleic acid having
XX CC two portions, involving providing nanoparticles having oligonucleotides
XX CC attached to it, which has a sequence complementary to sequence of two
XX CC portions of nucleic acid, contacting nucleic acid and nanoparticles, to
XX CC allow hybridization of oligonucleotides with two or more portions of
XX CC nucleic acid, and observing a detectable change brought about by
XX CC hybridization. (M1), nanoparticles (I), nanoparticle-oligonucleotide
XX CC conjugates (II) and the aggregate probe are useful for detecting two or
XX CC more nucleic acids (from a biological source) having at least two
XX CC portions, such as viral RNA, bacterial or fungal DNA, a gene associated
XX CC with a disease, synthetic, or structurally-modified natural or synthetic
XX CC RNA or DNA, or a product of a polymerase chain reaction amplification.
XX CC (II) is useful for preparing a nanoprobe conjugate for detecting an
XX CC analyte, and for detecting a nucleic acid bound to an electrode surface.
XX CC Nucleic acid having two portions from other nucleic acids. (I), (II) and
XX CC the aggregate probe are useful for detecting an analyte (especially
XX CC polyvalent analyte) in a sample. This sequence represents a
XX CC polynucleotide used to demonstrate the method of the invention.
XX SQ Sequence 22 BP; 13 A; 4 C; 1 G; 4 T; 0 other;

Query Match 1.4%; Score 15.8; DB 1; Length 22;
Best Local Similarity 89.5%; Pred. NO. 3.8e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1076 CAACTATTAAAAA 1094
Db ||||| ||||| ||||| |||||
4 CAACTCGTAAAAA 22

RESULT 646
ABS64691
ID ABS64691 standard; DNA; 22 BP.
XX AC ABS64691;
XX AC ABS64691;
XX DT 15-NOV-2002 (first entry)
XX DE Nucleic acid detection method associated polynucleotide #73.
XX KW Nucleic acid detection method; nanoparticle-oligonucleotide conjugate;

```

```

KW nanoparticle; viral RNA detection; bacterial DNA detection;
KW fungal DNA detection; nanoprobe conjugate; ss.
XX Synthetic.
XX WO200246472-A2.
XX 13-JUN-2002.
XX 07-DEC-2001; 2001WO-US46418.
XX 08-DEC-2000; 2000US-254392P.
XX 08-DEC-2000; 2000US-254418P.
XX 11-DEC-2000; 2000US-255235P.
XX 11-DEC-2000; 2000US-255236P.
XX 12-JAN-2001; 2001US-0760500.
XX 28-MAR-2001; 2001US-0820279.
XX 09-APR-2001; 2001US-282640P.
XX 10-AUG-2001; 2001US-0927777.
XX (NANO-) NANOSPHERE INC.
XX Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;
XX Taton TA, Garimella V, Li Z, Park S;
XX WPI; 2002-608256/65.
XX Detecting nucleic acid having two portions, by providing nanoparticles
XX having oligonucleotides attached to it, contacting nucleic acid and
XX nanoparticles to allow hybridization, and observing detectable change
XX .
XX Example 26; Fig 52B; 442pp; English.
XX The invention describes a method of detecting (M1) a nucleic acid having
XX two portions, involving providing nanoparticles having oligonucleotides
XX attached to it, which has a sequence complementary to sequence of two
XX portions of nucleic acid, contacting nucleic acid and nanoparticles, to
XX allow hybridisation of oligonucleotides with two or more portions of
XX nucleic acid, and observing a detectable change brought about by
XX hybridisation. (M1), nanoparticles (I), nanoparticle-oligonucleotide
XX conjugates (II) and the aggregate probe are useful for detecting two or
XX more nucleic acids (from a biological source) having at least two
XX portions, such as viral RNA, bacterial or fungal DNA, a gene associated
XX with a disease, synthetic, or structurally-modified natural or synthetic
XX RNA or DNA, or a product of a polymerase chain reaction amplification.
XX (II) is useful for preparing a nanoprobe conjugate for detecting an
XX analyte, and for detecting a nucleic acid bound to an electrode surface.
XX (I) and (II) are useful for fabrication, and for separating a selected
XX nucleic acid having two portions from other nucleic acids. (I), (II) and
XX the aggregate probe are useful for detecting an analyte (especially
XX polyvalent analyte) in a sample. This sequence represents a
XX polynucleotide used to demonstrate the method of the invention.
XX SQ Sequence 22 BP; 13 A; 4 C; 1 G; 4 T; 0 other;
XX Query Match 1.4%; Score 15.8; DB 1; Length 22;
XX Best Local Similarity 89.5%; Pred. No. 3.8e+02;
XX Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX QY 1076 CAACTATTAAAAAAA 1094
XX Db 4 CAACTCGTAAAAAAA 22
XX RESULT 647
XX ABK65023
XX ID ABK65023 standard; DNA; 22 BP.
XX AC ABK65023;
XX XX
XX 02-JUL-2002 (first entry)
XX DT

nanoparticle-oligonucleotide #43.
Nanoparticle-oligonucleotide; nanofabrication;
nucleic acid detection; ss.
Synthetic.
WO200218643-A2.
07-MAR-2002.
10-AUG-2001; 2001WO-US25237.
11-AUG-2000; 2000US-224631P.
08-DEC-2000; 2000US-254392P.
11-DEC-2000; 2000US-255235P.
12-JAN-2001; 2001US-0760500.
28-MAR-2001; 2001US-0820279.
(NANO-) NANOSPHERE INC.
Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;
Taton TA, Garimella V, Li Z, Park S;
WPI; 2002-259024/30.
Detecting nucleic acid, useful for diagnosis of genetic, viral or
bacterial diseases, comprises hybridising nanoparticles with attached
oligonucleotides to nucleic acid and detecting change brought about by
hybridisation .
Example 16; Page 407; 412pp; English.
The invention relates to a method of detecting a nucleic acid (NA) having
at least 2 portions comprising: (a) providing nanoparticles (NP) with
attached oligonucleotides (OGN), where OGN has a sequence complementary
to the sequence of NA; (b) contacting NA and NP under conditions
effective to allow hybridisation of OGN with NA; and (c) observing a
detectable change brought about by hybridisation of OGN with NA.
The method is useful for detecting a nucleic acid, separating a
selected nucleic acid from others and methods of nanofabrication.
Detecting analytes such as nucleic acids and proteins are useful for the
diagnosis of genetic, bacterial and viral diseases. The OGN-NP conjugates
that use cyclic disulphide linkers improve the sensitivity of diagnostic
assays. In particular assays using OGN-NP conjugates prepared using
linkers comprising a steroid residue attached to a cyclic disulphide have
been found to be approximately 10 times more sensitive than assays
employing conjugates prepared using alkanethiols or acyclic disulphides
as the linker. The OGN-NP conjugates are stable allowing them to be used
directly in PCR solutions. Therefore conjugates added as probes to a DNA
target to be PCR amplified can be carried through the 30 or 40 heating
cooling cycles of the PCR and are still able to detect the amplicons
without opening the tubes and causing contamination. ABK64981-ABK65055
represent nanoparticle-oligonucleotides of the invention.
XX SQ Sequence 22 BP; 13 A; 4 C; 1 G; 4 T; 0 other;
XX Query Match 1.4%; Score 15.8; DB 1; Length 22;
XX Best Local Similarity 89.5%; Pred. No. 3.8e+02;
XX Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX QY 1076 CAACTATTAAAAAAA 1094
XX Db 4 CAACTCGTAAAAAAA 22
XX RESULT 648
XX ABK65026
XX ID ABK65026 standard; DNA; 22 BP.
XX AC ABK65026;
XX XX
XX 02-JUL-2002 (first entry)
XX DT

```

```

XX DE Nanoparticle-oligonucleotide #46.
XX KW Nanoparticle-oligonucleotide; nanofabrication;
XX KW nucleic acid detection; ss.
XX OS Synthetic.
XX FN WO200218643-A2.
XX PD 07-MAR-2002.
XX PF 10-AUG-2001; 2001WO-US25237.
XX PR 11-AUG-2000; 2000US-224631P.
XX PR 08-DEC-2000; 2000US-254392P.
XX PR 11-DEC-2000; 2000US-255235P.
XX PR 12-JAN-2001; 2001US-0760500.
XX PR 28-MAR-2001; 2001US-0820279.
XX PA (NANO-) NANOSPHERE INC.
XX PI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;
XX PI Taton TA, Garimella V, Li Z, Park S;
XX DR WPI; 2002-258024/30.
XX KW Detecting nucleic acid, useful for diagnosis of genetic, viral or
XX PT bacterial disease, comprises hybridising nanoparticles with attached
XX PT oligonucleotides to nucleic acid and detecting change brought about by
XX PT hybridisation -
XX PS Example 17; Figure 26B; 412pp; English.
XX CC The invention relates to a method of detecting a nucleic acid (NA) having
XX CC at least 2 portions comprising: (a) providing nanoparticles (NP) with
XX CC attached oligonucleotides (OGN), where OGN has a sequence complementary
XX CC to the sequence of NA; (b) contacting NA and NP under conditions
XX CC effective to allow hybridisation of OGN with NA; and (c) observing a
XX CC detectable change brought about by hybridisation of OGN with NA.
XX CC The method is useful for detecting a nucleic acid, separating a
XX CC selected nucleic acid from others and methods of nanofabrication.
XX CC Detecting analytes such as nucleic acids and proteins are useful for the
XX CC diagnosis of genetic, bacterial and viral diseases. The OGN-NP conjugates
XX CC that use cyclic disulphide linkers improve the sensitivity of diagnostic
XX CC assays. In particular assays using OGN-NP conjugates prepared using
XX CC linkers comprising a steroid residue attached to a cyclic disulphide have
XX CC been found to be approximately 10 times more sensitive than assays
XX CC employing conjugates prepared using alkanethiols or acyclic disulphides
XX CC as the linker. The OGN-NP conjugates are stable allowing them to be used
XX CC directly in PCR solutions. Therefore conjugates added as probes to a DNA
XX CC target to be PCR amplified can be carried through the 30 or 40 heating
XX CC cooling cycles of the PCR and are still able to detect the amplicons
XX CC without opening the tubes and causing contamination. ABK64981-ABK65055
XX CC represent nanoparticle-oligonucleotides of the invention.
XX SQ Sequence 22 BP; 13 A; 4 C; 1 G; 4 T; 0 other;
Query Match 1.4%; Score 15.8; DB 1; Length 22;
Best Local Similarity 89.5%; Pred. No. 3.8e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1076 CCACTATTAAAAA 1094
DB 4 CCACTCGTAAAAA 22
RESULT 649
ABK65053
ID ABK65053 standard; DNA; 22 BP.
XX AC ABK65053;
XX AC ABK92165;

```

```

DT XX 02-JUL-2002 (first entry)
DE XX Nanoparticle-oligonucleotide #73.
KW KW Nanoparticle-oligonucleotide; nanofabrication;
KW KW nucleic acid detection; ss.
OS XX Synthetic.
FN FN WO200218643-A2.
XX PD 07-MAR-2002.
XX PF 10-AUG-2001; 2001WO-US25237.
XX PR 11-AUG-2000; 2000US-224631P.
XX PR 08-DEC-2000; 2000US-254392P.
XX PR 11-DEC-2000; 2000US-255235P.
XX PR 12-JAN-2001; 2001US-0760500.
XX PR 28-MAR-2001; 2001US-0820279.
XX PA (NANO-) NANOSPHERE INC.
XX PI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;
XX PI Taton TA, Garimella V, Li Z, Park S;
XX DR WPI; 2002-258024/30.
XX KW Detecting nucleic acid, useful for diagnosis of genetic, viral or
XX PT bacterial disease, comprises hybridising nanoparticles with attached
XX PT oligonucleotides to nucleic acid and detecting change brought about by
XX PT hybridisation -
XX PS Example 28; Figure 52; 412pp; English.
XX CC The invention relates to a method of detecting a nucleic acid (NA) having
XX CC at least 2 portions comprising: (a) providing nanoparticles (NP) with
XX CC attached oligonucleotides (OGN), where OGN has a sequence complementary
XX CC to the sequence of NA; (b) contacting NA and NP under conditions
XX CC effective to allow hybridisation of OGN with NA; and (c) observing a
XX CC detectable change brought about by hybridisation of OGN with NA.
XX CC The method is useful for detecting a nucleic acid, separating a
XX CC selected nucleic acid from others and methods of nanofabrication.
XX CC Detecting analytes such as nucleic acids and proteins are useful for the
XX CC diagnosis of genetic, bacterial and viral diseases. The OGN-NP conjugates
XX CC that use cyclic disulphide linkers improve the sensitivity of diagnostic
XX CC assays. In particular assays using OGN-NP conjugates prepared using
XX CC linkers comprising a steroid residue attached to a cyclic disulphide have
XX CC been found to be approximately 10 times more sensitive than assays
XX CC employing conjugates prepared using alkanethiols or acyclic disulphides
XX CC as the linker. The OGN-NP conjugates are stable allowing them to be used
XX CC directly in PCR solutions. Therefore conjugates added as probes to a DNA
XX CC target to be PCR amplified can be carried through the 30 or 40 heating
XX CC cooling cycles of the PCR and are still able to detect the amplicons
XX CC without opening the tubes and causing contamination. ABK64981-ABK65055
XX CC represent nanoparticle-oligonucleotides of the invention.
XX SQ Sequence 22 BP; 13 A; 4 C; 1 G; 4 T; 0 other;
Query Match 1.4%; Score 15.8; DB 1; Length 22;
Best Local Similarity 89.5%; Pred. No. 3.8e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1076 CCACTATTAAAAA 1094
DB 4 CCACTCGTAAAAA 22
RESULT 650
ABX92165
ID ABX92165 standard; DNA; 22 BP.
XX AC ABX92165;

```


XX DB 12-MAY-2003 (first entry)

XX DE Nanoparticle-associated oligonucleotide SEQ ID 43.

XX KW Nonparticle; nucleic acid detection; hybridisation; diagnosis;

XX KW sequencing; viral infection; human immunodeficiency virus; HIV;

XX KW hepatitis virus; herpes virus; cytomegalovirus; Epstein-Barr virus;

XX KW bacterial infection; sexually transmitted disease; inherited disorder;

XX KW forensic; paternity testing; cell line authentication; gene therapy; ss.

XX OS Synthetic.

XX PN US2002155458-A1.

XX PD 24-OCT-2002.

XX PF 28-SEP-2001; 2001US-0967409.

XX PR 29-JUL-1996; 96US-031809P.

XX PR 26-APR-2000; 2000US-200161P.

XX PR 26-JUN-2000; 2000US-0603830.

XX PR 21-JUL-1997; 97WO-US12783.

XX PR 29-JAN-1999; 99US-0240755.

XX PR 25-JUN-1999; 99US-0344667.

XX PA (NANO-) NANOSPHERE INC.

XX PI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;

XX PI Taton TA;

XX DR WPI; 2003-182627/18.

XX PT Detecting nucleic acids having at least two portions involves use of

XX PT nanoparticles which have oligonucleotides attached to them that are

XX PT complementary to portions of the nucleic acid sequence -

XX PS Example 16; Page 57; 130pp; English.

XX CC This invention describes a novel method of detecting nucleic acid having

XX CC at least two portions. The method involves providing nanoparticles

XX CC attached to oligonucleotides, where the oligonucleotide on each

XX CC nanoparticle have a sequence complementary to a sequence of at least two

XX CC portions of nucleic acid, contacting nucleic acid and nanoparticle to

XX CC allow hybridisation of the oligonucleotide on the nanoparticle with two

XX CC or more portions of nucleic acid and observing a detectable change

XX CC brought about by hybridisation of the oligonucleotide nanoparticle with

XX CC nucleic acid. The method is useful for separating a selected nucleic

XX CC acid having at least two portions, from other nucleic acids and for

XX CC detecting nucleic acids having at least two portions. The method is

XX CC useful for detecting any type of nucleic acids which may be used for

XX CC diagnosis of disease and in sequencing of nucleic acids. Preferably, the

XX CC method is useful for detecting nucleic acids for diagnosis and/or

XX CC monitoring of viral infections (human immunodeficiency virus (HIV),

XX CC hepatitis virus, herpes virus, cytomegalovirus and Epstein-Barr virus),

XX CC bacterial diseases, sexually transmitted diseases, inherited disorders,

XX CC in forensics, in DNA sequencing, for paternity testing, for cell line

XX CC authentication, and for monitoring gene therapy. The method is useful in

XX CC research and analytical laboratories in DNA sequencing, in the field to

XX CC detect the presence of specific pathogens. Detecting nucleic acids based

XX CC on observing a colour change with the naked eye is cheap, fast, simple

XX CC and robust and does not require specialised expensive equipment.

XX CC ABX92123-ABX92186 and ABQ77356 represent oligonucleotides used to

XX CC illustrate the method of the invention.

XX SQ Sequence 22 BP; 13 A; 4 C; 1 G; 4 T; 0 other;

XX Query Match 1.4%; Score 15.8; DB 1; Length 22;

XX Best Local Similarity 89.5%; Pred. No. 3.8e+02;

XX Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

XX 1076 CAACTATTAAAAAAA 1094

XX ||||| |||||||||

DB 4 CAACTCGTAAAAAAA 22

RESULT 651

ABX92168

ID ABX92168 standard; DNA; 22 BP.

XX AC ABX92168;

XX DT 12-MAY-2003 (first entry)

XX DE Nanoparticle-associated oligonucleotide SEQ ID 46.

XX KW Nonparticle; nucleic acid detection; hybridisation; diagnosis;

XX KW sequencing; viral infection; human immunodeficiency virus; HIV;

XX KW hepatitis virus; herpes virus; cytomegalovirus; Epstein-Barr virus;

XX KW bacterial infection; sexually transmitted disease; inherited disorder;

XX KW forensic; paternity testing; cell line authentication; gene therapy; ss.

XX OS Synthetic.

XX PN US2002155458-A1.

XX PD 24-OCT-2002.

XX PF 28-SEP-2001; 2001US-0967409.

XX PR 29-JUL-1996; 96US-031809P.

XX PR 26-APR-2000; 2000US-200161P.

XX PR 26-JUN-2000; 2000US-0603830.

XX PR 21-JUL-1997; 97WO-US12783.

XX PR 29-JAN-1999; 99US-0240755.

XX PR 25-JUN-1999; 99US-0344667.

XX PA (NANO-) NANOSPHERE INC.

XX PI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;

XX PI Taton TA;

XX DR WPI; 2003-182627/18.

XX PT Detecting nucleic acids having at least two portions involves use of

XX PT nanoparticles which have oligonucleotides attached to them that are

XX PT complementary to portions of the nucleic acid sequence -

XX PS Example 17; Figure 26; 130pp; English.

XX CC This invention describes a novel method of detecting nucleic acid having

XX CC at least two portions. The method involves providing nanoparticles

XX CC attached to oligonucleotides, where the oligonucleotide on each

XX CC nanoparticle have a sequence complementary to a sequence of at least two

XX CC portions of nucleic acid, contacting nucleic acid and nanoparticle to

XX CC allow hybridisation of the oligonucleotide on the nanoparticle with two

XX CC or more portions of nucleic acid and observing a detectable change

XX CC brought about by hybridisation of the oligonucleotide nanoparticle with

XX CC nucleic acid. The method is useful for separating a selected nucleic

XX CC acid having at least two portions, from other nucleic acids and for

XX CC detecting nucleic acids having at least two portions. The method is

XX CC useful for detecting any type of nucleic acids which may be used for

XX CC diagnosis of disease and in sequencing of nucleic acids. Preferably, the

XX CC method is useful for detecting nucleic acids for diagnosis and/or

XX CC monitoring of viral infections (human immunodeficiency virus (HIV),

XX CC hepatitis virus, herpes virus, cytomegalovirus and Epstein-Barr virus),

XX CC bacterial diseases, sexually transmitted diseases, inherited disorders,

XX CC in forensics, in DNA sequencing, for paternity testing, for cell line

XX CC authentication, and for monitoring gene therapy. The method is useful in

XX CC research and analytical laboratories in DNA sequencing, in the field to

XX CC detect the presence of specific pathogens. Detecting nucleic acids based

XX CC on observing a colour change with the naked eye is cheap, fast, simple

XX CC and robust and does not require specialised expensive equipment.

XX CC ABX92123-ABX92186 and ABQ77356 represent oligonucleotides used to

XX CC illustrate the method of the invention.

```

SQ Sequence 22 BP; 13 A; 4 C; 1 G; 4 T; 0 other;
Query Match 1.4%; Score 15.8; DB 1; Length 22;
Best Local Similarity 89.5%; Pred. No. 3.8e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1076 CAACTATTAAAAAAA 1094
||||| |||||||
4 CAACTCGTAAAAAAA 22

Db
RESULT 652
ABX98146
ID ABX98146 standard; DNA; 22 BP.
XX
AC ABX98146;
XX
DT 16-MAY-2003 (first entry)
XX
DE Nucleic acid detection method associated oligonucleotide #42.
XX
KW Nucleic acid detection; nanoparticle; HIV; bacterial disease;
KW inherited disease; cystic fibrosis; cancer; sequencing;
KW forensic; paternity testing; cell line authentication; gene therapy;
KW ss.
XX
OS Synthetic.
XX
PN US6495324-B1.
XX
PD 17-DEC-2002.
XX
PF 20-OCT-2000; 2000US-0693005.
XX
PR 29-JUL-1996; 96US-031809P.
PR 25-JUN-1999; 99US-0344667.
PR 21-JUL-1997; 97WO-US12783.
PR 29-JAN-1999; 99US-0240755.
XX
PA (NANO-) NANOSPHERE INC.
XX
PI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;
XX WPI; 2003-237646/23.
XX
PT Detecting a nucleic acid using oligonucleotides attached to
PT nanoparticles, where each oligonucleotide has a sequence complementary
PT to at least two portions of the nucleic acid being detected, useful in
PT diagnosis of a diseases (e.g. HIV) -
XX
PS Example 16; Column 60; 79pp; English.
XX
CC The invention describes a method of detecting a nucleic acid using
CC oligonucleotides (OG) attached to nanoparticles. The OG on each
CC nanoparticle have a sequence complementary to the sequences of at least
CC two portions of the nucleic acid being detected. Contacting between the
CC nanoparticle conjugated OG and nucleic acids takes place under
CC hybridisation conditions, where binding is detected via a colour change.
CC The method has applications in diagnosis of a diseases (e.g. diagnosing
CC and monitoring viral diseases such as HIV, bacterial diseases, inherited
CC diseases such as cystic fibrosis, cancers, etc.), in sequencing of
CC nucleic acids, in forensics for paternity testing, for cell line
CC authentication and for monitoring gene therapy. This sequence
CC represents a DNA associated with the nucleic acid detection method of
CC the invention.
XX
SQ Sequence 22 BP; 13 A; 4 C; 1 G; 4 T; 0 other;
Query Match 1.4%; Score 15.8; DB 1; Length 22;
Best Local Similarity 89.5%; Pred. No. 3.8e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1076 CAACTATTAAAAAAA 1094
||||| |||||||
4 CAACTCGTAAAAAAA 22

Db
RESULT 654
ABX79169
ID ABX79169 standard; DNA; 22 BP.

```

```

Db
||||| |||||||
4 CAACTCGTAAAAAAA 22

RESULT 653
ABX98149
ID ABX98149 standard; DNA; 22 BP.
XX
AC ABX98149;
XX
DT 16-MAY-2003 (first entry)
XX
DE Nucleic acid detection method associated oligonucleotide #45.
XX
KW Nucleic acid detection; nanoparticle; HIV; bacterial disease;
KW inherited disease; cystic fibrosis; cancer; sequencing;
KW forensic; paternity testing; cell line authentication; gene therapy;
KW ss.
XX
OS Synthetic.
XX
PN US6495324-B1.
XX
PD 17-DEC-2002.
XX
PF 20-OCT-2000; 2000US-0693005.
XX
PR 29-JUL-1996; 96US-031809P.
PR 25-JUN-1999; 99US-0344667.
PR 21-JUL-1997; 97WO-US12783.
PR 29-JAN-1999; 99US-0240755.
XX
PA (NANO-) NANOSPHERE INC.
XX
PI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;
XX WPI; 2003-237646/23.
XX
PT Detecting a nucleic acid using oligonucleotides attached to
PT nanoparticles, where each oligonucleotide has a sequence complementary
PT to at least two portions of the nucleic acid being detected, useful in
PT diagnosis of a diseases (e.g. HIV) -
XX
PS Example 17; Fig 26B; 79pp; English.
XX
CC The invention describes a method of detecting a nucleic acid using
CC oligonucleotides (OG) attached to nanoparticles. The OG on each
CC nanoparticle have a sequence complementary to the sequences of at least
CC two portions of the nucleic acid being detected. Contacting between the
CC nanoparticle conjugated OG and nucleic acids takes place under
CC hybridisation conditions, where binding is detected via a colour change.
CC The method has applications in diagnosis of a diseases (e.g. diagnosing
CC and monitoring viral diseases such as HIV, bacterial diseases, inherited
CC diseases such as cystic fibrosis, cancers, etc.), in sequencing of
CC nucleic acids, in forensics for paternity testing, for cell line
CC authentication and for monitoring gene therapy. This sequence
CC represents a DNA associated with the nucleic acid detection method of
CC the invention.
XX
SQ Sequence 22 BP; 13 A; 4 C; 1 G; 4 T; 0 other;
Query Match 1.4%; Score 15.8; DB 1; Length 22;
Best Local Similarity 89.5%; Pred. No. 3.8e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1076 CAACTATTAAAAAAA 1094
||||| |||||||
4 CAACTCGTAAAAAAA 22

Db
RESULT 654
ABX79169
ID ABX79169 standard; DNA; 22 BP.

```

XX AC ABX79169;
 XX DT 15-APR-2003 (first entry)
 XX DE Immobilised capture probe for assay involving silver staining.
 XX KW Nanoparticle; ss; nucleic acid detection; viral disease; probe;
 XX KW human immunodeficiency virus infection; hepatitis virus infection;
 XX KW herpes virus infection; cytomegalovirus infection; forensic science;
 XX KW Epstein-Barr virus infection; bacterial disease; gene therapy;
 XX KW sexually transmitted disease; inherited disorder; DNA sequencing;
 XX KW paternity testing; cell line authentication.
 XX OS Synthetic.
 XX PN US2002155462-A1.
 XX PD 24-OCT-2002.
 XX PF 12-OCT-2001; 2001US-0976577.
 XX PR 29-JUL-1996; 96US-031809P.
 XX PR 26-APR-2000; 2000US-200161P.
 XX PR 26-JUN-2000; 2000US-0603830.
 XX PR 21-JUL-1997; 97WO-US12783.
 XX PR 29-JAN-1999; 99US-0240755.
 XX PR 25-JUN-1999; 99US-0344667.
 XX PA (NANO-) NANOSPHERE INC.
 XX PI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;
 XX PI Taton TA;
 XX WPI; 2003-198491/19.
 XX PT Detecting nucleic acids having at least 2 portions comprises use of
 XX PT nanoparticles which have oligonucleotides attached to them that are
 XX PT complementary to portions of the nucleic acid sequence -
 XX PS Example 16; Page 37; 130pp; English.
 XX CC The invention relates to detecting a nucleic acid (NA) having at least
 XX CC 2 portions, comprises providing a type of nanoparticles (NP) having
 XX CC attached to oligonucleotides (O) ((O) on each NP has a sequence
 XX CC complementary to sequence of at least 2 portions of NA), contacting NA
 XX CC and NP to allow hybridisation of (O) on NP with 2 or more portions of NA,
 XX CC and observing a detectable change brought about by hybridisation of (O)
 XX CC on NP with NA. The nanoparticle is useful for separating a selected
 XX CC nucleic acid having at least 2 portions, from other nucleic acids, and
 XX CC for detecting nucleic acids having at least 2 portions. The method of
 XX CC using NP is useful for detecting any type of nucleic acids which may be
 XX CC used for diagnosis of disease and in sequencing of nucleic acids.
 XX CC Preferably, the method is useful for detecting nucleic acids for
 XX CC diagnosis and/or monitoring of viral diseases (human immunodeficiency
 XX CC virus), hepatitis virus, herpes virus, cytomegalovirus and Epstein-Barr
 XX CC virus), bacterial diseases, sexually transmitted diseases, inherited
 XX CC disorders, in forensics, in DNA sequencing, for paternity testing, for
 XX CC cell line authentication and for monitoring gene therapy. The method is
 XX CC useful in research and analytical laboratories in DNA sequencing and in
 XX CC the field to detect the presence of specific pathogens. Detecting nucleic
 XX CC acids based on observing a colour change with the naked eye is cheap,
 XX CC fast, simple and robust, and do not require specialised expensive
 XX CC equipment. The present sequence is a nanoparticle (e.g. gold
 XX CC particles) labelled probe used to demonstrate the method of the
 XX CC invention.
 XX SQ Sequence 22 BP; 13 A; 4 C; 1 G; 4 T; 0 other;
 XX Query Match 1.4%; Score 15.8; DB 1; Length 22;
 XX Best Local Similarity 89.5%; Pred. No. 3.8e+02;
 XX Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1076 CAACCTATTAAAAAAA 1094
 DB 4 CAACCTCGTAAAAAAA 22
 RESULT 655
 ABX79172
 ID ABX79172 standard; DNA; 22 BP.
 XX AC ABX79172;
 XX DT 15-APR-2003 (first entry)
 XX DE CdSe/ZnS core/shell quantum dots oligonucleotide #1.
 XX KW Nanoparticle; ss; nucleic acid detection; viral disease; probe;
 XX KW human immunodeficiency virus infection; hepatitis virus infection;
 XX KW herpes virus infection; cytomegalovirus infection; forensic science;
 XX KW Epstein-Barr virus infection; bacterial disease; gene therapy;
 XX KW sexually transmitted disease; inherited disorder; DNA sequencing;
 XX KW paternity testing; cell line authentication; quantum dot;
 XX KW semiconductor.
 XX OS Synthetic.
 XX PN US2002155462-A1.
 XX PD 24-OCT-2002.
 XX PF 12-OCT-2001; 2001US-0976577.
 XX PR 29-JUL-1996; 96US-031809P.
 XX PR 26-APR-2000; 2000US-200161P.
 XX PR 26-JUN-2000; 2000US-0603830.
 XX PR 21-JUL-1997; 97WO-US12783.
 XX PR 29-JAN-1999; 99US-0240755.
 XX PR 25-JUN-1999; 99US-0344667.
 XX PA (NANO-) NANOSPHERE INC.
 XX PI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;
 XX PI Taton TA;
 XX WPI; 2003-198491/19.
 XX PT Detecting nucleic acids having at least 2 portions comprises use of
 XX PT nanoparticles which have oligonucleotides attached to them that are
 XX PT complementary to portions of the nucleic acid sequence -
 XX PS Example 17; Fig 26; 130pp; English.
 XX CC The invention relates to detecting a nucleic acid (NA) having at least
 XX CC 2 portions, comprises providing a type of nanoparticles (NP) having
 XX CC attached to oligonucleotides (O) ((O) on each NP has a sequence
 XX CC complementary to sequence of at least 2 portions of NA), contacting NA
 XX CC and NP to allow hybridisation of (O) on NP with 2 or more portions of NA,
 XX CC and observing a detectable change brought about by hybridisation of (O)
 XX CC on NP with NA. The nanoparticle is useful for separating a selected
 XX CC nucleic acid having at least 2 portions, from other nucleic acids, and
 XX CC for detecting nucleic acids having at least 2 portions. The method of
 XX CC using NP is useful for detecting any type of nucleic acids which may be
 XX CC used for diagnosis of disease and in sequencing of nucleic acids.
 XX CC Preferably, the method is useful for detecting nucleic acids for
 XX CC diagnosis and/or monitoring of viral diseases (human immunodeficiency
 XX CC virus), hepatitis virus, herpes virus, cytomegalovirus and Epstein-Barr
 XX CC virus), bacterial diseases, sexually transmitted diseases, inherited
 XX CC disorders, in forensics, in DNA sequencing, for paternity testing, for
 XX CC cell line authentication and for monitoring gene therapy. The method is
 XX CC useful in research and analytical laboratories in DNA sequencing and in
 XX CC the field to detect the presence of specific pathogens. Detecting nucleic
 XX CC acids based on observing a colour change with the naked eye is cheap,
 XX CC fast, simple and robust, and do not require specialised expensive
 XX CC equipment. The present sequence is a nanoparticle (e.g. gold
 XX CC particles) labelled probe used to demonstrate the method of the
 XX CC invention.

CC particles) labelled probe used to demonstrate the method of the
 CC invention. In this case the oligonucleotides are immobilised onto
 CC semiconductor nanoparticle quantum dots.
 XX
 SQ Sequence 22 BP; 13 A; 4 C; 1 G; 4 T; 0 other;
 Query Match 1.4%; Score 15.8; DB 1; Length 22;
 Best Local Similarity 89.5%; Pred. No. 3.8e+02;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1076 CCACTATTAAAAA 1094
 Db 4 CCACTCTAAAAA 22
 RESULT 656
 ABV74140/c
 ID ABV74140 standard; DNA; 22 BP.
 XX
 AC ABV74140;
 XX
 DT 23-JAN-2003 (first entry)
 XX
 DE Oligonucleotide used in cDNA library array.
 XX
 KW G-protein coupled receptor; odourant; receptor; olfaction; array;
 KW microarray; anosmia; attractant; aromatic; pesticide; PCR; primer;
 KW ss.
 XX
 OS Synthetic.
 XX
 Key Location/Qualifiers
 modified_base 1.
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "5, polylinker"
 XX
 PN WO200277200-A2.
 XX
 PD 03-OCT-2002.
 XX
 PP 26-MAR-2002; 2002WO-US09559.
 XX
 PR 27-MAR-2001; 2001US-279168P.
 PR 31-JAN-2002; 2002US-353392P.
 XX
 PA (INSC-) INSCENT INC.
 XX
 PI Woods D, Dimitratos S;
 XX
 DR WPI; 2003-029930/02.
 XX
 PT Identifying nucleic acid encoding novel sex-linked-tissue-linked
 PT receptors, useful for isolating odourant binding proteins or pesticide
 PT alternatives, by analyzing sequences from a male- and female-specific
 PT nucleic acid library
 XX
 PS Disclosure; Fig 5; 83pp; English.
 XX
 CC The present sequence is that of an oligonucleotide used in a method
 CC designed to rapidly array and normalize a complex cDNA library
 CC obtained from a target species. Clones are arrayed into multi-well
 CC plates. Each well contains 16 oligonucleotides with a 5' polylinker,
 CC a poly-T run capable of binding cDNAs by their poly-A tail and a
 CC unique 3' sequence, which allows an anchored oligonucleotide in each
 CC well to selectively hybridise only to those cDNA clones with a
 CC complementary 5' end. The unique 3' key sequences are designed to
 CC give a comprehensive level of degeneracy since they are diverse and
 CC numerous enough to ensure that every possible cDNA sequence can be
 CC bound by an individual, specific oligonucleotide in a single well.
 CC The cDNA library is heated to denature the clones into single
 CC stranded DNA, and an aliquot is added to every well. The anchored
 CC oligonucleotide serves as the 3' primer in PCR, and the common 5'

CC region present in every cDNA clone serves as the 5' priming site.
 CC Denaturing and washing leave anchored cDNA in each well. The library
 CC is now arrayed and normalised. The method was used to identify and
 CC isolate clones encoding G-protein coupled receptors, especially
 CC odourant receptors, and active effectors involved in the olfactory
 CC pathway of invertebrates and vertebrates, e.g. odourant binding
 CC proteins, or other olfactory or neuronal proteins. The identified
 CC receptors and proteins are useful for identifying compounds that
 CC reduce a target animal's sensitivity to odours, for manufacturing
 CC compounds or devices that mask odours, or trapping invertebrates with
 CC odourants. Semiochemicals (e.g. aromatics or pheromone mimetics) can
 CC be developed with desirable effects on specific species, for the
 CC development of pest monitoring systems or non-toxic, species-specific
 CC pesticide alternatives, for controlling insect feeding and breeding
 CC behaviour, detecting the presence of small air-borne molecules, etc.
 XX
 SQ Sequence 22 BP; 2 A; 1 C; 3 G; 16 T; 0 other;

Query Match 1.4%; Score 15.8; DB 1; Length 22;
 Best Local Similarity 89.5%; Pred. No. 3.8e+02;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1080 TATTAAAAA 1098
 Db 19 TGTCAAAAAA 1

RESULT 657
 AAZ89372/c
 ID AAZ89372 standard; DNA; 17 BP.
 XX
 AC AAZ89372;
 XX
 DT 15-JUN-2000 (first entry)
 XX
 DE RNA detecting primer #2.
 XX
 KW Amplification; detection; gene expression; primer; ss.
 XX
 OS Unidentified.
 XX
 PN DE19840731-A1.
 XX
 PD 09-MAR-2000.
 XX
 PF 07-SEP-1998; 98DE-1040731.
 XX
 PR 07-SEP-1998; 98DE-1040731.
 XX
 PA (HMRI) HOECHST MARION ROUSSEL DEUT GMBH.
 XX
 DR WPI; 2000-257789/23.
 XX
 PT Analysis of RNA samples, useful for detection of differential gene
 PT expression uses two differently labeled primers
 XX
 PS Disclosure; Page 10; 10pp; German.
 XX

CC This invention describes a novel method for analysis of an RNA sample
 CC which comprises amplifying cDNA with first and second differently
 CC labeled primers and analysis of the amplified labeled cDNA. The method
 CC is useful for analyzing differential gene expression, for identifying
 CC and/or characterizing pharmacological activities or for identifying
 CC target genes. The use of different primer combinations allow more cDNAs
 CC to be amplified. The method also provides a more detailed analysis than
 CC prior art methods. This sequence represents a primer used to illustrate
 CC the method of the invention.
 XX
 SQ Sequence 17 BP; 0 A; 0 C; 0 G; 15 T; 2 other;

Query Match 1.4%; Score 15.6; DB 1; Length 17;
 Best Local Similarity 93.8%; Pred. No. 3.2e+02;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAA 1098
 Db 16 KAAAAA 1

RESULT 658
 AAQ82104/c
 ID AAQ82104 standard; DNA; 22 BP.
 XX
 AC AAQ82104;
 XX
 DT 25-MAR-2003 (updated)
 DT 31-AUG-1995 (first entry)
 XX
 DE Chromosome 11 (locus D11S1037) STS primer cSRL-2c7-tz.
 XX
 KW sequence sampled mapping; genomic analysis; complex genome mapping;
 KW cosmid library; chromosome 11; sequence tagged site; STS analysis; ss.
 XX
 OS Synthetic.
 XX
 FN W09429486-A1.
 XX
 PD 22-DEC-1994.
 XX
 XX 15-JUN-1994; 94WO-US06810.
 XX
 PR 15-JUN-1993; 93US-0078471.
 PR 07-SEP-1993; 93US-0117952.
 XX
 PA (SALK) SALK INST BIOLOGICAL STUDIES.
 XX
 PI Evans GA, Smith MW;
 XX
 DR WPI; 1995-036508/05.
 XX
 XX Sequencing complex genomes, present as fragments in a cosmid
 PT library - by sequencing end-specific nucleotides of each clone
 PT then correlating with spatial relationship of cosmid, esp. for
 PT mammalian chromosomes.
 XX
 XX Example 4; Page 66; 128pp; English.
 XX
 CC Sequences were determined from the ends of chromosome 11-specific
 CC cosmids by automated sequencing without intermediate subcloning.
 CC A sample of 371 DNA sequence fragments were determined and of
 CC these, 277 were suitable for STS primer prediction and of
 CC analysis (using the "Primer" program available from E.Lander, MIT).
 CC The STSs and cosmids were mapped by in situ hybridization, somatic
 CC cell hybrid analysis or both. Using this method, 370 STSs specific
 CC for human chromosome 11 were generated and most of them were
 CC regionally mapped. This procedure illustrates a novel method for
 CC sequencing complex genomes, designated "sequence sampled mapping".
 CC The sequence sampled mapping method is useful for the completion of
 CC high density sequence-based maps, and ultimately, for the complete
 CC sequencing of genomic DNA directly from cosmid clones.
 CC See AAQ82001-Q82706 for STS primers.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 22 BP; 5 A; 5 C; 4 G; 8 T; 0 other;
 XX

Query Match 1.4%; Score 15.6; DB 1; Length 22;
 Best Local Similarity 81.8%; Pred. No. 4.1e+02;
 Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 548 CTCTGTAGCCCAACAGACGGA 569
 Db 22 CTTTGTAGCACAAGACGGA 1

RESULT 659
 AAC69375

ID AAC69375 standard; DNA; 22 BP.
 XX
 AC AAC69375;
 XX
 DT 29-JAN-2001 (first entry)
 XX
 DE Human ABC1 BAC contig polymorphic site, SEQ ID NO:274.
 XX
 KW Human ABC1 cholesterol transporter; chromosome 9q31;
 KW ATP-binding cassette; HDL deficiency disorder; high density lipoprotein;
 KW Tangier disease; TD; familial HDL deficiency; FHD; polymorphism;
 KW cardiovascular disease; coronary artery disease; coronary restenosis;
 KW cerebrovascular disease; peripheral vascular disease;
 KW Alzheimer's disease; Niemann-Pick disease; Huntington's disease;
 KW X-linked adrenoleukodystrophy; cancer; gene therapy; genetic diagnosis;
 KW prognosis; prophylaxis; drug screening; transgenic animal; ds.
 XX
 OS Homo sapiens.
 XX
 PN W0200055318-A2.
 XX
 PD 21-SEP-2000.
 XX
 PF 15-MAR-2000; 2000WO-IB00532.
 XX
 PR 15-MAR-1999; 99US-0124702.
 PR 08-JUN-1999; 99US-0138048.
 PR 17-JUN-1999; 99US-0139600.
 PR 01-SEP-1999; 99US-0151977.
 XX
 PA (UYBR-) UNIV BRITISH COLUMBIA.
 PA (XENO-) XENON BIORESEARCH INC.
 XX
 PI Hayden MR, Wilson AR, Pimstone SN;
 XX
 DR WPI; 2000-587528/55.
 XX
 XX New ABC1 polypeptide is useful for treating diseases associated with
 PT ABC1 biological activity, e.g. Alzheimer's disease, Huntington's
 PT disease and cancer -
 XX
 PS Examples; Fig 11; 229pp; English.
 XX

The invention relates to the human ABC1 cholesterol transporter protein (B38082) and to nucleic acid sequences (C69120) which encode it. ABC1 is a member of the ATP-binding cassette (ABC transporter) superfamily of proteins, and plays a crucial role in cholesterol transport, particularly intracellular cholesterol trafficking in monocytes and fibroblasts, being involved in cholesterol efflux from the cell. The gene encoding ABC1 is located on chromosome 9q31, and mutations in this gene are associated with two genetic HDL (high density lipoprotein) deficiency disorders, Tangier disease (TD) and familial HDL deficiency (FHD). These diseases are distinguishable in that TD is an autosomal recessive disorder, while FHD is inherited as an autosomal dominant trait. Low levels of HDL ("good cholesterol") in the blood correlate with a high risk of cardiovascular disease, particularly coronary artery disease, but also cerebrovascular disease, coronary restenosis, and peripheral vascular disease. Conversely, a high level of HDL has protective effects against cardiovascular disease. The invention provides genetic constructs and transgenic cells and non-human animals comprising human ABC1 nucleic acids, and methods of gene therapy for the treatment or prevention of cardiovascular disease comprising the administration of an expression vector encoding ABC1 or an active fragment thereof. The invention also encompasses compounds which mimic ABC1 activity, compounds which stimulate ABC1 expression and methods of screening for such compounds. It further relates to methods for determining whether a patient has an increased risk for cardiovascular disease due to polymorphisms in the ABC1 gene. Human ABC1 proteins and nucleotides can be used to treat or prevent cardiovascular disease, especially coronary artery disease, cerebrovascular disease, coronary restenosis or peripheral vascular disease. They may also be used in the treatment of diseases associated with ABC1 biological activity, such as Alzheimer's disease, Niemann-Pick disease, Huntington's disease, X-linked adrenoleukodystrophy and cancer.

CC The invention specifically excludes proteins with the exact amino acid
CC sequences of GenBank Accession No: CAA10005.1 and X75926, and the nucleic
CC acid with the exact sequence as GenBank Accession No: AJ012376.1.
CC The present sequence represents a polymorphic site of the human ABC1
CC gene.
XX

SQ Sequence 22 BP; 7 A; 2 C; 10 G; 3 T; 0 other;

Query Match 1.4%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 4.1e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 991 TTGGAGCTCAGGCTGAGAA 1012
|||||
Db 1 TTGGAGGCTAAGCAGGAGAA 22

RESULT 660

AAA57767/C

ID AAA57767 standard; DNA; 22 BP.

XX AAA57767;

AC

XX 20-OCT-2000 (first entry)

DT

XX Nucleotide sequence which is bound by Z2 domain of RIP60 polypeptide.

DE

XX Human; RIP60; zinc finger protein; nucleic acid delivery complex;

KW nucleic acid binding domain; nucleic acid condensation domain; ss.

KW

XX Synthetic.

OS

XX WO200040723-A2.

PN

XX 13-JUL-2000.

XX 04-JAN-2000; 2000WO-US00212.

XX 04-JAN-1999; 99US-0114743.

PR 04-JAN-1999; 99US-0114745.

XX (UYVE-) UNIV VERMONT & STATE AGRIC COLLEGE.

PA

XX Heintz NH, Houchens CR;

PI

XX WPI; 2000-465985/40.

DR

XX Non-viral nucleic acid delivery complex for delivering a nucleic acid

PT molecule into a cell comprises a modular polypeptide -

PT

XX Example 17; Page 74; 115pp; English.

PS

XX The present sequence is bound by the Z2 domain of the human RIP60

CC polypeptide. RIP60 is a zinc finger protein. The nucleic acid

CC binding domain of the RIP60 polypeptide is used to construct a

CC non-viral nucleic acid delivery complex comprising a modular

CC polypeptide. The complex comprises a modular peptide containing

CC a nucleic acid binding domain and a nucleic acid condensation domain

CC that bind with and condense a nucleic acid molecule of more than

CC 50 kilobases in length. The complex also comprises one or more

CC polypeptides selected from a cell recognition domain, a protein

CC transduction domain, a protein degradation domain, an intracellular

CC targeting domain, a protein interaction domain, an epitope domain and

CC a protein purification domain. The complexes are used to deliver a

CC nucleic acid to a cell. The nucleic acids delivered are of various

CC sizes and preferably greater than 50 kilobases, especially more than

CC 100 or more than 200 kilobases in length.

XX

SQ Sequence 22 BP; 5 A; 0 C; 1 G; 16 T; 0 other;

Query Match 1.4%; Score 15.6; DB 1; Length 22;

Best Local Similarity 81.8%; Pred. No. 4.1e+02;

Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

CC The invention specifically excludes proteins with the exact amino acid
CC sequences of GenBank Accession No: CAA10005.1 and X75926, and the nucleic
CC acid with the exact sequence as GenBank Accession No: AJ012376.1.
CC The present sequence represents a polymorphic site of the human ABC1
CC gene.
XX

SQ Sequence 22 BP; 7 A; 2 C; 10 G; 3 T; 0 other;

Query Match 1.4%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 4.1e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 991 TTGGAGCTCAGGCTGAGAA 1012
|||||
Db 1 TTGGAGGCTAAGCAGGAGAA 22

RESULT 660

AAA57767/C

ID AAA57767 standard; DNA; 22 BP.

XX AAA57767;

AC

XX 20-OCT-2000 (first entry)

DT

XX Nucleotide sequence which is bound by Z2 domain of RIP60 polypeptide.

DE

XX Human; RIP60; zinc finger protein; nucleic acid delivery complex;

KW nucleic acid binding domain; nucleic acid condensation domain; ss.

KW

XX Synthetic.

OS

XX WO200040723-A2.

PN

XX 13-JUL-2000.

XX 04-JAN-2000; 2000WO-US00212.

XX 04-JAN-1999; 99US-0114743.

PR 04-JAN-1999; 99US-0114745.

XX (UYVE-) UNIV VERMONT & STATE AGRIC COLLEGE.

PA

XX Heintz NH, Houchens CR;

PI

XX WPI; 2000-465985/40.

DR

XX Non-viral nucleic acid delivery complex for delivering a nucleic acid

PT molecule into a cell comprises a modular polypeptide -

PT

XX Example 17; Page 74; 115pp; English.

PS

XX The present sequence is bound by the Z2 domain of the human RIP60

CC polypeptide. RIP60 is a zinc finger protein. The nucleic acid

CC binding domain of the RIP60 polypeptide is used to construct a

CC non-viral nucleic acid delivery complex comprising a modular

CC polypeptide. The complex comprises a modular peptide containing

CC a nucleic acid binding domain and a nucleic acid condensation domain

CC that bind with and condense a nucleic acid molecule of more than

CC 50 kilobases in length. The complex also comprises one or more

CC polypeptides selected from a cell recognition domain, a protein

CC transduction domain, a protein degradation domain, an intracellular

CC targeting domain, a protein interaction domain, an epitope domain and

CC a protein purification domain. The complexes are used to deliver a

CC nucleic acid to a cell. The nucleic acids delivered are of various

CC sizes and preferably greater than 50 kilobases, especially more than

CC 100 or more than 200 kilobases in length.

XX

SQ Sequence 22 BP; 5 A; 0 C; 1 G; 16 T; 0 other;

Query Match 1.4%; Score 15.6; DB 1; Length 22;

Best Local Similarity 81.8%; Pred. No. 4.1e+02;

Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1078 ACTATTAAAAA 1099
|||||
Db 22 ACTAATAATAATAAAAAA 1

RESULT 661

ABQ93623/C

ID ABQ93623 standard; DNA; 22 BP.

XX ABQ93623;

AC

XX 16-OCT-2002 (first entry)

DT

XX Human DISC1/DISC2 PCR primer disc25 f2.

DE

XX Human; Disrupted In Schizophrenia 1; DISC1; neuroleptic; gene therapy;

KW neuropsychiatric disorder; schizoaffective disorder; bipolar disorder;

KW unipolar affective disorder; adolescent conduct disorder;

KW schizophrenia; PCR; primer; ss.

KW

XX Homo sapiens.

OS

XX WO200258637-A2.

PN

XX 01-AUG-2002.

XX 23-JAN-2002; 2002WO-US02186.

PF

XX 24-JAN-2001; 2001US-0770107.

XX (MILL-) MILLENIUM PHARM INC.

XX

XX Meyer JM, Barrington-martin R, Parker A, Barnes GT;

PI

XX WPI; 2002-590791/63.

XX New human Disrupted-In-Schizophrenia (DISC) 1 and DISC2 genes

XX containing single nucleotide polymorphisms, useful for preventing or

XX treating neuropsychiatric disorders e.g. schizophrenia -

XX

XX Claim 17; Figure 4; 169pp; English.

PS

XX The invention relates to a novel Disrupted-In-Schizophrenia (DISC) 1

XX allelic variant polynucleotide. The polypeptides of the invention have

XX neuroleptic activity. The polynucleotides may have a use in gene therapy.

XX DISC1 or DISC2 nucleic acid molecules are useful for diagnosing or

XX treating a subject having a disease or disorder associated with specific

XX DISC1 or DISC2 alleles and/or aberrant DISC1 expression or activity e.g.

XX neuropsychiatric disorder such as schizoaffective, bipolar, unipolar

XX affective or adolescent conduct disorder or schizophrenia. Similarly,

XX the compound that inhibits DISC1 protein activity may be used in the

XX method for treating such neuropsychiatric disorders. The sequences shown

XX in ABQ93575-ABQ93658 represent the PCR primers used in the invention to

XX amplify the sequences of DISC2 and DISC2.

XX

SQ Sequence 22 BP; 5 A; 6 C; 6 G; 5 T; 0 other;

Query Match 1.4%; Score 15.6; DB 1; Length 22;

Best Local Similarity 81.8%; Pred. No. 4.1e+02;

Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1030 GCCTGGCTTTCATAGTGAGGCT 1051

Db 22 GCCTAGACTTCACAGTGAGGCT 1

RESULT 662

AAD31453

ID AAD31453 standard; DNA; 22 BP.

XX AAD31453;

AC

XX

```

DT 31-MAY-2002 (first entry)
XX Human chromosome 17 92Kb gene fragment amplifying PCR primer, wt1r.
DE
XX
XX Human; Van Buchem's disease; genomic deletion; craniotubular hypertosis;
KW autosomal recessive disorder; Chromosome 17; chromosome 17q21;
KW bone dysplasia; 92Kb gene fragment; PCR primer; ss.
OS Homo sapiens.
XX
XX WO200210455-A2.
XX
XX 07-FEB-2002.
XX
XX 30-JUL-2001; 2001WO-US23968.
XX
XX 28-JUL-2000; 2000US-221855P.
XX
XX 06-JUL-2001; 2001US-303386P.
XX
XX (CELL-) CELLTECH R & D INC.
XX (STRA/) STRAEHLING HAMPTON K.
XX
XX Brunkow ME, Proll S, Paepers B;
XX WPI; 2002-227089/28.
XX
XX Methods for identifying subjects who are afflicted with or carriers of
XX diseases associated with genomic deletion(s), e.g. Van Buchem's
XX disease, by determining the presence of a deletion in the 92 kb region
XX of human chromosome 17 at 17q21.
XX
XX Example 3; Page 26; 109pp; English.
XX
XX The present invention relates to methods for distinguishing between
XX individuals homozygous for and therefore afflicted with Van Buchem's
XX disease, individuals heterozygous for and therefore carriers of Van
XX Buchem's disease and individuals who are not afflicted with Van Buchem's
XX disease comprise identifying a large genomic deletion in chromosome 17 at
XX 17q21. The method is useful for identifying individuals who are afflicted
XX with or carriers of diseases associated with one or more genomic
XX deletion, particularly Van Buchem's disease, which is a rare autosomal
XX recessive disorder that results in a bone dysplasia referred to as
XX craniotubular hypertosis. The present sequence is a PCR primer used to
XX amplify 92kb gene fragment in human chromosome 17 at 17q21.
XX
XX Sequence 22 BP; 7 A; 2 C; 10 G; 3 T; 0 other;
XX
XX Query Match 1.4%; Score 15.6; DB 1; Length 22;
XX Best Local Similarity 81.8%; Pred. No. 4.1e+02;
XX Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX QY 992 TGGAGTCTGAGGCTGGAGAAAT 1013
XX Db 1 TGGAGGCTGAGGCAAGAGAAAT 22
XX
XX RESULT 663
XX AAD31457
XX ID AAD31457 standard; DNA; 22 BP.
XX
XX AC AAD31457;
XX
XX 31-MAY-2002 (first entry)
XX
XX Human chromosome 17 92Kb gene fragment amplifying PCR primer, wt3R.
DE
XX
XX Human; Van Buchem's disease; genomic deletion; craniotubular hypertosis;
KW autosomal recessive disorder; Chromosome 17; chromosome 17q21;
KW bone dysplasia; 92Kb gene fragment; PCR primer; ss.
OS Homo sapiens.
XX
XX WO200210455-A2.
XX

```

```

XX 07-FEB-2002.
XX
XX 30-JUL-2001; 2001WO-US23968.
XX
XX 28-JUL-2000; 2000US-221855P.
XX
XX 06-JUL-2001; 2001US-303386P.
XX
XX (CELL-) CELLTECH R & D INC.
XX (STRA/) STRAEHLING HAMPTON K.
XX
XX Brunkow ME, Proll S, Paepers B;
XX WPI; 2002-227089/28.
XX
XX Methods for identifying subjects who are afflicted with or carriers of
XX diseases associated with genomic deletion(s), e.g. Van Buchem's
XX disease, by determining the presence of a deletion in the 92 kb region
XX of human chromosome 17 at 17q21.
XX
XX Example 3; Page 26; 109pp; English.
XX
XX The present invention relates to methods for distinguishing between
XX individuals homozygous for and therefore afflicted with Van Buchem's
XX disease, individuals heterozygous for and therefore carriers of Van
XX Buchem's disease and individuals who are not afflicted with Van Buchem's
XX disease comprise identifying a large genomic deletion in chromosome 17 at
XX 17q21. The method is useful for identifying individuals who are afflicted
XX with or carriers of diseases associated with one or more genomic
XX deletion, particularly Van Buchem's disease, which is a rare autosomal
XX recessive disorder that results in a bone dysplasia referred to as
XX craniotubular hypertosis. The present sequence is a PCR primer used to
XX amplify 92kb gene fragment in human chromosome 17 at 17q21.
XX
XX Sequence 22 BP; 7 A; 2 C; 10 G; 3 T; 0 other;
XX
XX Query Match 1.4%; Score 15.6; DB 1; Length 22;
XX Best Local Similarity 81.8%; Pred. No. 4.1e+02;
XX Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX QY 992 TGGAGTCTGAGGCTGGAGAAAT 1013
XX Db 1 TGGAGGCTGAGGCAAGAGAAAT 22
XX
XX RESULT 664
XX AAA25452/c
XX ID AAA25452 standard; DNA; 17 BP.
XX
XX AC AAA25452;
XX
XX 19-JUL-2000 (first entry)
XX
XX Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1950.
XX
XX Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage;
XX hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
XX gene expression modification; cancer; phosphorothioate; endonuclease;
XX anticancer; breast cancer; endometrium cancer; ss.
XX
XX Homo sapiens.
XX
XX WO9954459-A2.
XX
XX 28-OCT-1999.
XX
XX 19-APR-1999; 99WO-US08547.
XX
XX 20-APR-1998; 98US-0082404.
XX
XX 23-JUN-1998; 98US-0103636.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX

```

```

PI Thompson JD, Beigelman L, McSwiggen JA, Karpeisky A, Bellon L;
PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haerberli P;
PI Matulic-Adamic J;
XX WPI; 2000-013248/01.
XX
XX New nucleic acids that interact, and optionally cleave, target
XX sequences, used to treat cancer -
XX
XX Claim 77; Page 79; 148pp; English.
XX
XX The present invention describes nucleic acids (A) that interact stably
XX with a target sequence and contain at least one phosphorodithioate
XX link, having endonuclease activity. (A), and more generally any
XX catalytic nucleic acid (A') that modulates expression of the oestrogen
XX receptor gene, are used to treat cancer (particularly of breast or
XX endometrium), in vivo or by transforming cells ex vivo and implanting
XX treated cells, or for other conditions associated with levels of
XX oestrogen receptor. Because of the high selectivity for targeted RNA, (A)
XX can also be used to correlate inhibition of gene expression with
XX alterations in phenotype, particularly for identification of therapeutic
XX targets, and as research reagents (for RNA, in the same way that
XX restriction endonucleases are used with DNA). The combination of
XX modifications in (A) improves resistance to nucleases, binding affinity
XX and/or activity. AAA23503 to AAA24747 represent oestrogen receptor
XX hammerhead ribozyme sequences, and AAA24748 to AAA25992 represent their
XX corresponding target sequences. AAA25993 to AAA26105 represent oestrogen
XX receptor hairpin ribozyme sequences, and AAA26107 to AAA26218 represent
XX their corresponding target sequences. AAA26219 to AAA26271 represent
XX other ribozyme sequences and antisense oligonucleotides used in the
XX exemplification of the present invention.
XX
XX Sequence 17 BP; 0 A; 0 C; 1 G; 16 T; 0 other;
SQ
Query Match 1.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 3.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1084 AAAAAAAAAAAAAA 1100
DB 17 AAAAAAAAAAAAAA 1
RESULT 665
AAA25453/c
ID AAA25453 standard; DNA; 17 BP.
XX
XX AAA25453;
XX
XX 19-JUL-2000 (first entry)
XX
XX Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1951.
XX
XX Oestrogen receptor; c-ras; bcl-2; ribozyme; cleavage;
XX hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
XX gene expression modification; cancer; phosphorothioate; endonuclease;
XX anticancer; breast cancer; endometrium cancer; ss.
XX
XX Homo sapiens.
XX
XX WO9954459-A2.
XX
XX 28-OCT-1999.
XX
XX 19-APR-1999; 99WO-US08547.
XX
XX 20-APR-1998; 98US-0082404.
XX 23-JUN-1998; 98US-0103636.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Thompson JD, Beigelman L, McSwiggen JA, Karpeisky A, Bellon L;
PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haerberli P;

```

```

PI Matulic-Adamic J;
XX WPI; 2000-013248/01.
XX
XX New nucleic acids that interact, and optionally cleave, target
XX sequences, used to treat cancer -
XX
XX Claim 77; Page 79; 148pp; English.
XX
XX The present invention describes nucleic acids (A) that interact stably
XX with a target sequence and contain at least one phosphorodithioate
XX link, having endonuclease activity. (A), and more generally any
XX catalytic nucleic acid (A') that modulates expression of the oestrogen
XX receptor gene, are used to treat cancer (particularly of breast or
XX endometrium), in vivo or by transforming cells ex vivo and implanting
XX treated cells, or for other conditions associated with levels of
XX oestrogen receptor. Because of the high selectivity for targeted RNA, (A)
XX can also be used to correlate inhibition of gene expression with
XX alterations in phenotype, particularly for identification of therapeutic
XX targets, and as research reagents (for RNA, in the same way that
XX restriction endonucleases are used with DNA). The combination of
XX modifications in (A) improves resistance to nucleases, binding affinity
XX and/or activity. AAA23503 to AAA24747 represent oestrogen receptor
XX hammerhead ribozyme sequences, and AAA24748 to AAA25992 represent their
XX corresponding target sequences. AAA25993 to AAA26105 represent oestrogen
XX receptor hairpin ribozyme sequences, and AAA26107 to AAA26218 represent
XX their corresponding target sequences. AAA26219 to AAA26271 represent
XX other ribozyme sequences and antisense oligonucleotides used in the
XX exemplification of the present invention.
XX
XX Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 other;
SQ
Query Match 1.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 3.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1083 TAAAAAAAAAAAAA 1099
DB 17 TACAAAAAAAAAAAAA 1
RESULT 666
AAD44151/c
ID AAD44151 standard; DNA; 17 BP.
XX
XX AAD44151;
XX
XX 13-DEC-2002 (first entry)
XX
XX Oligo-AT PCR primer #2 used to illustrate the method of the invention.
XX
XX Sequential consensus region-directed amplification; gene expression;
XX disease diagnosis; gene analysis; human; matrix metalloproteinase;
XX PCR; primer; ss.
XX
XX Unidentified.
XX
XX US6277571-B1.
XX
XX 21-AUG-2001.
XX
XX 30-SBP-1998; 98US-0163485.
XX
XX 03-OCT-1997; 97US-108152P.
XX
XX (UTVI-) UNIV VIRGINIA COMMONWEALTH INTELLECTUAL.
XX
XX Fillmore H, Broadus W, Gillies G;
XX WPI; 2002-412824/44.
XX
XX Sequential consensus region-directed amplification for sorting mixture
XX of DNAs into 2 or more subsets or distinguishing gene expression
XX

```


PT patterns in 2 samples, useful for disease diagnosis and gene analysis -
 XX
 XX Example; Fig 1D; 19pp; English.
 XX
 CC The invention relates to a method of sequential consensus region-directed
 CC amplification for sorting a mixture of DNAs into 2 or more subsets or
 CC distinguishing gene expression patterns in 2 samples. The methods, kits
 CC and oligonucleotides are useful for sorting a mixture of DNAs into 2 or
 CC more subsets or distinguishing gene expression patterns in 2 samples
 CC e.g. for disease diagnosis and gene analysis. The present sequence is
 CC oligo AT PCR primer used to illustrate the method of the invention.
 XX
 SQ Sequence 17 BP; 0 A; 0 C; 0 G; 16 T; 1 other;
 Query Match 1.4%; Score 15.4; DB 1; Length 17;
 Best Local Similarity 94.1%; Pred. No. 3.4e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1084 AAAAAAAAAAAAAA 1100
 Db 17 AAAAAAAAAAAAAA 1
 RESULT 667
 ABA91530/c
 ID ABA91530 standard; DNA; 17 BP.
 AC ABA91530;
 DT 23-APR-2002 (first entry)
 DE DNA-RNA-DNA oligonucleotide AGT02014 used to test RNase H cleavage.
 XX DNA-RNA hybrid; RNase H; nucleic acid detection; ss.
 XX Synthetic.
 OS
 FH Key Location/Qualifiers
 FT misc_RNA 8
 FT /*tag= a
 FT /label= "RNA"
 XX
 PN WO200206531-A2.
 XX 24-JAN-2002.
 PD
 PF 12-JUL-2001; 2001WO-US22166.
 XX
 PR 14-JUL-2000; 2000US-0616761.
 PR 30-MAR-2001; 2001US-0823647.
 XX
 PA (GENE-) APPLIED GENE TECHNOLOGIES INC.
 XX
 PI Dattagupta N;
 XX
 DR WPI; 2002-171819/22.
 XX
 PT Probes for detecting target nucleotide sequence in sample, has sequence
 PT that forms hairpin structure having a double-stranded segment and
 PT single-stranded loop collectively forming region complementary to
 PT target sequence -
 XX
 PS Example 4; Page 49; 72pp; English.
 XX
 CC The present sequence is that of DNA-RNA-DNA hybrid oligonucleotide
 CC AGT02014. This is one of a set of oligonucleotides (see
 CC ABA91527-30) used to assess the minimum number of ribonucleotides
 CC in DNA-RNA chimeric oligonucleotides required for RNase H cleavage.
 CC Each oligonucleotide of the set had a different number of
 CC ribonucleotides, 1 in the present case. The oligonucleotides were
 CC mixed with target DNA oligonucleotide AGT02009 (see ABA91531) and
 CC incubated with RNase H (5 U/ml) at 37 degrees C for 30 minutes.
 CC The results showed that 4 ribonucleotides were the minimum number

CC for RNA cleavage. The invention provides probes for nucleic acid
 CC hybridisation. The probes form a hairpin structure comprising a
 CC double-stranded stem and a single-stranded loop, and are capable of
 CC both intramolecular and intermolecular hybridisation. The
 CC double-stranded stem may comprise a methylphosphonate DNA:RNA hybrid
 CC that is resistant to RNase H cleavage. When the probe hybridises
 CC with a target DNA, the RNA strand in the DNA:RNA duplex becomes
 CC sensitive to RNase H treatment and can be removed. Arrays and
 CC methods for nucleic acid hybridisation using the probes are provided.
 XX
 SQ Sequence 17 BP; 1 A; 0 C; 0 G; 16 T; 0 other;
 Query Match 1.4%; Score 15.4; DB 1; Length 17;
 Best Local Similarity 94.1%; Pred. No. 3.4e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1084 AAAAAAAAAAAAAA 1100
 Db 17 AAAAAAAAAAAAAA 1
 RESULT 668
 AAQ20108/c
 ID AAQ20108 standard; DNA; 18 BP.
 AC AAQ20108;
 XX
 DT 01-APR-1992 (first entry)
 DE
 DE Cross-linking oligomer 942 to target human TNF Receptor mRNA.
 XX deoxyribonucleic acid; major groove; ethanoino group;
 KW tumour necrosis factor; receptor; messenger RNA; aziridinylcytosine;
 KW cross-linking group; ss.
 XX Synthetic.
 OS
 FH Key Location/Qualifiers
 FT modified_base 5
 FT /*tag= a
 FT /mod_base= m5c
 FT modified_base 18
 FT /*tag= b
 FT /mod_base= OTHER
 FT /note= "N4N4-ethanocytosine"
 XX
 PN WO9118997-A.
 XX
 PD 12-DEC-1991.
 XX
 PF 24-MAY-1991; 91WO-1003680.
 XX
 PR 14-JAN-1991; 91US-0640654.
 PR 25-MAY-1990; 90US-0529346.
 XX
 PA (GILE-) GILEAD SCIE INC.
 XX
 PI Matteucci MD, Krawczyk S;
 XX
 DR WPI; 1992-007480/01.
 XX
 PT New sequence-specific non-photo-activated crosslinking agents -
 PT bind to the major groove of duplex DNA and are esp. useful for
 PT treating latent infections e.g. HIV
 XX
 PS Example 4; Page 27; 42pp; English.
 XX
 CC The oligomer was designed to target human TNF receptor mRNA
 CC beginning at nucleotide 2354 and to covalently cross-link to
 CC the target via the N4N4-ethanocytosine group. See also AAQ20109.
 XX
 SQ Sequence 18 BP; 0 A; 2 C; 0 G; 16 T; 0 other;

Query Match 1.4%; Score 15.4; DB 1; Length 18;
 Best Local Similarity 94.1%; Pred. No. 3.6e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
 DB 17 AAAAAAAAAAGAAAAA 1

RESULT 669

AAQ20109/c
 ID AAQ20109 standard; DNA; 18 BP.
 XX
 AC AAQ20109;
 XX
 DT 01-APR-1992 (first entry)
 XX
 DE Cross-linking oligomer 943 to target human TNF Receptor mRNA.
 XX
 KW deoxyribonucleic acid; major groove; ethanoino group;
 XX
 KW tumour necrosis factor; receptor; messenger RNA; aziridinylcytosine;
 XX
 KW cross-linking group; ss.
 OS Synthetic.

Key Location/Qualifiers
 modified_base 5 /*tag= a
 FT /mod_base= OTHER
 FT /note= "N-methyl-8-oxo-2'-deoxyadenine"
 FT modified_base 18
 FT /*tag= b
 FT /mod_base= OTHER
 FT /note= "N4N4-ethanocytosine"

XX
 PN WO9118997-A.
 XX
 XX
 PD 12-DEC-1991.
 XX
 XX
 PF 24-MAY-1991; 91WO-1003680.
 XX
 XX
 PR 14-JAN-1991; 91US-0640654.
 PR 25-MAY-1990; 90US-0529346.
 XX
 XX
 PA (GILE-) GILEAD SCIE INC.
 XX
 PI Matteucci MD, Krawczyk S;
 XX
 DR WPI; 1992-007480/01.
 XX
 XX
 PT New sequence-specific non-photo-activated crosslinking agents -
 PT bind to the major groove of duplex DNA and are esp. useful for
 PT treating latent infections e.g. HIV
 XX
 PS Example 4; Page 27; 42pp; English.
 XX
 CC The oligomer was designed to target human TNF receptor mRNA
 CC beginning at nucleotide 2354 and to covalently cross-link to
 CC the target via the N4N4-ethanocytosine group. See also AAQ20108.
 XX
 SQ Sequence 18 BP; 1 A; 1 C; 0 G; 16 T; 0 other;

Query Match 1.4%; Score 15.4; DB 1; Length 18;
 Best Local Similarity 94.1%; Pred. No. 3.6e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
 DB 17 AAAAAAAAAATATAA 1

RESULT 670
 AAQ25501

ID AAQ25501 standard; DNA; 18 BP.
 XX
 AC AAQ25501;

XX
 DT 25-MAR-2003 (updated)
 DT 07-DEC-1992 (first entry)
 XX

DE Purine rich HUMNFR target duplex sequence.

XX
 KW Target; human tumour necrosis factor receptor mRNA; AIDS; triplex;
 KW HIV; hepatitis; malignancy; inflammation; ds.
 XX
 OS Synthetic.

XX
 PN WO9209705-A1.
 XX

PD 11-JUN-1992.

XX
 PF 25-NOV-1991; 91WO-US08811.

XX
 PR 23-NOV-1990; 90US-0617907.

PR 18-JAN-1991; 91US-0643382.

PR 08-APR-1991; 91US-0683420.

PR 17-APR-1991; 91US-0686544.

PR 17-APR-1991; 91US-0686546.

PR 17-APR-1991; 91US-0686547.

PR 27-SEP-1991; 91US-0766733.

XX
 PA (GILE-) GILEAD SCI INC.

XX
 PI Froehler B, Krawczyk S, Matteucci MD, Milligan J;

XX
 DR WPI; 1992-217083/26.

XX
 PT New oligomers contg. modified bases - which form a triplex with
 PT G-C doublet in a DNA duplex, for treating and diagnosing HIV,
 PT hepatitis, herpes, malignancy and inflammation
 XX

PS Claim 11; Page 64; 77pp; English.

XX
 CC The sequence depicts a HUMNFR (tumour necrosis factor receptor) mRNA
 CC sequence beginning at nucleotide 2354. The sequence is a viral duplex
 CC sequence contg. a purine-rich region concentrated on one chain of the
 CC duplex. The sequence may be prep'd. by standard DNA synthesis. The
 CC HUMNFR duplex sequence is used as a target for novel oligomers which
 CC are capable of forming a triplex at physiological pH by coupling into
 CC the major groove of the DNA duplex. Three such oligomers TNFR 941-32
 CC are capable of forming a triplex with this sequence. The oligomers
 CC are used in the treatment of inflammation. Similar oligomers may
 CC be used to target viral DNA duplexes specific for HIV, herpes and
 CC other viruses. The triple helices form under mild conditions thus
 CC assays may be carried out without subjecting the test specimen to
 CC harsh conditions. The oligomer is able to inhibit gene expression,
 CC as verified by in vitro systems.
 CC See also AAQ25452-25500 and AAQ30226-448.
 CC (Updated on 25-MAR-2003 to correct PN field.)

XX
 SQ Sequence 18 BP; 16 A; 0 C; 2 G; 0 U; 0 other;

Query Match 1.4%; Score 15.4; DB 1; Length 18;
 Best Local Similarity 94.1%; Pred. No. 3.6e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
 DB 1 AAAAAAAAAAAAAAAAAA 17

RESULT 671
 AAQ30447/C
 ID AAQ30447 standard; DNA; 18 BP.
 XX
 AC AAQ30447;

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 8, 2004, 16:08:28 ; Search time 35 Seconds
(without alignments)

1.937 Million cell updates/sec

Title: us-09-904-568-1

Perfect score: 1100

Sequence: 1 gcacgagccacgcagcagctta.....attaaaaa1100

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 0.5

Searched: 1682 seqs, 30821 residues

Total number of hits satisfying chosen parameters: 3364

Minimum DB seq length: 12

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1690 summaries

Database : rng1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| C 1 | 21 | 1.9 | 21 | 1 | AAQ75728 |
| C 2 | 21 | 1.9 | 30 | 1 | AAQ71444 |
| C 3 | 20.2 | 1.8 | 25 | 1 | AAH38447 |
| C 4 | 20 | 1.8 | 20 | 1 | AAQ75581 |
| C 5 | 20 | 1.8 | 21 | 1 | AAQ75727 |
| C 6 | 20 | 1.8 | 21 | 1 | AAQ75729 |
| C 7 | 20 | 1.8 | 21 | 1 | AAQ75730 |
| C 8 | 19.6 | 1.8 | 27 | 1 | AAV71936 |
| C 9 | 19.6 | 1.8 | 27 | 1 | ABK52620 |
| C 10 | 19.4 | 1.8 | 21 | 1 | AAQ75724 |
| C 11 | 19.4 | 1.8 | 21 | 1 | AAQ75732 |
| C 12 | 19.4 | 1.8 | 21 | 1 | AAQ75760 |
| C 13 | 19.4 | 1.8 | 21 | 1 | AAQ75696 |
| C 14 | 19.4 | 1.8 | 21 | 1 | AAQ75712 |
| C 15 | 19.4 | 1.8 | 21 | 1 | AAQ75720 |
| C 16 | 19.4 | 1.8 | 21 | 1 | AAQ75680 |
| C 17 | 19.4 | 1.8 | 21 | 1 | AAQ75675 |
| C 18 | 19.4 | 1.8 | 21 | 1 | AAQ75632 |
| C 19 | 19.4 | 1.8 | 24 | 1 | ABK12409 |
| C 20 | 19.4 | 1.8 | 24 | 1 | RAI66361 |
| C 21 | 19.2 | 1.7 | 25 | 1 | ABK86170 |
| C 22 | 19.2 | 1.7 | 27 | 1 | ABX79828 |
| C 23 | 19 | 1.7 | 19 | 1 | AAQ75552 |
| C 24 | 19 | 1.7 | 20 | 1 | AAQ75580 |
| C 25 | 19 | 1.7 | 20 | 1 | AAQ75582 |
| C 26 | 19 | 1.7 | 20 | 1 | AAQ75579 |
| C 27 | 19 | 1.7 | 21 | 1 | AAQ75723 |
| C 28 | 19 | 1.7 | 21 | 1 | AAQ75725 |
| C 29 | 19 | 1.7 | 21 | 1 | AAQ75726 |
| C 30 | 19 | 1.7 | 21 | 1 | AAQ75731 |
| C 31 | 19 | 1.7 | 21 | 1 | AAQ75733 |
| C 32 | 19 | 1.7 | 21 | 1 | AAQ75734 |
| C 33 | 19 | 1.7 | 21 | 1 | AAQ75719 |

| | | | | | | |
|-------|------|-----|----|---|----------|---------------------|
| C 34 | 19 | 1.7 | 21 | 1 | AAQ75721 | Reverse transcript |
| C 35 | 19 | 1.7 | 21 | 1 | AAQ75722 | Reverse transcript |
| C 36 | 19 | 1.7 | 24 | 1 | ABK86168 | Oligo dt primer #1 |
| C 37 | 19 | 1.7 | 24 | 1 | ABK86169 | Oligo dt primer #2 |
| C 38 | 19 | 1.7 | 27 | 1 | AAV71935 | Anchored poly T RT |
| C 39 | 19 | 1.7 | 27 | 1 | ABK65992 | Human gene specific |
| C 40 | 18.8 | 1.7 | 24 | 1 | AAU47515 | Human cyclophilin- |
| C 41 | 18.6 | 1.7 | 25 | 1 | AAK84258 | PCR primer for hum |
| C 42 | 18.6 | 1.7 | 25 | 1 | AAK96240 | 16s rRNA gene PCR |
| C 43 | 18.6 | 1.7 | 26 | 1 | AAK78723 | Human pancreatic p |
| C 44 | 18.6 | 1.7 | 26 | 1 | AAK07466 | Human BS124 specif |
| C 45 | 18.4 | 1.7 | 20 | 1 | AAQ75697 | Reverse transcript |
| C 46 | 18.4 | 1.7 | 20 | 1 | AAQ75697 | Reverse transcript |
| C 47 | 18.4 | 1.7 | 20 | 1 | AAQ75684 | Reverse transcript |
| C 48 | 18.4 | 1.7 | 20 | 1 | AAQ75589 | Reverse transcript |
| C 49 | 18.4 | 1.7 | 20 | 1 | AAQ75577 | Reverse transcript |
| C 50 | 18.4 | 1.7 | 20 | 1 | AAQ75565 | Reverse transcript |
| C 51 | 18.4 | 1.7 | 21 | 1 | AAQ75757 | Reverse transcript |
| C 52 | 18.4 | 1.7 | 21 | 1 | AAQ75759 | Reverse transcript |
| C 53 | 18.4 | 1.7 | 21 | 1 | AAQ75761 | Reverse transcript |
| C 54 | 18.4 | 1.7 | 21 | 1 | AAQ75762 | Reverse transcript |
| C 55 | 18.4 | 1.7 | 21 | 1 | AAQ75695 | Reverse transcript |
| C 56 | 18.4 | 1.7 | 21 | 1 | AAQ75697 | Reverse transcript |
| C 57 | 18.4 | 1.7 | 21 | 1 | AAQ75698 | Reverse transcript |
| C 58 | 18.4 | 1.7 | 21 | 1 | AAQ75711 | Reverse transcript |
| C 59 | 18.4 | 1.7 | 21 | 1 | AAQ75713 | Reverse transcript |
| C 60 | 18.4 | 1.7 | 21 | 1 | AAQ75714 | Reverse transcript |
| C 61 | 18.4 | 1.7 | 21 | 1 | AAQ75678 | Reverse transcript |
| C 62 | 18.4 | 1.7 | 21 | 1 | AAQ75679 | Reverse transcript |
| C 63 | 18.4 | 1.7 | 21 | 1 | AAQ75681 | Reverse transcript |
| C 64 | 18.4 | 1.7 | 21 | 1 | AAQ75682 | Reverse transcript |
| C 65 | 18.4 | 1.7 | 21 | 1 | AAQ75676 | Reverse transcript |
| C 66 | 18.4 | 1.7 | 21 | 1 | AAQ75677 | Reverse transcript |
| C 67 | 18.4 | 1.7 | 21 | 1 | AAQ75629 | Reverse transcript |
| C 68 | 18.4 | 1.7 | 21 | 1 | AAQ75631 | Reverse transcript |
| C 69 | 18.4 | 1.7 | 21 | 1 | AAQ75633 | Reverse transcript |
| C 70 | 18.4 | 1.7 | 21 | 1 | AAQ75634 | Reverse transcript |
| C 71 | 18.4 | 1.7 | 22 | 1 | ABK92338 | Reverse transcript |
| C 72 | 18.4 | 1.7 | 24 | 1 | ABV77669 | PolyA adaptor olig |
| C 73 | 18.4 | 1.7 | 25 | 1 | AAH39959 | Human zinc finger |
| C 74 | 18.2 | 1.7 | 24 | 1 | AAH76998 | SNP specific SNPE |
| C 75 | 18.2 | 1.7 | 25 | 1 | AAC96060 | Human amyloid prec |
| C 76 | 18.2 | 1.7 | 25 | 1 | AAC96085 | 16s rRNA gene PCR |
| C 77 | 18 | 1.6 | 18 | 1 | AAK94667 | 16s rRNA gene PCR |
| C 78 | 18 | 1.6 | 18 | 1 | AAK18372 | Anchored poly (T) o |
| C 79 | 18 | 1.6 | 19 | 1 | AAQ75553 | RT-PCR primer of t |
| C 80 | 18 | 1.6 | 19 | 1 | AAQ75554 | Reverse transcript |
| C 81 | 18 | 1.6 | 19 | 1 | AAQ75551 | Reverse transcript |
| C 82 | 18 | 1.6 | 20 | 1 | AAQ49436 | Reverse transcript |
| C 83 | 18 | 1.6 | 20 | 1 | AAK04916 | Cytochrome P450 se |
| C 84 | 18 | 1.6 | 20 | 1 | AAQ75583 | Mammalian stem cel |
| C 85 | 18 | 1.6 | 20 | 1 | AAQ75586 | Reverse transcript |
| C 86 | 18 | 1.6 | 20 | 1 | AAQ75587 | Reverse transcript |
| C 87 | 18 | 1.6 | 20 | 1 | AAQ75588 | Reverse transcript |
| C 88 | 18 | 1.6 | 20 | 1 | AAQ75590 | Reverse transcript |
| C 89 | 18 | 1.6 | 20 | 1 | AAQ75575 | Reverse transcript |
| C 90 | 18 | 1.6 | 20 | 1 | AAQ75576 | Reverse transcript |
| C 91 | 18 | 1.6 | 20 | 1 | AAQ75578 | Reverse transcript |
| C 92 | 18 | 1.6 | 20 | 1 | AAV07752 | Phosphorothioate o |
| C 93 | 18 | 1.6 | 20 | 1 | AAAL3753 | Stem cell factor u |
| C 94 | 18 | 1.6 | 20 | 1 | AAAL0448 | Human stem cell fa |
| C 95 | 18 | 1.6 | 20 | 1 | AAH41332 | Universal stem cel |
| C 96 | 18 | 1.6 | 20 | 1 | AAK04112 | Human SCF (stem ce |
| C 97 | 18 | 1.6 | 20 | 1 | AAK04213 | Human SCF (stem ce |
| C 98 | 18 | 1.6 | 20 | 1 | AAH23890 | Human SCF (stem ce |
| C 99 | 18 | 1.6 | 20 | 1 | AAK89092 | Mammalian stem cel |
| C 100 | 18 | 1.6 | 20 | 1 | ABK73849 | SCF universal olig |
| C 101 | 18 | 1.6 | 20 | 1 | ABK35465 | Rat SCF 5' cDNA am |
| C 102 | 18 | 1.6 | 21 | 1 | AAQ75691 | Reverse transcript |
| C 103 | 18 | 1.6 | 21 | 1 | AAQ75692 | Reverse transcript |
| C 104 | 18 | 1.6 | 21 | 1 | AAQ75693 | Reverse transcript |
| C 105 | 18 | 1.6 | 21 | 1 | AAQ75694 | Reverse transcript |
| C 106 | 18 | 1.6 | 21 | 1 | AAQ75699 | Reverse transcript |

| | | | | | | | | | | | | |
|-------|----|-----|----|----------|--------------------|-------|------|-----|----|---|----------|--------------------|
| C 107 | 18 | 1.6 | 1 | AAQ75700 | Reverse transcript | C 180 | 17.6 | 1.6 | 25 | 1 | AAQ96858 | HLA HLA-C gene PCR |
| C 108 | 18 | 1.6 | 21 | AAQ75701 | Reverse transcript | C 181 | 17.6 | 1.6 | 25 | 1 | AAA39306 | Rapid capture prob |
| C 109 | 18 | 1.6 | 21 | AAQ75702 | Reverse transcript | C 182 | 17.6 | 1.6 | 25 | 1 | AAZ30267 | Capture probe Cpl2 |
| C 110 | 18 | 1.6 | 21 | AAQ75703 | Reverse transcript | C 183 | 17.6 | 1.6 | 25 | 1 | ABK49986 | Example oligonucle |
| C 111 | 18 | 1.6 | 21 | AAQ75704 | Reverse transcript | C 184 | 17.4 | 1.6 | 19 | 1 | AAQ75556 | Reverse transcript |
| C 112 | 18 | 1.6 | 21 | AAQ75705 | Reverse transcript | C 185 | 17.4 | 1.6 | 19 | 1 | AAQ75558 | Reverse transcript |
| C 113 | 18 | 1.6 | 21 | AAQ75706 | Reverse transcript | C 186 | 17.4 | 1.6 | 20 | 1 | AAQ75596 | Reverse transcript |
| C 114 | 18 | 1.6 | 21 | AAQ75707 | Reverse transcript | C 187 | 17.4 | 1.6 | 20 | 1 | AAQ75598 | Reverse transcript |
| C 115 | 18 | 1.6 | 21 | AAQ75708 | Reverse transcript | C 188 | 17.4 | 1.6 | 20 | 1 | AAQ75595 | Reverse transcript |
| C 116 | 18 | 1.6 | 21 | AAQ75709 | Reverse transcript | C 189 | 17.4 | 1.6 | 20 | 1 | AAQ75596 | Reverse transcript |
| C 117 | 18 | 1.6 | 21 | AAQ75710 | Reverse transcript | C 190 | 17.4 | 1.6 | 20 | 1 | AAQ75566 | Reverse transcript |
| C 118 | 18 | 1.6 | 21 | AAQ75711 | Reverse transcript | C 191 | 17.4 | 1.6 | 20 | 1 | AAQ75564 | Reverse transcript |
| C 119 | 18 | 1.6 | 21 | AAQ75712 | Reverse transcript | C 192 | 17.4 | 1.6 | 20 | 1 | AAQ91207 | Reverse transcript |
| C 120 | 18 | 1.6 | 21 | AAQ75713 | Reverse transcript | C 193 | 17.4 | 1.6 | 21 | 1 | AAQ75751 | Antisense IGFBP-5 |
| C 121 | 18 | 1.6 | 21 | AAQ75714 | Reverse transcript | C 194 | 17.4 | 1.6 | 21 | 1 | AAQ75753 | Reverse transcript |
| C 122 | 18 | 1.6 | 21 | AAQ75715 | Reverse transcript | C 195 | 17.4 | 1.6 | 21 | 1 | AAQ75753 | Reverse transcript |
| C 123 | 18 | 1.6 | 21 | AAQ75716 | Reverse transcript | C 196 | 17.4 | 1.6 | 21 | 1 | AAQ75754 | Reverse transcript |
| C 124 | 18 | 1.6 | 21 | AAQ75717 | Reverse transcript | C 197 | 17.4 | 1.6 | 21 | 1 | AAQ75772 | Reverse transcript |
| C 125 | 18 | 1.6 | 21 | AAQ75718 | Reverse transcript | C 198 | 17.4 | 1.6 | 21 | 1 | AAQ75755 | Reverse transcript |
| C 126 | 18 | 1.6 | 21 | AAQ75719 | Reverse transcript | C 199 | 17.4 | 1.6 | 21 | 1 | AAQ75758 | Reverse transcript |
| C 127 | 18 | 1.6 | 21 | AAQ75720 | Reverse transcript | C 200 | 17.4 | 1.6 | 21 | 1 | AAQ75763 | Reverse transcript |
| C 128 | 18 | 1.6 | 21 | AAQ75721 | Reverse transcript | C 201 | 17.4 | 1.6 | 21 | 1 | AAQ75765 | Reverse transcript |
| C 129 | 18 | 1.6 | 21 | AAQ75722 | Reverse transcript | C 202 | 17.4 | 1.6 | 21 | 1 | AAQ75766 | Reverse transcript |
| C 130 | 18 | 1.6 | 21 | AAQ75723 | Reverse transcript | C 203 | 17.4 | 1.6 | 21 | 1 | AAQ75630 | Reverse transcript |
| C 131 | 18 | 1.6 | 21 | AAQ75724 | Reverse transcript | C 204 | 17.4 | 1.6 | 21 | 1 | AAQ75635 | Reverse transcript |
| C 132 | 18 | 1.6 | 21 | AAQ75725 | Reverse transcript | C 205 | 17.4 | 1.6 | 21 | 1 | AAQ75637 | Reverse transcript |
| C 133 | 18 | 1.6 | 21 | AAQ75726 | Reverse transcript | C 206 | 17.4 | 1.6 | 21 | 1 | AAQ75638 | Reverse transcript |
| C 134 | 18 | 1.6 | 21 | AAQ75727 | Reverse transcript | C 207 | 17.4 | 1.6 | 21 | 1 | AAQ75623 | Reverse transcript |
| C 135 | 18 | 1.6 | 21 | AAQ75728 | Reverse transcript | C 208 | 17.4 | 1.6 | 21 | 1 | AAQ75625 | Reverse transcript |
| C 136 | 18 | 1.6 | 21 | AAQ75729 | Reverse transcript | C 209 | 17.4 | 1.6 | 21 | 1 | AAQ75626 | Reverse transcript |
| C 137 | 18 | 1.6 | 21 | AAQ75730 | Reverse transcript | C 210 | 17.4 | 1.6 | 21 | 1 | AAQ75627 | Reverse transcript |
| C 138 | 18 | 1.6 | 21 | AAQ75731 | Reverse transcript | C 211 | 17.4 | 1.6 | 21 | 1 | AAQ75644 | Reverse transcript |
| C 139 | 18 | 1.6 | 21 | AAQ75732 | Reverse transcript | C 212 | 17.4 | 1.6 | 21 | 1 | AAQ75644 | Reverse transcript |
| C 140 | 18 | 1.6 | 21 | AAQ75733 | Reverse transcript | C 213 | 17.4 | 1.6 | 21 | 1 | AAQ75644 | Reverse transcript |
| C 141 | 18 | 1.6 | 21 | AAQ75734 | Reverse transcript | C 214 | 17.4 | 1.6 | 21 | 1 | AAQ75644 | Reverse transcript |
| C 142 | 18 | 1.6 | 21 | AAQ75735 | Reverse transcript | C 215 | 17.2 | 1.6 | 19 | 1 | AAQ75644 | Reverse transcript |
| C 14 | | | | | | | | | | | | |

| | | | | | | |
|-------|----|-----|----|---|-----------|--------------------|
| C 253 | 17 | 1.5 | 18 | 1 | AAX19943 | Primer SEQ ID NO:3 |
| C 254 | 17 | 1.5 | 18 | 1 | AAX18373 | RT-PCR primer of t |
| C 255 | 17 | 1.5 | 18 | 1 | AAA40563 | Human adult ovary |
| C 256 | 17 | 1.5 | 18 | 1 | AAX290646 | Human adipose ti |
| C 257 | 17 | 1.5 | 18 | 1 | AAX287161 | Oligoarabinonucleo |
| C 258 | 17 | 1.5 | 18 | 1 | AAX287162 | Oligoarabinonucleo |
| C 259 | 17 | 1.5 | 18 | 1 | AAX287166 | Deoxyarabinonucleo |
| C 260 | 17 | 1.5 | 18 | 1 | AAX287167 | Deoxyarabinonucleo |
| C 261 | 17 | 1.5 | 18 | 1 | AAD20091 | mRNA fragment used |
| C 262 | 17 | 1.5 | 18 | 1 | AAF82472 | Phagemid vector pC |
| C 263 | 17 | 1.5 | 18 | 1 | AAD03565 | Oligonucleotide #6 |
| C 264 | 17 | 1.5 | 18 | 1 | AAF99708 | Immunostimulatory |
| C 265 | 17 | 1.5 | 18 | 1 | AAF99734 | Immunostimulatory |
| C 266 | 17 | 1.5 | 18 | 1 | ABL17014 | Oligonucleotide A1 |
| C 267 | 17 | 1.5 | 18 | 1 | ABS78429 | Angiogenesis inhib |
| C 268 | 17 | 1.5 | 18 | 1 | ABS78455 | Angiogenesis inhib |
| C 269 | 17 | 1.5 | 18 | 1 | ABS53437 | Poly d(T) primer. |
| C 270 | 17 | 1.5 | 18 | 1 | AAD41497 | Oligonucleotide us |
| C 271 | 17 | 1.5 | 18 | 1 | AS94743 | Rat secreted facto |
| C 272 | 17 | 1.5 | 18 | 1 | ABA93239 | Adaptor oligonucle |
| C 273 | 17 | 1.5 | 18 | 1 | ABL39401 | Immunostimulatory |
| C 274 | 17 | 1.5 | 18 | 1 | AAQ75555 | Reverse transcript |
| C 275 | 17 | 1.5 | 19 | 1 | AAQ75557 | Reverse transcript |
| C 276 | 17 | 1.5 | 19 | 1 | AAQ75558 | Reverse transcript |
| C 277 | 17 | 1.5 | 19 | 1 | AAQ75549 | Reverse transcript |
| C 278 | 17 | 1.5 | 19 | 1 | AAQ75550 | Reverse transcript |
| C 279 | 17 | 1.5 | 19 | 1 | AAQ75547 | Reverse transcript |
| C 280 | 17 | 1.5 | 19 | 1 | AAAT10757 | Reverse transcript |
| C 281 | 17 | 1.5 | 19 | 1 | AAV07878 | Oligonucleotide pr |
| C 282 | 17 | 1.5 | 19 | 1 | AAV06820 | Aminoxy-modified |
| C 283 | 17 | 1.5 | 19 | 1 | AAZ01358 | Oligonucleotide CO |
| C 284 | 17 | 1.5 | 19 | 1 | AXH81927 | PCR primer for FG1 |
| C 285 | 17 | 1.5 | 19 | 1 | AXH81316 | Polynucleotide str |
| C 286 | 17 | 1.5 | 19 | 1 | AAAB8947 | 5' amino oligonucl |
| C 287 | 17 | 1.5 | 19 | 1 | AAAB8947 | Oligonucleotide IS |
| C 288 | 17 | 1.5 | 19 | 1 | AAA88948 | Oligonucleotide IS |
| C 289 | 17 | 1.5 | 19 | 1 | AAA88949 | Oligonucleotide IS |
| C 290 | 17 | 1.5 | 19 | 1 | AAA88950 | Oligonucleotide IS |
| C 291 | 17 | 1.5 | 19 | 1 | AAA88951 | Oligonucleotide IS |
| C 292 | 17 | 1.5 | 19 | 1 | AAA88952 | Oligonucleotide IS |
| C 293 | 17 | 1.5 | 19 | 1 | AAA88965 | Oligonucleotide IS |
| C 294 | 17 | 1.5 | 19 | 1 | AAC62422 | 2'-Modified chimer |
| C 295 | 17 | 1.5 | 19 | 1 | AAC62454 | T19 diester for us |
| C 296 | 17 | 1.5 | 19 | 1 | AAH71630 | Cleavage of nucle |
| C 297 | 17 | 1.5 | 19 | 1 | AAA06839 | Phosphorothioate 2 |
| C 298 | 17 | 1.5 | 19 | 1 | AZ613390 | Modified T-contain |
| C 299 | 17 | 1.5 | 19 | 1 | AZ61404 | Uniform phosphodi |
| C 300 | 17 | 1.5 | 19 | 1 | AZ95240 | 2'-O-modified ribo |
| C 301 | 17 | 1.5 | 19 | 1 | AZ95241 | Modified oligonucl |
| C 302 | 17 | 1.5 | 19 | 1 | AAH46460 | Modified oligonucl |
| C 303 | 17 | 1.5 | 19 | 1 | AAH25737 | Oligonucleotide #8 |
| C 304 | 17 | 1.5 | 19 | 1 | AAH25738 | Human type II RNas |
| C 305 | 17 | 1.5 | 19 | 1 | AF31458 | Human type II RNas |
| C 306 | 17 | 1.5 | 19 | 1 | AAF31564 | Oligonucleotide IS |
| C 307 | 17 | 1.5 | 19 | 1 | AAC83664 | ISIS sequence 3232 |
| C 308 | 17 | 1.5 | 19 | 1 | AAD41998 | 2'-O-N-[2-(dimethy |
| C 309 | 17 | 1.5 | 19 | 1 | AAD41999 | Oligonucleotide #1 |
| C 310 | 17 | 1.5 | 19 | 1 | AAD42000 | Oligonucleotide #2 |
| C 311 | 17 | 1.5 | 19 | 1 | AAD42001 | Oligonucleotide #3 |
| C 312 | 17 | 1.5 | 19 | 1 | AAD42002 | Oligonucleotide #4 |
| C 313 | 17 | 1.5 | 19 | 1 | AAD42003 | Oligonucleotide #5 |
| C 314 | 17 | 1.5 | 19 | 1 | AAD42004 | Oligonucleotide #6 |
| C 315 | 17 | 1.5 | 19 | 1 | AAD42005 | Oligonucleotide #7 |
| C 316 | 17 | 1.5 | 19 | 1 | AAD42009 | Oligonucleotide #8 |
| C 317 | 17 | 1.5 | 19 | 1 | AAD42010 | Oligonucleotide #1 |
| C 318 | 17 | 1.5 | 19 | 1 | AAD42011 | Oligonucleotide #1 |
| C 319 | 17 | 1.5 | 19 | 1 | AAD42020 | Oligonucleotide #2 |
| C 320 | 17 | 1.5 | 19 | 1 | ABK94423 | Human MLH1 DNA mi |
| C 321 | 17 | 1.5 | 19 | 1 | ABL51520 | Tailing reaction r |
| C 322 | 17 | 1.5 | 19 | 1 | ABL51521 | Tailing reaction r |
| C 323 | 17 | 1.5 | 19 | 1 | ABA91949 | Methyl thioethyl m |
| C 324 | 17 | 1.5 | 19 | 1 | ABA91950 | Methoxyethoxy modi |
| C 325 | 17 | 1.5 | 19 | 1 | AAK98526 | Dimethylaminoprop |
| | | | | | | Nucleic acid quant |

| | | | | | | |
|-------|----|-----|----|---|----------|--------------------|
| C 326 | 17 | 1.5 | 19 | 1 | ABZ75398 | Synthetic nuclease |
| C 327 | 17 | 1.5 | 19 | 1 | ABZ75399 | Synthetic nuclease |
| C 328 | 17 | 1.5 | 19 | 1 | ABZ75399 | Oligonucleotide wi |
| C 329 | 17 | 1.5 | 20 | 1 | AAQ25565 | Dye-coupled 3'-am |
| C 330 | 17 | 1.5 | 20 | 1 | AAQ33554 | Microsatellite seq |
| C 331 | 17 | 1.5 | 20 | 1 | AAQ33554 | Sequence of synthe |
| C 332 | 17 | 1.5 | 20 | 1 | AAQ58578 | Mammalian stem cel |
| C 333 | 17 | 1.5 | 20 | 1 | AAQ58578 | Mammalian stem cel |
| C 334 | 17 | 1.5 | 20 | 1 | AAQ58578 | Mammalian stem cel |
| C 335 | 17 | 1.5 | 20 | 1 | AAQ58578 | Mammalian stem cel |
| C 336 | 17 | 1.5 | 20 | 1 | AAQ58578 | Mammalian stem cel |
| C 337 | 17 | 1.5 | 20 | 1 | AAQ58578 | Mammalian stem cel |
| C 338 | 17 | 1.5 | 20 | 1 | AAQ58578 | Mammalian stem cel |
| C 339 | 17 | 1.5 | 20 | 1 | AAQ58578 | Mammalian stem cel |
| C 340 | 17 | 1.5 | 20 | 1 | AAQ58578 | Mammalian stem cel |
| C 341 | 17 | 1.5 | 20 | 1 | AAQ58578 | Mammalian stem cel |
| C 342 | 17 | 1.5 | 20 | 1 | AAQ58578 | Mammalian stem cel |
| C 343 | 17 | 1.5 | 20 | 1 | AAQ58578 | Mammalian stem cel |
| C 344 | 17 | 1.5 | 20 | 1 | AAQ58578 | Mammalian stem cel |
| C 345 | 17 | 1.5 | 20 | 1 | AAQ58578 | Mammalian stem cel |
| C 346 | 17 | 1.5 | 20 | 1 | AAQ58578 | Mammalian stem cel |
| C 347 | 17 | 1.5 | 20 | 1 | AAQ58578 | Mammalian stem cel |
| C 348 | 17 | 1.5 | 20 | 1 | AAQ58578 | Mammalian stem cel |
| C 349 | 17 | 1.5 | 20 | 1 | AAQ58578 | Mammalian stem cel |
| C 350 | 17 | 1.5 | 20 | 1 | AAQ58578 | Mammalian stem cel |
| C 351 | 17 | 1.5 | 20 | 1 | AAQ58578 | Mammalian stem cel |
| C 352 | 17 | 1.5 | 20 | 1 | AAQ58578 | Mammalian stem cel |
| C 353 | 17 | 1.5 | 20 | 1 | AAQ58578 | Mammalian stem cel |
| C 354 | 17 | 1.5 | 20 | 1 | AAQ58578 | Mammalian stem cel |
| C 355 | 17 | 1.5 | 20 | 1 | AAQ58578 | Mammalian stem cel |
| C 356 | 17 | 1.5 | 20 | 1 | AAQ58578 | Mammalian stem cel |
| C 357 | 17 | 1.5 | 20 | 1 | AAQ58578 | Mammalian stem cel |
| C 358 | 17 | 1.5 | 20 | 1 | AAQ58578 | Mammalian stem cel |
| C 359 | 17 | 1.5 | 20 | 1 | AAQ58578 | Mammalian stem cel |
| C 360 | 17 | 1.5 | 20 | 1 | AAQ58578 | Mammalian stem cel |
| C 361 | 17 | 1.5 | 20 | 1 | AAQ58578 | Mammalian stem cel |
| C 362 | 17 | 1.5 | 20 | 1 | AAQ58578 | Mammalian stem cel |
| C 363 | 17 | 1.5 | 20 | 1 | AAQ58578 | Mammalian stem cel |
| C 364 | 17 | 1.5 | 20 | 1 | AAQ58578 | Mammalian stem cel |
| C 365 | 17 | 1.5 | 20 | 1 | AAQ58578 | Mammalian stem cel |
| C 366 | 17 | 1.5 | 20 | 1 | AAQ58578 | Mammalian stem cel |
| C 367 | 17 | 1.5 | 20 | 1 | AAQ58578 | Mammalian stem cel |
| C 368 | 17 | 1.5 | 20 | 1 | AAQ58578 | Mammalian stem cel |
| C 369 | 17 | 1.5 | 20 | 1 | AAQ58578 | Mammalian stem cel |
| C 370 | 17 | 1.5 | 20 | 1 | AAQ58578 | Mammalian stem cel |
| C 371 | 17 | 1.5 | 20 | 1 | AAQ58578 | Mammalian stem cel |
| C 372 | 17 | 1.5 | 20 | 1 | AAQ58578 | Mammalian stem cel |
| C 373 | 17 | 1.5 | 20 | 1 | AAQ58578 | Mammalian stem cel |
| C 374 | 17 | 1.5 | 20 | 1 | AAQ58578 | Mammalian stem cel |
| C 375 | 17 | 1.5 | 20 | 1 | AAQ58578 | Mammalian stem cel |
| C 376 | 17 | 1.5 | 20 | 1 | AAQ58578 | Mammalian stem cel |
| C 377 | 17 | 1.5 | 20 | 1 | AAQ58578 | Mammalian stem cel |
| C 378 | 17 | 1.5 | 20 | 1 | AAQ58578 | Mammalian stem cel |
| C 379 | 17 | 1.5 | 20 | 1 | AAQ58578 | Mammalian stem cel |
| C 380 | 17 | 1.5 | 20 | 1 | AAQ58578 | Mammalian stem cel |
| C 381 | 17 | 1.5 | 20 | 1 | AAQ58578 | Mammalian stem cel |
| C 382 | 17 | 1.5 | 20 | 1 | AAQ58578 | Mammalian stem cel |
| C 383 | 17 | 1.5 | 20 | 1 | AAQ58578 | Mammalian stem cel |
| C 384 | 17 | 1.5 | 20 | 1 | AAQ58578 | Mammalian stem cel |
| C 385 | 17 | 1.5 | 20 | 1 | AAQ58578 | Mammalian stem cel |
| C 386 | 17 | 1.5 | 20 | 1 | AAQ58578 | Mammalian stem cel |
| C 387 | 17 | 1.5 | 20 | 1 | AAQ58578 | Mammalian stem cel |
| C 388 | 17 | 1.5 | 20 | 1 | AAQ58578 | Mammalian stem cel |
| C 389 | 17 | 1.5 | 20 | 1 | AAQ58578 | Mammalian stem cel |
| C 390 | 17 | 1.5 | 20 | 1 | AAQ58578 | Mammalian stem cel |
| C 391 | 17 | 1.5 | 20 | 1 | AAQ58578 | Mammalian stem cel |
| C 392 | 17 | 1.5 | 20 | 1 | AAQ58578 | Mammalian stem cel |
| C 393 | 17 | 1.5 | 20 | 1 | AAQ58578 | Mammalian stem cel |
| C 394 | 17 | 1.5 | 20 | 1 | AAQ58578 | Mammalian stem cel |
| C 395 | 17 | 1.5 | 20 | 1 | AAQ58578 | Mammalian stem cel |
| C 396 | 17 | 1.5 | 20 | 1 | AAQ58578 | Mammalian stem cel |
| C 397 | 17 | 1.5 | 20 | 1 | AAQ58578 | Mammalian stem cel |
| C 398 | 17 | 1.5 | 20 | 1 | AAQ58578 | Mammalian stem cel |

| | | | | | | | | | | | | | |
|-------|------|-----|----|---|--------------------|---------------------|-------|------|-----|----|---|----------|--------------------|
| c 545 | 17 | 1.5 | 24 | 1 | ABK86172 | Oligo dT primer #4 | c 618 | 16 | 1.5 | 18 | 1 | ABK13935 | 5'-PCR primer used |
| c 546 | 17 | 1.5 | 24 | 1 | ABN85073 | Human S4 ribosomal | c 619 | 16 | 1.5 | 18 | 1 | AAD52799 | Primer used to pre |
| c 547 | 17 | 1.5 | 24 | 1 | AAD33505 | HT18Apad_P512-24- | c 620 | 16 | 1.5 | 20 | 1 | AAS05714 | Aminopurine substi |
| c 548 | 17 | 1.5 | 24 | 1 | ABL55130 | Human gonadotropin | c 621 | 16 | 1.5 | 20 | 1 | AAC82923 | Human S-9 derived |
| c 549 | 17 | 1.5 | 24 | 1 | ABX79809 | EST polymorphic DN | c 622 | 16 | 1.5 | 20 | 1 | AAD33499 | HT18Apad_P527-20- |
| c 550 | 16.8 | 1.5 | 20 | 1 | AAZ37719 | Human mdm2 phospho | c 623 | 16 | 1.5 | 20 | 1 | ABA05917 | Hepatitis B virus |
| c 551 | 16.8 | 1.5 | 20 | 1 | AAS29488 | Human mdm2 antisen | c 624 | 16 | 1.5 | 21 | 1 | AAZ09196 | Oligonucleotide 8 |
| c 552 | 16.8 | 1.5 | 20 | 1 | AAF83959 | BAP28 gene fragmen | c 625 | 16 | 1.5 | 21 | 1 | AAD33500 | HT18Apad_P526-21- |
| c 553 | 16.8 | 1.5 | 20 | 1 | AAF80873 | Human mdm2 phospho | c 626 | 16 | 1.5 | 22 | 1 | AAD33501 | HT18Apad_P525-22- |
| c 554 | 16.8 | 1.5 | 20 | 1 | AAS97833 | Murine SAC1 gene-s | c 627 | 15.8 | 1.4 | 19 | 1 | AAT29081 | Primer for tyrosin |
| c 555 | 16.8 | 1.5 | 20 | 1 | AAS97860 | Murine SAC1 gene-s | c 628 | 15.8 | 1.4 | 19 | 1 | AAV01125 | Elastin PCR primer |
| c 556 | 16.8 | 1.5 | 20 | 1 | AAZ26500 | Human polymorphic | c 629 | 15.8 | 1.4 | 19 | 1 | ABT13587 | Liver regeneration |
| c 557 | 16.8 | 1.5 | 21 | 1 | AAH88803 | Human polymorphic | c 630 | 15.8 | 1.4 | 20 | 1 | AAT32535 | Primer for exon 12 |
| c 558 | 16.8 | 1.5 | 23 | 1 | AAH64547 | Nucleotide sequenc | c 631 | 15.8 | 1.4 | 20 | 1 | AAZ44829 | Human FADD primer |
| c 559 | 16.8 | 1.5 | 24 | 1 | AAV06320 | Human prollyl 4-hyd | c 632 | 15.8 | 1.4 | 20 | 1 | AAS05713 | Polypyrimidine Cri |
| c 560 | 16.8 | 1.5 | 24 | 1 | ABN85224 | Human translation | c 633 | 15.8 | 1.4 | 21 | 1 | AAT48469 | Third-strand oligo |
| c 561 | 16.4 | 1.5 | 18 | 1 | AAR30446 | Oligomer TNFR941 f | c 634 | 15.8 | 1.4 | 21 | 1 | AAZ26632 | Human polymorphic |
| c 562 | 16.4 | 1.5 | 18 | 1 | AAQ33975 | Binary encoded seq | c 635 | 15.8 | 1.4 | 21 | 1 | AAZ14729 | Triple helix third |
| c 563 | 16.4 | 1.5 | 20 | 1 | AAF75598 | 8-aminopurine subs | c 636 | 15.8 | 1.4 | 22 | 1 | AAZ27844 | Oligonucleotide-na |
| c 564 | 16.4 | 1.5 | 20 | 1 | AAS05715 | Synthetic oligonuc | c 637 | 15.8 | 1.4 | 22 | 1 | AAS63416 | Oligonucleotide-na |
| c 565 | 16.4 | 1.5 | 20 | 1 | ABA05916 | Hepatitis B virus | c 638 | 15.8 | 1.4 | 22 | 1 | AAS63419 | Oligonucleotide-na |
| c 566 | 16.4 | 1.5 | 23 | 1 | AAZ33577 | Deletion sequence | c 639 | 15.8 | 1.4 | 22 | 1 | AAS10359 | Oligonucleotide-go |
| c 567 | 16.4 | 1.5 | 23 | 1 | AAZ39753 | Synthetic oligonuc | c 640 | 15.8 | 1.4 | 22 | 1 | AAZ10362 | Oligonucleotide-go |
| c 568 | 16.4 | 1.5 | 23 | 1 | AAH30031 | Human interleukin | c 641 | 15.8 | 1.4 | 22 | 1 | AAZ28471 | Random oligonucleo |
| c 569 | 16.4 | 1.5 | 23 | 1 | AAH30035 | Human myelin prote | c 642 | 15.8 | 1.4 | 22 | 1 | AAZ28474 | Random oligonucleo |
| c 570 | 16.2 | 1.5 | 18 | 1 | AAZ18389 | RT-PCR primer of t | c 643 | 15.8 | 1.4 | 22 | 1 | ABT54436 | Silver staining me |
| c 571 | 16.2 | 1.5 | 21 | 1 | AAZ26563 | Human polymorphic | c 644 | 15.8 | 1.4 | 22 | 1 | ABT54436 | Nucleic acid detec |
| c 572 | 16.2 | 1.5 | 22 | 1 | AAZ26563 | Polymorphic sequen | c 645 | 15.8 | 1.4 | 22 | 1 | ABT54436 | Nucleic acid detec |
| c 573 | 16 | 1.5 | 16 | 1 | AAZ07568 | Homo sapiens fetal | c 646 | 15.8 | 1.4 | 22 | 1 | ABT54436 | Nucleic acid detec |
| c 574 | 16 | 1.5 | 16 | 1 | AAZ07568 | DNA chip primer #4 | c 647 | 15.8 | 1.4 | 22 | 1 | ABT54436 | Nucleic acid detec |
| c 575 | 16 | 1.5 | 16 | 1 | AAZ07568 | Human polymorphic | c 648 | 15.8 | 1.4 | 22 | 1 | ABT54436 | Nucleic acid detec |
| c 576 | 16 | 1.5 | 16 | 1 | AAZ42481 | Oligonucleotide us | c 649 | 15.8 | 1.4 | 22 | 1 | ABT54436 | Nucleic acid detec |
| c 577 | 16 | 1.5 | 16 | 1 | AAZ42481 | Oligonucleotide po | c 650 | 15.8 | 1.4 | 22 | 1 | ABT54436 | Nucleic acid detec |
| c 578 | 16 | 1.5 | 16 | 1 | AAZ42481 | Oligonucleotide-mi | c 651 | 15.8 | 1.4 | 22 | 1 | ABT54436 | Nucleic acid detec |
| c 579 | 16 | 1.5 | 16 | 1 | AAZ42481 | Oligonucleotide #5 | c 652 | 15.8 | 1.4 | 22 | 1 | ABT54436 | Nucleic acid detec |
| c 580 | 16 | 1.5 | 16 | 1 | AAZ42481 | Nucleotide sequenc | c 653 | 15.8 | 1.4 | 22 | 1 | ABT54436 | Nucleic acid detec |
| c 581 | 16 | 1.5 | 16 | 1 | AAZ42481 | Oligo-homodeoxyrib | c 654 | 15.8 | 1.4 | 22 | 1 | ABT54436 | Nucleic acid detec |
| c 582 | 16 | 1.5 | 17 | 1 | AAZ42481 | Human flt1 VEGF re | c 655 | 15.8 | 1.4 | 22 | 1 | ABT54436 | Nucleic acid detec |
| c 583 | 16 | 1.5 | 17 | 1 | AAZ42481 | Human flt1 VEGF re | c 656 | 15.8 | 1.4 | 22 | 1 | ABT54436 | Nucleic acid detec |
| c 584 | 16 | 1.5 | 17 | 1 | AAZ42481 | Human eosinophil c | c 657 | 15.8 | 1.4 | 22 | 1 | ABT54436 | Nucleic acid detec |
| c 585 | 16 | 1.5 | 17 | 1 | AAZ42481 | RT-PCR primer of t | c 658 | 15.8 | 1.4 | 22 | 1 | ABT54436 | Nucleic acid detec |
| c 586 | 16 | 1.5 | 17 | 1 | AAZ42481 | PCR anchor primer, | c 659 | 15.8 | 1.4 | 22 | 1 | ABT54436 | Nucleic acid detec |
| c 587 | 16 | 1.5 | 17 | 1 | AAZ42481 | PCR anchor primer, | c 660 | 15.8 | 1.4 | 22 | 1 | ABT54436 | Nucleic acid detec |
| c 588 | 16 | 1.5 | 17 | 1 | AAZ42481 | PCR anchor primer, | c 661 | 15.8 | 1.4 | 22 | 1 | ABT54436 | Nucleic acid detec |
| c 589 | 16 | 1.5 | 17 | 1 | AAZ42481 | PCR anchor primer, | c 662 | 15.8 | 1.4 | 22 | 1 | ABT54436 | Nucleic acid detec |
| c 590 | 16 | 1.5 | 17 | 1 | AAZ42481 | PCR anchor primer, | c 663 | 15.8 | 1.4 | 22 | 1 | ABT54436 | Nucleic acid detec |
| c 591 | 16 | 1.5 | 17 | 1 | AAZ42481 | Human Iga nephropa | c 664 | 15.8 | 1.4 | 22 | 1 | ABT54436 | Nucleic acid detec |
| c 592 | 16 | 1.5 | 17 | 1 | AAZ42481 | PCR primer GT15A u | c 665 | 15.8 | 1.4 | 22 | 1 | ABT54436 | Nucleic acid detec |
| c 593 | 16 | 1.5 | 17 | 1 | AAZ42481 | Oestrogen receptor | c 666 | 15.8 | 1.4 | 22 | 1 | ABT54436 | Nucleic acid detec |
| c 594 | 16 | 1.5 | 17 | 1 | AAZ42481 | Oestrogen receptor | c 667 | 15.8 | 1.4 | 22 | 1 | ABT54436 | Nucleic acid detec |
| c 595 | 16 | 1.5 | 17 | 1 | AAZ42481 | Oestrogen receptor | c 668 | 15.8 | 1.4 | 22 | 1 | ABT54436 | Nucleic acid detec |
| c 596 | 16 | 1.5 | 17 | 1 | AAZ42481 | Anchored oligo(dn) | c 669 | 15.8 | 1.4 | 22 | 1 | ABT54436 | Nucleic acid detec |
| c 597 | 16 | 1.5 | 17 | 1 | AAZ42481 | Human polinosis-a | c 670 | 15.8 | 1.4 | 22 | 1 | ABT54436 | Nucleic acid detec |
| c 598 | 16 | 1.5 | 17 | 1 | AAZ42481 | PCR anchor primer, | c 671 | 15.8 | 1.4 | 22 | 1 | ABT54436 | Nucleic acid detec |
| c 599 | 16 | 1.5 | 17 | 1 | AAZ42481 | Human polinosis-a | c 672 | 15.8 | 1.4 | 22 | 1 | ABT54436 | Nucleic acid detec |
| c 600 | 16 | 1.5 | 17 | 1 | AAZ42481 | Nucleotide sequenc | c 673 | 15.8 | 1.4 | 22 | 1 | ABT54436 | Nucleotide sequenc |
| c 601 | 16 | 1.5 | 17 | 1 | AAZ42481 | Human B153 expres | c 674 | 15.8 | 1.4 | 22 | 1 | ABT54436 | Nucleotide sequenc |
| c 602 | 16 | 1.5 | 17 | 1 | AAZ42481 | Allergic disease e | c 675 | 15.8 | 1.4 | 22 | 1 | ABT54436 | Nucleotide sequenc |
| c 603 | 16 | 1.5 | 17 | 1 | AAZ42481 | Nucleotide sequenc | c 676 | 15.8 | 1.4 | 22 | 1 | ABT54436 | Nucleotide sequenc |
| c 604 | 16 | 1.5 | 17 | 1 | AAZ42481 | Human allergic dis | c 677 | 15.8 | 1.4 | 22 | 1 | ABT54436 | Nucleotide sequenc |
| c 605 | 16 | 1.5 | 17 | 1 | AAZ42481 | Human atopic transf | c 678 | 15.8 | 1.4 | 22 | 1 | ABT54436 | Nucleotide sequenc |
| c 606 | 16 | 1.5 | 17 | 1 | AAZ42481 | Human atopic derma | c 679 | 15.8 | 1.4 | 22 | 1 | ABT54436 | Nucleotide sequenc |
| c 607 | 16 | 1.5 | 17 | 1 | AAZ42481 | 5'-PCR primer used | c 680 | 15.8 | 1.4 | 22 | 1 | ABT54436 | Nucleotide sequenc |
| c 608 | 16 | 1.5 | 17 | 1 | AAZ42481 | Primer, Synthetic | c 681 | 15.8 | 1.4 | 22 | 1 | ABT54436 | Nucleotide sequenc |
| c 609 | 16 | 1.5 | 18 | 1 | AAZ42481 | Sequence derived f | c 682 | 15.8 | 1.4 | 22 | 1 | ABT54436 | Nucleotide sequenc |
| c 610 | 16 | 1.5 | 18 | 1 | AAZ42481 | Nucleotide sequenc | c 683 | 15.8 | 1.4 | 22 | 1 | ABT54436 | Nucleotide sequenc |
| c 611 | 16 | 1.5 | 18 | 1 | AAZ42481 | Nucleotide sequenc | c 684 | 15.8 | 1.4 | 22 | 1 | ABT54436 | Nucleotide sequenc |
| c 612 | 16 | 1.5 | 18 | 1 | AAZ42481 | Human adipose tiss | c 685 | 15.8 | 1.4 | 22 | 1 | ABT54436 | Nucleotide sequenc |
| c 613 | 16 | 1.5 | 18 | 1 | AAZ42481 | Human adipose tiss | c 686 | 15.8 | 1.4 | 22 | 1 | ABT54436 | Nucleotide sequenc |
| c 614 | 16 | 1.5 | 18 | 1 | AAZ42481 | Human adipose tiss | c 687 | 15.8 | 1.4 | 22 | 1 | ABT54436 | Nucleotide sequenc |
| c 615 | 16 | 1.5 | 18 | 1 | AAZ42481 | Human adipose tiss | c 688 | 15.8 | 1.4 | 22 | 1 | ABT54436 | Nucleotide sequenc |
| c 616 | 16 | 1.5 | 18 | 1 | AAZ42481 | Binary encoded seq | c 689 | 15.8 | 1.4 | 22 | 1 | ABT54436 | Nucleotide sequenc |
| c 617 | 16 | 1.5 | 18 | 1 | AAZ42481 | Binary encoded seq | c 690 | 15.8 | 1.4 | 22 | 1 | ABT54436 | Nucleotide sequenc |
| | | | | | Human cytomagalovi | | | | | | | | |

| | | | | | | | | | | | | |
|-------|------|----|---|-----------|--------------------|-------|----|-----|----|---|----------|---------------------|
| C 691 | 1.4 | 16 | 1 | AAH27758 | Primer used in hum | C 764 | 15 | 1.4 | 15 | 1 | ABK98184 | Triple helix formi |
| C 692 | 15.2 | 16 | 1 | AAH28119 | Human TSA7005 gene | C 765 | 15 | 1.4 | 15 | 1 | ABL57054 | Hydrazide phosphor |
| C 693 | 15.2 | 17 | 1 | AAH18388 | RT-PCR primer of t | C 766 | 15 | 1.4 | 15 | 1 | ABL57056 | Hydrazide phosphor |
| C 694 | 15.2 | 17 | 1 | AAH14174 | Modified Poly-T Pr | C 767 | 15 | 1.4 | 15 | 1 | ABL57059 | Hydrazide precursor |
| C 695 | 15.2 | 20 | 1 | AAH09195 | Oligonucleotide 7 | C 768 | 15 | 1.4 | 15 | 1 | ABL57060 | Hydrazide precursor |
| C 696 | 15.2 | 20 | 1 | AAH09195 | Human PRO1410 forw | C 769 | 15 | 1.4 | 15 | 1 | ABL57061 | Hydrazide precursor |
| C 697 | 15.2 | 20 | 1 | AAH082154 | Zmx1 gene region | C 770 | 15 | 1.4 | 15 | 1 | ABL57063 | Hydrazide precursor |
| C 698 | 15.2 | 20 | 1 | AAH082154 | Primer #132 used i | C 771 | 15 | 1.4 | 15 | 1 | ABL57064 | Hydrazide precursor |
| C 699 | 15.2 | 20 | 1 | AAH082154 | Human beta-actin d | C 772 | 15 | 1.4 | 15 | 1 | ABL57066 | Hydrazide precursor |
| C 700 | 15.2 | 20 | 1 | AAH082154 | Human S-9 derived | C 773 | 15 | 1.4 | 15 | 1 | ABL57066 | Amino-C6-modified |
| C 701 | 15.2 | 20 | 1 | AAH082154 | Human onco-gene p1 | C 774 | 15 | 1.4 | 15 | 1 | ABL57066 | Chicken heparanase |
| C 702 | 15.2 | 20 | 1 | AAH082154 | Human Zmx1 cDNA f | C 775 | 15 | 1.4 | 15 | 1 | ABL57066 | Nucleotide sequenc |
| C 703 | 15.2 | 20 | 1 | AAH082154 | Hepatitis B virus | C 776 | 15 | 1.4 | 15 | 1 | ABL57066 | Primer used for th |
| C 704 | 15.2 | 20 | 1 | AAH082154 | Capture oligonucle | C 777 | 15 | 1.4 | 15 | 1 | ABL57066 | Retroviral reverse |
| C 705 | 15.2 | 20 | 1 | AAH082154 | Human chromosome 2 | C 778 | 15 | 1.4 | 15 | 1 | ABL57066 | Oligonucleotide SE |
| C 706 | 15.2 | 20 | 1 | AAH082154 | Human HBM STS mark | C 779 | 15 | 1.4 | 15 | 1 | ABL57066 | Oligonucleotide T1 |
| C 707 | 15.2 | 20 | 1 | AAH082154 | DNA mutation detec | C 780 | 15 | 1.4 | 15 | 1 | ABL57066 | Oligonucleotide us |
| C 708 | 15.2 | 20 | 1 | AAH082154 | Human polymorphic | C 781 | 15 | 1.4 | 15 | 1 | ABL57066 | 5' End of cDNA lib |
| C 709 | 15.2 | 20 | 1 | AAH082154 | PCR primer used to | C 782 | 15 | 1.4 | 15 | 1 | ABL57066 | RT-PCR primer of t |
| C 710 | 15.2 | 20 | 1 | AAH082154 | Oligo JT-296 for c | C 783 | 15 | 1.4 | 15 | 1 | ABL57066 | RT-PCR primer of t |
| C 711 | 15.2 | 20 | 1 | AAH082154 | Anchored oligo-dt | C 784 | 15 | 1.4 | 15 | 1 | ABL57066 | Molecular beacon t |
| C 712 | 15.2 | 20 | 1 | AAH082154 | Nuclease resistant | C 785 | 15 | 1.4 | 15 | 1 | ABL57066 | Human flt1 VEGF re |
| C 713 | 15.2 | 20 | 1 | AAH082154 | Nuclease resistant | C 786 | 15 | 1.4 | 15 | 1 | ABL57066 | Primer of the spec |
| C 714 | 15.2 | 20 | 1 | AAH082154 | Nuclease resistant | C 787 | 15 | 1.4 | 15 | 1 | ABL57066 | Anchored oligo(T) |
| C 715 | 15.2 | 20 | 1 | AAH082154 | Nuclease resistant | C 788 | 15 | 1.4 | 15 | 1 | ABL57066 | PCR anchor primer, |
| C 716 | 15.2 | 20 | 1 | AAH082154 | Nuclease resistant | C 789 | 15 | 1.4 | 15 | 1 | ABL57066 | PCR anchor primer, |
| C 717 | 15.2 | 20 | 1 | AAH082154 | Nuclease resistant | C 790 | 15 | 1.4 | 15 | 1 | ABL57066 | PCR anchor primer, |
| C 718 | 15.2 | 20 | 1 | AAH082154 | Nuclease resistant | C 791 | 15 | 1.4 | 15 | 1 | ABL57066 | PCR anchor primer, |
| C 719 | 15.2 | 20 | 1 | AAH082154 | Nuclease resistant | C 792 | 15 | 1.4 | 15 | 1 | ABL57066 | PCR anchor primer, |
| C 720 | 15.2 | 20 | 1 | AAH082154 | Nuclease resistant | C 793 | 15 | 1.4 | 15 | 1 | ABL57066 | PCR anchor primer, |
| C 721 | 15.2 | 20 | 1 | AAH082154 | Nuclease resistant | C 794 | 15 | 1.4 | 15 | 1 | ABL57066 | PCR anchor primer, |
| C 722 | 15.2 | 20 | 1 | AAH082154 | Nuclease resistant | C 795 | 15 | 1.4 | 15 | 1 | ABL57066 | PCR anchor primer, |
| C 723 | 15.2 | 20 | 1 | AAH082154 | Nuclease resistant | C 796 | 15 | 1.4 | 15 | 1 | ABL57066 | PCR anchor primer, |
| C 724 | 15.2 | 20 | 1 | AAH082154 | Nuclease resistant | C 797 | 15 | 1.4 | 15 | 1 | ABL57066 | PCR anchor primer, |
| C 725 | 15.2 | 20 | 1 | AAH082154 | Nuclease resistant | C 798 | 15 | 1.4 | 15 | 1 | ABL57066 | PCR anchor primer, |
| C 726 | 15.2 | 20 | 1 | AAH082154 | Nuclease resistant | C 799 | 15 | 1.4 | 15 | 1 | ABL57066 | PCR anchor primer, |
| C 727 | 15.2 | 20 | 1 | AAH082154 | Nuclease resistant | C 800 | 15 | 1.4 | 15 | 1 | ABL57066 | PCR anchor primer, |
| C 728 | 15.2 | 20 | 1 | AAH082154 | Nuclease resistant | C 801 | 15 | 1.4 | 15 | 1 | ABL57066 | PCR anchor primer, |
| C 729 | 15.2 | 20 | 1 | AAH082154 | Nuclease resistant | C 802 | 15 | 1.4 | 15 | 1 | ABL57066 | PCR anchor primer, |
| C 730 | 15.2 | 20 | 1 | AAH082154 | Nuclease resistant | C 803 | 15 | 1.4 | 15 | 1 | ABL57066 | PCR anchor primer, |
| C 731 | 15.2 | 20 | 1 | AAH082154 | Nuclease resistant | C 804 | 15 | 1.4 | 15 | 1 | ABL57066 | PCR anchor primer, |
| C 732 | 15.2 | 20 | 1 | AAH082154 | Nuclease resistant | C 805 | 15 | 1.4 | 15 | 1 | ABL57066 | PCR anchor primer, |
| C 733 | 15.2 | 20 | 1 | AAH082154 | Nuclease resistant | C 806 | 15 | 1.4 | 15 | 1 | ABL57066 | PCR anchor primer, |
| C 734 | 15.2 | 20 | 1 | AAH082154 | Nuclease resistant | C 807 | 15 | 1.4 | 15 | 1 | ABL57066 | PCR anchor primer, |
| C 735 | 15.2 | 20 | 1 | AAH082154 | Nuclease resistant | C 808 | 15 | 1.4 | 15 | 1 | ABL57066 | PCR anchor primer, |
| C 736 | 15.2 | 20 | 1 | AAH082154 | Nuclease resistant | C 809 | 15 | 1.4 | 15 | 1 | ABL57066 | PCR anchor primer, |
| C 737 | 15.2 | 20 | 1 | AAH082154 | Nuclease resistant | C 810 | 15 | 1.4 | 15 | 1 | ABL57066 | PCR anchor primer, |
| C 738 | 15.2 | 20 | 1 | AAH082154 | Nuclease resistant | C 811 | 15 | 1.4 | 15 | 1 | ABL57066 | PCR anchor primer, |
| C 739 | 15.2 | 20 | 1 | AAH082154 | Nuclease resistant | C 812 | 15 | 1.4 | 15 | 1 | ABL57066 | PCR anchor primer, |
| C 740 | 15.2 | 20 | 1 | AAH082154 | Nuclease resistant | C 813 | 15 | 1.4 | 15 | 1 | ABL57066 | PCR anchor primer, |
| C 741 | 15.2 | 20 | 1 | AAH082154 | Nuclease resistant | C 814 | 15 | 1.4 | 15 | 1 | ABL57066 | PCR anchor primer, |
| C 742 | 15.2 | 20 | 1 | AAH082154 | Nuclease resistant | C 815 | 15 | 1.4 | 15 | 1 | ABL57066 | PCR anchor primer, |
| C 743 | 15.2 | 20 | 1 | AAH082154 | Nuclease resistant | C 816 | 15 | 1.4 | 15 | 1 | ABL57066 | PCR anchor primer, |
| C 744 | 15.2 | 20 | 1 | AAH082154 | Nuclease resistant | C 817 | 15 | 1.4 | 15 | 1 | ABL57066 | PCR anchor primer, |
| C 745 | 15.2 | 20 | 1 | AAH082154 | Nuclease resistant | C 818 | 15 | 1.4 | 15 | 1 | ABL57066 | PCR anchor primer, |
| C 746 | 15.2 | 20 | 1 | AAH082154 | Nuclease resistant | C 819 | 15 | 1.4 | 15 | 1 | ABL57066 | PCR anchor primer, |
| C 747 | 15.2 | 20 | 1 | AAH082154 | Nuclease resistant | C 820 | 15 | 1.4 | 15 | 1 | ABL57066 | PCR anchor primer, |
| C 748 | 15.2 | 20 | 1 | AAH082154 | Nuclease resistant | C 821 | 15 | 1.4 | 15 | 1 | ABL57066 | PCR anchor primer, |
| C 749 | 15.2 | 20 | 1 | AAH082154 | Nuclease resistant | C 822 | 15 | 1.4 | 15 | 1 | ABL57066 | PCR anchor primer, |
| C 750 | 15.2 | 20 | 1 | AAH082154 | Nuclease resistant | C 823 | 15 | 1.4 | 15 | 1 | ABL57066 | PCR anchor primer, |
| C 751 | 15.2 | 20 | 1 | AAH082154 | Nuclease resistant | C 824 | 15 | 1.4 | 15 | 1 | ABL57066 | PCR anchor primer, |
| C 752 | 15.2 | 20 | 1 | AAH082154 | Nuclease resistant | C 825 | 15 | 1.4 | 15 | 1 | ABL57066 | PCR anchor primer, |
| C 753 | 15.2 | 20 | 1 | AAH082154 | Nuclease resistant | C 826 | 15 | 1.4 | 15 | 1 | ABL57066 | PCR anchor primer, |
| C 754 | 15.2 | 20 | 1 | AAH082154 | Nuclease resistant | C 827 | 15 | 1.4 | 15 | 1 | ABL57066 | PCR anchor primer, |
| C 755 | 15.2 | 20 | 1 | AAH082154 | Nuclease resistant | C 828 | 15 | 1.4 | 15 | 1 | ABL57066 | PCR anchor primer, |
| C 756 | 15.2 | 20 | 1 | AAH082154 | Nuclease resistant | C 829 | 15 | 1.4 | 15 | 1 | ABL57066 | PCR anchor primer, |
| C 757 | 15.2 | 20 | 1 | AAH082154 | Nuclease resistant | C 830 | 15 | 1.4 | 15 | 1 | ABL57066 | PCR anchor primer, |
| C 758 | 15.2 | 20 | 1 | AAH082154 | Nuclease resistant | C 831 | 15 | 1.4 | 15 | 1 | ABL57066 | PCR anchor primer, |
| C 759 | 15.2 | 20 | 1 | AAH082154 | Nuclease resistant | C 832 | 15 | 1.4 | 15 | 1 | ABL57066 | PCR anchor primer, |
| C 760 | 15.2 | 20 | 1 | AAH082154 | Nuclease resistant | C 833 | 15 | 1.4 | 15 | 1 | ABL57066 | PCR anchor primer, |
| C 761 | 15.2 | 20 | 1 | AAH082154 | Nuclease resistant | C 834 | 15 | 1.4 | 15 | 1 | ABL57066 | PCR anchor primer, |
| C 762 | 15.2 | 20 | 1 | AAH082154 | Nuclease resistant | C 835 | 15 | 1.4 | 15 | 1 | ABL57066 | PCR anchor primer, |
| C 763 | 15.2 | 20 | 1 | AAH082154 | Nuclease resistant | C 836 | 15 | 1.4 | 15 | 1 | ABL57066 | PCR anchor primer, |

| | | | | | | |
|-------|----|-----|----|---|----------|---------------------|
| C 837 | 15 | 1.4 | 18 | 1 | AAZ90650 | Human adipose tiss |
| C 838 | 15 | 1.4 | 18 | 1 | AAZ90651 | Human adipose tiss |
| C 839 | 15 | 1.4 | 18 | 1 | ABT11136 | Human 5-lipoxygena |
| C 840 | 15 | 1.4 | 20 | 1 | AAZ73293 | Primer for pUC19 D |
| C 841 | 15 | 1.4 | 20 | 1 | AAZ32003 | MSH2 gene specific |
| C 842 | 15 | 1.4 | 20 | 1 | AAZ32010 | MSH2 gene specific |
| C 843 | 15 | 1.4 | 20 | 1 | AAZ32010 | Human beta-actin d |
| C 844 | 15 | 1.4 | 20 | 1 | AAZ32010 | Human beta-actin d |
| C 845 | 15 | 1.4 | 20 | 1 | AAZ32010 | Human beta-actin d |
| C 846 | 15 | 1.4 | 20 | 1 | AAZ32010 | Human beta-actin d |
| C 847 | 15 | 1.4 | 20 | 1 | AAZ32010 | Human beta-actin d |
| C 848 | 15 | 1.4 | 20 | 1 | AAZ32010 | Human beta-actin d |
| C 849 | 15 | 1.4 | 20 | 1 | AAZ32010 | Human S-9 derived |
| C 850 | 15 | 1.4 | 20 | 1 | AAZ32010 | Human S-9 derived |
| C 851 | 15 | 1.4 | 20 | 1 | AAZ32010 | Human S-9 derived |
| C 852 | 15 | 1.4 | 20 | 1 | AAZ32010 | Human S-9 derived |
| C 853 | 15 | 1.4 | 20 | 1 | AAZ32010 | Human S-9 derived |
| C 854 | 15 | 1.4 | 20 | 1 | AAZ32010 | Human glutathione |
| C 855 | 15 | 1.4 | 20 | 1 | AAZ32010 | HR15-C downstream |
| C 856 | 15 | 1.4 | 20 | 1 | AAZ32010 | Molecular beacon t |
| C 857 | 15 | 1.4 | 20 | 1 | AAZ32010 | Human GLUT1 10 SSCP |
| C 858 | 15 | 1.4 | 20 | 1 | AAZ32010 | Capture oligonucle |
| C 859 | 15 | 1.4 | 20 | 1 | AAZ32010 | Human gene single |
| C 860 | 15 | 1.4 | 20 | 1 | AAZ32010 | Histamine N-methyl |
| C 861 | 15 | 1.4 | 20 | 1 | AAZ32010 | Histamine N-methyl |
| C 862 | 15 | 1.4 | 20 | 1 | AAZ32010 | Molecular beacon t |
| C 863 | 15 | 1.4 | 20 | 1 | AAZ32010 | Cross-linking olig |
| C 864 | 15 | 1.4 | 20 | 1 | AAZ32010 | Oligomer HUM beta |
| C 865 | 15 | 1.4 | 20 | 1 | AAZ32010 | Oligomer HUM beta |
| C 866 | 15 | 1.4 | 20 | 1 | AAZ32010 | Oligomer HUM beta |
| C 867 | 15 | 1.4 | 20 | 1 | AAZ32010 | Oligomer HUM beta |
| C 868 | 15 | 1.4 | 20 | 1 | AAZ32010 | Oligomer HUM beta |
| C 869 | 15 | 1.4 | 20 | 1 | AAZ32010 | Oligomer HUM beta |
| C 870 | 15 | 1.4 | 20 | 1 | AAZ32010 | Oligomer HUM beta |
| C 871 | 15 | 1.4 | 20 | 1 | AAZ32010 | Oligomer HUM beta |
| C 872 | 15 | 1.4 | 20 | 1 | AAZ32010 | Oligomer HUM beta |
| C 873 | 15 | 1.4 | 20 | 1 | AAZ32010 | Oligomer HUM beta |
| C 874 | 15 | 1.4 | 20 | 1 | AAZ32010 | Oligomer HUM beta |
| C 875 | 15 | 1.4 | 20 | 1 | AAZ32010 | Oligomer HUM beta |
| C 876 | 15 | 1.4 | 20 | 1 | AAZ32010 | Oligomer HUM beta |
| C 877 | 15 | 1.4 | 20 | 1 | AAZ32010 | Oligomer HUM beta |
| C 878 | 15 | 1.4 | 20 | 1 | AAZ32010 | Oligomer HUM beta |
| C 879 | 15 | 1.4 | 20 | 1 | AAZ32010 | Oligomer HUM beta |
| C 880 | 15 | 1.4 | 20 | 1 | AAZ32010 | Oligomer HUM beta |
| C 881 | 15 | 1.4 | 20 | 1 | AAZ32010 | Oligomer HUM beta |
| C 882 | 15 | 1.4 | 20 | 1 | AAZ32010 | Oligomer HUM beta |
| C 883 | 15 | 1.4 | 20 | 1 | AAZ32010 | Oligomer HUM beta |
| C 884 | 15 | 1.4 | 20 | 1 | AAZ32010 | Oligomer HUM beta |
| C 885 | 15 | 1.4 | 20 | 1 | AAZ32010 | Oligomer HUM beta |
| C 886 | 15 | 1.4 | 20 | 1 | AAZ32010 | Oligomer HUM beta |
| C 887 | 15 | 1.4 | 20 | 1 | AAZ32010 | Oligomer HUM beta |
| C 888 | 15 | 1.4 | 20 | 1 | AAZ32010 | Oligomer HUM beta |
| C 889 | 15 | 1.4 | 20 | 1 | AAZ32010 | Oligomer HUM beta |
| C 890 | 15 | 1.4 | 20 | 1 | AAZ32010 | Oligomer HUM beta |
| C 891 | 15 | 1.4 | 20 | 1 | AAZ32010 | Oligomer HUM beta |
| C 892 | 15 | 1.4 | 20 | 1 | AAZ32010 | Oligomer HUM beta |
| C 893 | 15 | 1.4 | 20 | 1 | AAZ32010 | Oligomer HUM beta |
| C 894 | 15 | 1.4 | 20 | 1 | AAZ32010 | Oligomer HUM beta |
| C 895 | 15 | 1.4 | 20 | 1 | AAZ32010 | Oligomer HUM beta |
| C 896 | 15 | 1.4 | 20 | 1 | AAZ32010 | Oligomer HUM beta |
| C 897 | 15 | 1.4 | 20 | 1 | AAZ32010 | Oligomer HUM beta |
| C 898 | 15 | 1.4 | 20 | 1 | AAZ32010 | Oligomer HUM beta |
| C 899 | 15 | 1.4 | 20 | 1 | AAZ32010 | Oligomer HUM beta |
| C 900 | 15 | 1.4 | 20 | 1 | AAZ32010 | Oligomer HUM beta |
| C 901 | 15 | 1.4 | 20 | 1 | AAZ32010 | Oligomer HUM beta |
| C 902 | 15 | 1.4 | 20 | 1 | AAZ32010 | Oligomer HUM beta |
| C 903 | 15 | 1.4 | 20 | 1 | AAZ32010 | Oligomer HUM beta |
| C 904 | 15 | 1.4 | 20 | 1 | AAZ32010 | Oligomer HUM beta |
| C 905 | 15 | 1.4 | 20 | 1 | AAZ32010 | Oligomer HUM beta |
| C 906 | 15 | 1.4 | 20 | 1 | AAZ32010 | Oligomer HUM beta |
| C 907 | 15 | 1.4 | 20 | 1 | AAZ32010 | Oligomer HUM beta |
| C 908 | 15 | 1.4 | 20 | 1 | AAZ32010 | Oligomer HUM beta |
| C 909 | 15 | 1.4 | 20 | 1 | AAZ32010 | Oligomer HUM beta |

Murine IL-5 antise
Ribonucleotide red
Human S-9 derived
Gene 216 SSCP sequ
Human helicase-moi
Human calreticulin
Capture oligonucle
Human matrix metal
Human gene 216 pol
Human matrix metal
Mouse interleukin
Oligo d(T) primer
RT-PCR primer of t
Escherichia coli 2
Human biallelic ma
Legionella 23S rRN
C. trachomatis 23S
Fungal 28S rRNA sp
Universal probe 10
Probe d. Unidenti
Bacteriophage M4 v
Cross-linking olig
Oligomer HUM beta
Gene detection seq
Antisense oligonuc
Human papilloma vi
Human chromosome 1
Internal PCR prime
Auxotrophic ORF TR
Retinoblastoma 1 P
Probe for detectin
Internal PCR prime
Variant #5 of univ
N-ras probe 665T
Primer MY48 for hu
Human mdm2 phospho
Human mdm2 phospho
PCR primer used to
PCR primer used to
PCR primer used to
PCR primer used to
PCR primer used to
PCR primer used to
Primer 128 for PDZ
Human ras oncogene
Human ras oncogene
Human STAT3 phosph
Human Ig H chain s
Human TNFalpha ant
Reverse primer for
PCR primer for bet
Human mdm2 antisen
Human mdm2 antisen
Human glycogen syn
Human c-ski oncop
Follicular conjunc
Human E2F-2 gene P
Human mdm2 antisen
Human mdm2 phospho
Human mdm2 phospho
Oligonucleotide in
Human PLA2, group
Human RECOL2 antis
Human RAIDD antis
Mouse syntaxin 4 i
ABQ62490
Human Her-1 antis
Human Stat3 antis
DST CHS1 23 cDNA s
Murine SAC1 gene-s
Mouse pancreatic p

| | | | | | | | | | | | | | |
|------|------|-----|----|---|-----------|-----------------------|-------|------|-----|----|---|----------|--------------------|
| 983 | 14.2 | 1.3 | 20 | 1 | AA696792 | Human STAT3 antisense | 1056 | 13.8 | 1.3 | 17 | 1 | ABA78137 | BRCA1 mutation cor |
| 984 | 14.2 | 1.3 | 20 | 1 | ABL44478 | Human chromosome 1 | c1057 | 13.8 | 1.3 | 17 | 1 | ABA78138 | BRCA1 mutation cor |
| 985 | 14.2 | 1.3 | 20 | 1 | ABV77208 | PCR primer used to | c1058 | 13.8 | 1.3 | 17 | 1 | AA511599 | Porcine reproducti |
| 986 | 14 | 1.3 | 14 | 1 | AAQ33508 | Sequence of micros | c1059 | 13.8 | 1.3 | 17 | 1 | AAH95016 | Human Chk1 ribozym |
| 987 | 14 | 1.3 | 14 | 1 | AAV09230 | 3' poly(T) primer | c1060 | 13.8 | 1.3 | 17 | 1 | AAH80147 | Oligonucleotide hy |
| 988 | 14 | 1.3 | 14 | 1 | AAV12222 | Poly(T) oligonucle | c1061 | 13.8 | 1.3 | 17 | 1 | ABK02484 | Human NOGO Ambery |
| 989 | 14 | 1.3 | 14 | 1 | AAK57019 | WO9923258 oligonuc | c1062 | 13.8 | 1.3 | 17 | 1 | ABS74958 | Human PAPP-Ea asso |
| 990 | 14 | 1.3 | 14 | 1 | AAK19465 | Human senescence f | c1063 | 13.8 | 1.3 | 17 | 1 | ABT06038 | Human Igm heavy ch |
| 991 | 14 | 1.3 | 14 | 1 | AAK14688 | Triple helix formi | c1064 | 13.8 | 1.3 | 17 | 1 | ABT06038 | Human Igm heavy ch |
| 992 | 14 | 1.3 | 14 | 1 | AAK14689 | Triple helix formi | c1065 | 13.8 | 1.3 | 17 | 1 | ABT06038 | Human Igm heavy ch |
| 993 | 14 | 1.3 | 14 | 1 | AAK622349 | Triple helix third | c1066 | 13.8 | 1.3 | 17 | 1 | ABT06038 | Human Igm heavy ch |
| 994 | 14 | 1.3 | 14 | 1 | AAK622349 | Oligonucleotide #1 | c1067 | 13.8 | 1.3 | 17 | 1 | ABT06038 | Human Igm heavy ch |
| 995 | 14 | 1.3 | 14 | 1 | AAK622349 | Oligonucleotide #2 | c1068 | 13.8 | 1.3 | 17 | 1 | ABT06038 | Human Igm heavy ch |
| 996 | 14 | 1.3 | 14 | 1 | ABQ833269 | RNA oligonucleotid | c1069 | 13.8 | 1.3 | 17 | 1 | ABT06038 | Human Igm heavy ch |
| 997 | 14 | 1.3 | 14 | 1 | ABQ833275 | EG1 cDNA tag relat | c1070 | 13.8 | 1.3 | 17 | 1 | ABT06038 | Human Igm heavy ch |
| 998 | 14 | 1.3 | 14 | 1 | ABQ833278 | EG1 cDNA tag relat | c1071 | 13.8 | 1.3 | 17 | 1 | ABT06038 | Human Igm heavy ch |
| 999 | 14 | 1.3 | 14 | 1 | ABU88471 | EG1 cDNA tag relat | c1072 | 13.8 | 1.3 | 17 | 1 | ABT06038 | Human Igm heavy ch |
| 1000 | 14 | 1.3 | 14 | 1 | ABA933701 | Oligo dt 3p1 prime | c1073 | 13.8 | 1.3 | 17 | 1 | ABT06038 | Human Igm heavy ch |
| 1001 | 14 | 1.3 | 14 | 1 | AAK24492 | Light responsive o | c1074 | 13.8 | 1.3 | 17 | 1 | ABT06038 | Human Igm heavy ch |
| 1002 | 14 | 1.3 | 14 | 1 | AAK24492 | Retinoid-regulated | c1075 | 13.8 | 1.3 | 17 | 1 | ABT06038 | Human Igm heavy ch |
| 1003 | 14 | 1.3 | 14 | 1 | AAK24492 | Human ICAM hammerh | c1076 | 13.8 | 1.3 | 17 | 1 | ABT06038 | Human Igm heavy ch |
| 1004 | 14 | 1.3 | 14 | 1 | AAK24492 | IGF-1 oligonucleot | c1077 | 13.8 | 1.3 | 17 | 1 | ABT06038 | Human Igm heavy ch |
| 1005 | 14 | 1.3 | 14 | 1 | AAK24492 | IGF-1 oligonucleot | c1078 | 13.8 | 1.3 | 17 | 1 | ABT06038 | Human Igm heavy ch |
| 1006 | 14 | 1.3 | 14 | 1 | AAK24492 | IGF-1 oligonucleot | c1079 | 13.8 | 1.3 | 17 | 1 | ABT06038 | Human Igm heavy ch |
| 1007 | 14 | 1.3 | 14 | 1 | AAK24492 | Triple helix formi | c1080 | 13.8 | 1.3 | 17 | 1 | ABT06038 | Human Igm heavy ch |
| 1008 | 14 | 1.3 | 14 | 1 | AAK24492 | Triple helix formi | c1081 | 13.8 | 1.3 | 17 | 1 | ABT06038 | Human Igm heavy ch |
| 1009 | 14 | 1.3 | 14 | 1 | AAK24492 | Triple helix formi | c1082 | 13.8 | 1.3 | 17 | 1 | ABT06038 | Human Igm heavy ch |
| 1010 | 14 | 1.3 | 14 | 1 | AAK24492 | Triple helix formi | c1083 | 13.8 | 1.3 | 17 | 1 | ABT06038 | Human Igm heavy ch |
| 1011 | 14 | 1.3 | 14 | 1 | AAK24492 | Triple helix formi | c1084 | 13.8 | 1.3 | 17 | 1 | ABT06038 | Human Igm heavy ch |
| 1012 | 14 | 1.3 | 14 | 1 | AAK24492 | EST polymorphic DN | c1085 | 13.8 | 1.3 | 17 | 1 | ABT06038 | Human Igm heavy ch |
| 1013 | 14 | 1.3 | 14 | 1 | AAK24492 | RT-PCR primer of t | c1086 | 13.8 | 1.3 | 17 | 1 | ABT06038 | Human Igm heavy ch |
| 1014 | 14 | 1.3 | 14 | 1 | AAK24492 | RT-PCR primer of t | c1087 | 13.8 | 1.3 | 17 | 1 | ABT06038 | Human Igm heavy ch |
| 1015 | 14 | 1.3 | 14 | 1 | AAK24492 | Oligo-dt PCR prime | c1088 | 13.8 | 1.3 | 17 | 1 | ABT06038 | Human Igm heavy ch |
| 1016 | 14 | 1.3 | 14 | 1 | AAK24492 | Oligo-dt PCR prime | c1089 | 13.8 | 1.3 | 17 | 1 | ABT06038 | Human Igm heavy ch |
| 1017 | 14 | 1.3 | 14 | 1 | AAK24492 | Oligo-dt PCR prime | c1090 | 13.8 | 1.3 | 17 | 1 | ABT06038 | Human Igm heavy ch |
| 1018 | 14 | 1.3 | 14 | 1 | AAK24492 | Human flt1 VEGF re | c1091 | 13.8 | 1.3 | 17 | 1 | ABT06038 | Human Igm heavy ch |
| 1019 | 14 | 1.3 | 14 | 1 | AAK24492 | Human flt1 VEGF re | c1092 | 13.8 | 1.3 | 17 | 1 | ABT06038 | Human Igm heavy ch |
| 1020 | 14 | 1.3 | 14 | 1 | AAK24492 | Oestrogen receptor | c1093 | 13.8 | 1.3 | 17 | 1 | ABT06038 | Human Igm heavy ch |
| 1021 | 14 | 1.3 | 14 | 1 | AAK24492 | DNA sequence of ca | c1094 | 13.8 | 1.3 | 17 | 1 | ABT06038 | Human Igm heavy ch |
| 1022 | 14 | 1.3 | 14 | 1 | AAK24492 | HIV-1 related bind | c1095 | 13.8 | 1.3 | 17 | 1 | ABT06038 | Human Igm heavy ch |
| 1023 | 14 | 1.3 | 14 | 1 | AAK24492 | HIV-1 related bind | c1096 | 13.8 | 1.3 | 17 | 1 | ABT06038 | Human Igm heavy ch |
| 1024 | 14 | 1.3 | 14 | 1 | AAK24492 | Human protective D | c1097 | 13.8 | 1.3 | 17 | 1 | ABT06038 | Human Igm heavy ch |
| 1025 | 14 | 1.3 | 14 | 1 | AAK24492 | Ribozyme substrate | c1098 | 13.8 | 1.3 | 17 | 1 | ABT06038 | Human Igm heavy ch |
| 1026 | 14 | 1.3 | 14 | 1 | AAK24492 | AL1-1 exon 3 neste | c1099 | 13.8 | 1.3 | 17 | 1 | ABT06038 | Human Igm heavy ch |
| 1027 | 14 | 1.3 | 14 | 1 | AAK24492 | Human AL1-1 gene e | c1100 | 13.8 | 1.3 | 17 | 1 | ABT06038 | Human Igm heavy ch |
| 1028 | 14 | 1.3 | 14 | 1 | AAK24492 | Primer 1 for pUC19 | c1101 | 13.8 | 1.3 | 17 | 1 | ABT06038 | Human Igm heavy ch |
| 1029 | 14 | 1.3 | 14 | 1 | AAK24492 | Primer 2 for pUC19 | c1102 | 13.8 | 1.3 | 17 | 1 | ABT06038 | Human Igm heavy ch |
| 1030 | 14 | 1.3 | 14 | 1 | AAK24492 | Oligonucleotide pr | c1103 | 13.8 | 1.3 | 17 | 1 | ABT06038 | Human Igm heavy ch |
| 1031 | 14 | 1.3 | 14 | 1 | AAK24492 | PCR primer used to | c1104 | 13.8 | 1.3 | 17 | 1 | ABT06038 | Human Igm heavy ch |
| 1032 | 14 | 1.3 | 14 | 1 | AAK24492 | 5' RACE primer CHI | c1105 | 13.8 | 1.3 | 17 | 1 | ABT06038 | Human Igm heavy ch |
| 1033 | 14 | 1.3 | 14 | 1 | AAK24492 | Human PTP1B antisense | c1106 | 13.8 | 1.3 | 17 | 1 | ABT06038 | Human Igm heavy ch |
| 1034 | 14 | 1.3 | 14 | 1 | AAK24492 | Immunostimulatory | c1107 | 13.8 | 1.3 | 17 | 1 | ABT06038 | Human Igm heavy ch |
| 1035 | 14 | 1.3 | 14 | 1 | AAK24492 | Angiogenesis inhib | c1108 | 13.8 | 1.3 | 17 | 1 | ABT06038 | Human Igm heavy ch |
| 1036 | 14 | 1.3 | 14 | 1 | AAK24492 | Human PTP1B antisense | c1109 | 13.8 | 1.3 | 17 | 1 | ABT06038 | Human Igm heavy ch |
| 1037 | 14 | 1.3 | 14 | 1 | AAK24492 | Human PTP1B mRNA 1 | c1110 | 13.8 | 1.3 | 17 | 1 | ABT06038 | Human Igm heavy ch |
| 1038 | 14 | 1.3 | 14 | 1 | AAK24492 | Capture oligonucle | c1111 | 13.8 | 1.3 | 17 | 1 | ABT06038 | Human Igm heavy ch |
| 1039 | 14 | 1.3 | 14 | 1 | AAK24492 | Immunostimulatory | c1112 | 13.8 | 1.3 | 17 | 1 | ABT06038 | Human Igm heavy ch |
| 1040 | 13.8 | 1.3 | 17 | 1 | AAK24492 | Probe yz30 to N-ra | c1113 | 13.8 | 1.3 | 17 | 1 | ABT06038 | Human Igm heavy ch |
| 1041 | 13.8 | 1.3 | 17 | 1 | AAK24492 | Detection probe fo | c1114 | 13.8 | 1.3 | 17 | 1 | ABT06038 | Human Igm heavy ch |
| 1042 | 13.8 | 1.3 | 17 | 1 | AAK24492 | Detection probe fo | c1115 | 13.8 | 1.3 | 17 | 1 | ABT06038 | Human Igm heavy ch |
| 1043 | 13.8 | 1.3 | 17 | 1 | AAK24492 | Mouse flt-1 VEGF r | c1116 | 13.8 | 1.3 | 17 | 1 | ABT06038 | Human Igm heavy ch |
| 1044 | 13.8 | 1.3 | 17 | 1 | AAK24492 | Mouse flt-1 VEGF r | c1117 | 13.8 | 1.3 | 17 | 1 | ABT06038 | Human Igm heavy ch |
| 1045 | 13.8 | 1.3 | 17 | 1 | AAK24492 | Human flt1 VEGF re | c1118 | 13.8 | 1.3 | 17 | 1 | ABT06038 | Human Igm heavy ch |
| 1046 | 13.8 | 1.3 | 17 | 1 | AAK24492 | Granule bound star | c1119 | 13.8 | 1.3 | 17 | 1 | ABT06038 | Human Igm heavy ch |
| 1047 | 13.8 | 1.3 | 17 | 1 | AAK24492 | Integrin subunit b | c1120 | 13.8 | 1.3 | 17 | 1 | ABT06038 | Human Igm heavy ch |
| 1048 | 13.8 | 1.3 | 17 | 1 | AAK24492 | Hammerhead ribozym | c1121 | 13.8 | 1.3 | 17 | 1 | ABT06038 | Human Igm heavy ch |
| 1049 | 13.8 | 1.3 | 17 | 1 | AAK24492 | Hammerhead ribozym | c1122 | 13.8 | 1.3 | 17 | 1 | ABT06038 | Human Igm heavy ch |
| 1050 | 13.8 | 1.3 | 17 | 1 | AAK24492 | Hammerhead ribozym | c1123 | 13.8 | 1.3 | 17 | 1 | ABT06038 | Human Igm heavy ch |
| 1051 | 13.8 | 1.3 | 17 | 1 | AAK24492 | Oestrogen receptor | c1124 | 13.8 | 1.3 | 17 | 1 | ABT06038 | Human Igm heavy ch |
| 1052 | 13.8 | 1.3 | 17 | 1 | AAK24492 | Oestrogen receptor | c1125 | 13.8 | 1.3 | 17 | 1 | ABT06038 | Human Igm heavy ch |
| 1053 | 13.8 | 1.3 | 17 | 1 | AAK24492 | Oestrogen receptor | c1126 | 13.8 | 1.3 | 17 | 1 | ABT06038 | Human Igm heavy ch |
| 1054 | 13.8 | 1.3 | 17 | 1 | AAK24492 | Oestrogen receptor | c1127 | 13.8 | 1.3 | 17 | 1 | ABT06038 | Human Igm heavy ch |
| 1055 | 13.8 | 1.3 | 17 | 1 | AAK24492 | Oestrogen receptor | c1128 | 13.8 | 1.3 | 17 | 1 | ABT06038 | Human Igm heavy ch |

| | | | |
|----|---|----------|---------------------|
| 17 | 1 | ABA78137 | BRCA1 mutation corr |
| 17 | 1 | ABA78138 | BRCA1 mutation corr |
| 17 | 1 | AA511599 | Porcine reproducti |
| 17 | 1 | AAH95016 | Human Chk1 ribozym |
| 17 | 1 | AAH80147 | Oligonucleotide hy |
| 17 | 1 | ABK02484 | Human NOGO Ambery |
| 17 | 1 | ABS74958 | Human PAPP-Ea asso |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | ABT06038 | Human Igm heavy ch |
| 17 | 1 | | |

[illegible]

| | | | | | | | | | | | | |
|----|-----|----|---|----------|--------------------|------|------|-----|----|---|----------|--------------------|
| 13 | 1.2 | 14 | 1 | AAV12223 | Poly(T) oligonucle | 1348 | 12.8 | 1.2 | 16 | 1 | AAA33723 | Low adenosine anti |
| 13 | 1.2 | 14 | 1 | AAV12224 | Poly(T) oligonucle | 1349 | 12.8 | 1.2 | 16 | 1 | ABL57868 | Human ABCA7 gene P |
| 13 | 1.2 | 14 | 1 | AAV04013 | Oligo-dr primer us | 1350 | 12.8 | 1.2 | 17 | 1 | AAQ13796 | Probe 83-4A for ce |
| 13 | 1.2 | 14 | 1 | AAZ23414 | Integrin subunit b | 1351 | 12.8 | 1.2 | 17 | 1 | AAQ20006 | Oligonucleotide #2 |
| 13 | 1.2 | 14 | 1 | AAZ08326 | Human lung tumour | 1352 | 12.8 | 1.2 | 17 | 1 | AAQ20005 | Oligonucleotide #1 |
| 13 | 1.2 | 14 | 1 | AAZ18181 | Primer for Mouse t | 1353 | 12.8 | 1.2 | 17 | 1 | AAQ26203 | HUA-DR beta sub-ty |
| 13 | 1.2 | 14 | 1 | AAZ19471 | Human senescence f | 1354 | 12.8 | 1.2 | 17 | 1 | AAQ75070 | Mouse flt-1 VEGF r |
| 13 | 1.2 | 14 | 1 | AAZ19474 | Human senescence f | 1355 | 12.8 | 1.2 | 17 | 1 | AAQ75070 | Human KDR VEGF rec |
| 13 | 1.2 | 14 | 1 | AAZ02695 | Human senescence f | 1356 | 12.8 | 1.2 | 17 | 1 | AAQ75070 | Human flt1 VEGF re |
| 13 | 1.2 | 14 | 1 | AAZ02697 | Barley HPD primer | 1357 | 12.8 | 1.2 | 17 | 1 | AAQ69805 | Human flt1 VEGF re |
| 13 | 1.2 | 14 | 1 | AAZ79077 | Barley HPD primer | 1358 | 12.8 | 1.2 | 17 | 1 | AAQ69438 | Human flt1 VEGF re |
| 13 | 1.2 | 14 | 1 | AAZ80852 | (dr)12AG primer. | 1359 | 12.8 | 1.2 | 17 | 1 | AAQ62988 | Human flt1 VEGF re |
| 13 | 1.2 | 14 | 1 | AAZ60813 | Human B18Ag1 cDNA | 1360 | 12.8 | 1.2 | 17 | 1 | AAQ62988 | Delta-9 desaturase |
| 13 | 1.2 | 14 | 1 | AAZ23152 | 3' PCR primer used | 1361 | 12.8 | 1.2 | 17 | 1 | AAQ62988 | Granule bound star |
| 13 | 1.2 | 14 | 1 | ABQ83270 | Human lung tumour- | 1362 | 12.8 | 1.2 | 17 | 1 | AAQ62988 | DNA probe 1 specif |
| 13 | 1.2 | 14 | 1 | ABQ83271 | EGF cDNA tag relat | 1363 | 12.8 | 1.2 | 17 | 1 | AAQ62988 | Human EGF-R target |
| 13 | 1.2 | 14 | 1 | ABQ83272 | EGF cDNA tag relat | 1364 | 12.8 | 1.2 | 17 | 1 | AAQ62988 | Human TTF-2 substr |
| 13 | 1.2 | 14 | 1 | ABQ83276 | EGF cDNA tag relat | 1365 | 12.8 | 1.2 | 17 | 1 | AAQ62988 | Potato citrate syn |
| 13 | 1.2 | 14 | 1 | ABQ83277 | EGF cDNA tag relat | 1366 | 12.8 | 1.2 | 17 | 1 | AAQ62988 | Human TTF-2 substr |
| 13 | 1.2 | 14 | 1 | ABV73026 | EGF cDNA tag relat | 1367 | 12.8 | 1.2 | 17 | 1 | AAQ62988 | Integrin alpha 6 s |
| 13 | 1.2 | 14 | 1 | ABV54141 | Murine SPRP-1 diff | 1368 | 12.8 | 1.2 | 17 | 1 | AAQ62988 | Integrin subunit b |
| 13 | 1.2 | 14 | 1 | ABX46742 | Human breast tumou | 1369 | 12.8 | 1.2 | 17 | 1 | AAQ62988 | Integrin subunit b |
| 13 | 1.2 | 14 | 1 | ABU88472 | Human breast tumou | 1370 | 12.8 | 1.2 | 17 | 1 | AAQ62988 | Human A-Raf substr |
| 13 | 1.2 | 14 | 1 | AAD24491 | Oligo dt 3pi prime | 1371 | 12.8 | 1.2 | 17 | 1 | AAQ62988 | Hammerhead ribozym |
| 13 | 1.2 | 14 | 1 | AAD24493 | Retinoid-regulated | 1372 | 12.8 | 1.2 | 17 | 1 | AAQ62988 | Hammerhead ribozym |
| 13 | 1.2 | 14 | 1 | AAD24494 | Retinoid-regulated | 1373 | 12.8 | 1.2 | 17 | 1 | AAQ62988 | Hammerhead ribozym |
| 13 | 1.2 | 14 | 1 | AAZ99698 | Breast tumour-spec | 1374 | 12.8 | 1.2 | 17 | 1 | AAQ62988 | Hammerhead ribozym |
| 13 | 1.2 | 14 | 1 | ABZ79769 | EST polymorphic DN | 1375 | 12.8 | 1.2 | 17 | 1 | AAQ62988 | Hammerhead ribozym |
| 13 | 1.2 | 14 | 1 | ABZ23321 | Reverse transcript | 1376 | 12.8 | 1.2 | 17 | 1 | AAQ62988 | Hammerhead ribozym |
| 13 | 1.2 | 15 | 1 | AAZ51332 | Human ICAM hammerh | 1377 | 12.8 | 1.2 | 17 | 1 | AAQ62988 | Human genomic SNP |
| 13 | 1.2 | 15 | 1 | AAZ18364 | RT-PCR primer of t | 1378 | 12.8 | 1.2 | 17 | 1 | AAQ62988 | Oestrogen receptor |
| 13 | 1.2 | 15 | 1 | AAZ18361 | RT-PCR primer of t | 1379 | 12.8 | 1.2 | 17 | 1 | AAQ62988 | Oestrogen receptor |
| 13 | 1.2 | 15 | 1 | AAZ62987 | Substrate for HH r | 1380 | 12.8 | 1.2 | 17 | 1 | AAQ62988 | Oestrogen receptor |
| 13 | 1.2 | 15 | 1 | AAZ64410 | Substrate for ham | 1381 | 12.8 | 1.2 | 17 | 1 | AAQ62988 | Oestrogen receptor |
| 13 | 1.2 | 15 | 1 | AAZ69537 | Human IL4Ralpha ge | 1382 | 12.8 | 1.2 | 17 | 1 | AAQ62988 | Retinob |

| | | | | | | | | | | | | | |
|-------|------|-----|----|---|-----------|--------------------|-------|------|-----|----|---|----------|----------------------|
| c1421 | 12.8 | 1.2 | 17 | 1 | ABK18569 | Human ERG G-cleave | c1494 | 12.8 | 1.2 | 18 | 1 | ABK98126 | Triple helix formi |
| c1422 | 12.8 | 1.2 | 17 | 1 | ABK18966 | Human ERG DNzyme | c1495 | 12.8 | 1.2 | 18 | 1 | AB159012 | Oligonucleotide SE |
| c1423 | 12.8 | 1.2 | 17 | 1 | ABK19138 | Human ERG Amberzym | c1496 | 12.8 | 1.2 | 18 | 1 | ABK30214 | CYP2D6 gene polymo |
| c1424 | 12.8 | 1.2 | 17 | 1 | ABK26335 | Waxy starch produc | c1497 | 12.8 | 1.2 | 18 | 1 | ABU43118 | Human chromosome 1 |
| c1425 | 12.8 | 1.2 | 17 | 1 | ABK26336 | Waxy starch produc | c1498 | 12.8 | 1.2 | 18 | 1 | ABU44184 | Human chromosome 1 |
| c1426 | 12.8 | 1.2 | 17 | 1 | ABK26635 | Waxy starch produc | c1499 | 12.8 | 1.2 | 18 | 1 | ABX96428 | Human obese (ob) g |
| c1427 | 12.8 | 1.2 | 17 | 1 | ABK26636 | Waxy starch produc | c1500 | 12.8 | 1.2 | 18 | 1 | ABX10913 | Novel human membra |
| c1428 | 12.8 | 1.2 | 17 | 1 | AA18428 | PCR primer 415 use | c1501 | 12.8 | 1.2 | 18 | 1 | ABX15434 | Human Syk CDNA spe |
| c1429 | 12.8 | 1.2 | 17 | 1 | ABT34698 | Tumour suppression | c1502 | 12.8 | 1.2 | 18 | 1 | AA154275 | Mouse Bsp PCR prim |
| c1430 | 12.8 | 1.2 | 17 | 1 | ABT35200 | Tumour suppression | c1503 | 12.8 | 1.2 | 21 | 1 | ACG91374 | Oligo JT-296 for c |
| c1431 | 12.8 | 1.2 | 17 | 1 | ABT35608 | Tumour suppression | c1504 | 12.6 | 1.1 | 13 | 1 | ABC13098 | Oligonucleotide SE |
| c1432 | 12.8 | 1.2 | 17 | 1 | ABT37161 | Tumour suppression | c1505 | 12.6 | 1.1 | 13 | 1 | ABC13099 | Oligonucleotide SE |
| c1433 | 12.8 | 1.2 | 17 | 1 | ABT37451 | Tumour suppression | c1506 | 12.6 | 1.1 | 13 | 1 | ABC97302 | Oligonucleotide SE |
| c1434 | 12.8 | 1.2 | 17 | 1 | ABT38498 | Tumour suppression | c1507 | 12.6 | 1.1 | 13 | 1 | ABC97303 | Oligonucleotide SE |
| c1435 | 12.8 | 1.2 | 17 | 1 | ABT38748 | Tumour suppression | c1508 | 12.6 | 1.1 | 13 | 1 | ABC97303 | Oligonucleotide SE |
| c1436 | 12.8 | 1.2 | 17 | 1 | ABT39374 | Tumour suppression | c1509 | 12.6 | 1.1 | 13 | 1 | ABF14878 | Oligonucleotide SE |
| c1437 | 12.8 | 1.2 | 17 | 1 | ACR06327 | NFKB sub-unit modu | c1510 | 12.6 | 1.1 | 13 | 1 | ABF14879 | Oligonucleotide SE |
| c1438 | 12.8 | 1.2 | 17 | 1 | ACR06327 | NFKB sub-unit modu | c1511 | 12.6 | 1.1 | 13 | 1 | ABF49492 | Oligonucleotide SE |
| c1439 | 12.8 | 1.2 | 17 | 1 | ACA06768 | NFKB sub-unit modu | c1512 | 12.6 | 1.1 | 13 | 1 | ABF49493 | Oligonucleotide SE |
| c1440 | 12.8 | 1.2 | 17 | 1 | ACA06768 | NFKB sub-unit modu | c1513 | 12.6 | 1.1 | 13 | 1 | ABF77924 | Oligonucleotide SE |
| c1441 | 12.8 | 1.2 | 17 | 1 | ABX16358 | Human checkpoint g | c1514 | 12.6 | 1.1 | 13 | 1 | ABF77925 | Oligonucleotide SE |
| c1442 | 12.8 | 1.2 | 17 | 1 | ABX172106 | Human tumour endot | c1515 | 12.6 | 1.1 | 13 | 1 | ABF99038 | Oligonucleotide SE |
| c1443 | 12.8 | 1.2 | 17 | 1 | ABZ61500 | Human H-Ras DNzyme | c1516 | 12.6 | 1.1 | 14 | 1 | ABF99039 | Oligonucleotide SE |
| c1444 | 12.8 | 1.2 | 17 | 1 | ABZ64967 | Human HER2 DNzyme | c1517 | 12.6 | 1.1 | 14 | 1 | AAV10121 | Oligonucleotide SE |
| c1445 | 12.8 | 1.2 | 17 | 1 | ABZ65388 | Human HER2 DNzyme | c1518 | 12.6 | 1.1 | 14 | 1 | AZ89371 | Human retinoid rec |
| c1446 | 12.8 | 1.2 | 17 | 1 | ABZ65433 | Human HER2 DNzyme | c1519 | 12.6 | 1.1 | 14 | 1 | AZ89371 | RNA detecting prim |
| c1447 | 12.8 | 1.2 | 17 | 1 | ABZ65433 | Human HER2 DNzyme | c1520 | 12.6 | 1.1 | 15 | 1 | ABK15060 | Reverse transcript |
| c1448 | 12.8 | 1.2 | 17 | 1 | ABZ65527 | Human HER2 DNzyme | c1521 | 12.6 | 1.1 | 15 | 1 | ABA81571 | Human phospholipid |
| c1449 | 12.8 | 1.2 | 17 | 1 | ABZ65527 | Human HER2 DNzyme | c1522 | 12.6 | 1.1 | 20 | 1 | AAS94583 | Human PLTP gene al |
| c1450 | 12.8 | 1.2 | 18 | 1 | AAQ20007 | Human HER2 DNzyme | c1523 | 12.4 | 1.1 | 14 | 1 | AAH45766 | Human E2F-2 gene p |
| c1451 | 12.8 | 1.2 | 18 | 1 | AAQ26202 | Oligonucleotide #3 | c1524 | 12.4 | 1.1 | 14 | 1 | AAQ45287 | Sequence of minina |
| c1452 | 12.8 | 1.2 | 18 | 1 | AAQ41404 | HLA-DR beta sub-ty | c1525 | 12.4 | 1.1 | 14 | 1 | AAQ45287 | Degenerate 3' olig |
| c1453 | 12.8 | 1.2 | 18 | 1 | AAQ67186 | Monomer DRB3705 fo | c1526 | 12.4 | 1.1 | 14 | 1 | AAQ45287 | 3' primer for DUB- |
| c1454 | 12.8 | 1.2 | 18 | 1 | AAQ67186 | Human CD40 hairpin | c1527 | 12.4 | 1.1 | 14 | 1 | AAQ45287 | 3' poly(T) primer |
| c1455 | 12.8 | 1.2 | 18 | 1 | AAQ67186 | Triple helix formi | c1528 | 12.4 | 1.1 | 14 | 1 | AAQ45287 | 3' poly(T) primer |
| c1456 | 12.8 | 1.2 | 18 | 1 | AAQ67186 | Triple helix formi | c1529 | 12.4 | 1.1 | 14 | 1 | AAQ45287 | 3' poly(T) primer |
| c1457 | 12.8 | 1.2 | 18 | 1 | AAQ67186 | DNA sequencing "pr | c1530 | 12.4 | 1.1 | 14 | 1 | AAQ45287 | Poly(T) oligonucle |
| c1458 | 12.8 | 1.2 | 18 | 1 | AAQ67186 | Primer #2 for sWSS | c1531 | 12.4 | 1.1 | 14 | 1 | AAQ45287 | Poly(T) oligonucle |
| c1459 | 12.8 | 1.2 | 18 | 1 | AAQ67186 | CDNA3 sense primer | c1532 | 12.4 | 1.1 | 14 | 1 | AAQ45287 | Poly(T) oligonucle |
| c1460 | 12.8 | 1.2 | 18 | 1 | AAQ67186 | Human KDR VEGF rec | c1533 | 12.4 | 1.1 | 14 | 1 | AAQ45287 | Poly(T) oligonucle |
| c1461 | 12.8 | 1.2 | 18 | 1 | AAQ67186 | Sense primer Exon | c1534 | 12.4 | 1.1 | 14 | 1 | AAQ45287 | Oligo-dr primer us |
| c1462 | 12.8 | 1.2 | 18 | 1 | AAQ67186 | Mouse Pax4 PCR sen | c1535 | 12.4 | 1.1 | 14 | 1 | AAQ45287 | PCR primer for DNA |
| c1463 | 12.8 | 1.2 | 18 | 1 | AAQ67186 | LDR oligonucleotid | c1536 | 12.4 | 1.1 | 14 | 1 | AAQ45287 | Human senescence f |
| c1464 | 12.8 | 1.2 | 18 | 1 | AAQ67186 | Human AKT-1 phosph | c1537 | 12.4 | 1.1 | 14 | 1 | AAQ45287 | Human senescence f |
| c1465 | 12.8 | 1.2 | 18 | 1 | AAQ67186 | Human Akt-1 mRNA i | c1538 | 12.4 | 1.1 | 14 | 1 | AAQ45287 | Human senescence f |
| c1466 | 12.8 | 1.2 | 18 | 1 | AAQ67186 | PCR primer for Pax | c1539 | 12.4 | 1.1 | 14 | 1 | AAQ45287 | Barley HPD primer |
| c1467 | 12.8 | 1.2 | 18 | 1 | AAQ67186 | STK 8 gene specif | c1540 | 12.4 | 1.1 | 14 | 1 | AAQ45287 | Anti-gammaPDE codi |
| c1468 | 12.8 | 1.2 | 18 | 1 | AAQ67186 | STK 9 gene specif | c1541 | 12.4 | 1.1 | 14 | 1 | AAQ45287 | RNA oligonucleotid |
| c1469 | 12.8 | 1.2 | 18 | 1 | AAQ67186 | STK 10 gene specif | c1542 | 12.4 | 1.1 | 14 | 1 | AAQ45287 | EGI CDNA tag relat |
| c1470 | 12.8 | 1.2 | 18 | 1 | AAQ67186 | STK 11 gene specif | c1543 | 12.4 | 1.1 | 14 | 1 | AAQ45287 | PCR primer #2 used |
| c1471 | 12.8 | 1.2 | 18 | 1 | AAQ67186 | STK 12 gene specif | c1544 | 12.4 | 1.1 | 14 | 1 | AAQ45287 | MARS gene intron |
| c1472 | 12.8 | 1.2 | 18 | 1 | AAQ67186 | STK 13 gene specif | c1545 | 12.4 | 1.1 | 14 | 1 | AAQ45287 | Retinoid-regulated |
| c1473 | 12.8 | 1.2 | 18 | 1 | AAQ67186 | STK 14 gene specif | c1546 | 12.4 | 1.1 | 14 | 1 | AAQ45287 | Retinoid-regulated |
| c1474 | 12.8 | 1.2 | 18 | 1 | AAQ67186 | PCR primer Syk-H f | c1547 | 12.4 | 1.1 | 14 | 1 | AAQ45287 | Retinoid-regulated |
| c1475 | 12.8 | 1.2 | 18 | 1 | AAQ67186 | Human biallelic ma | c1548 | 12.4 | 1.1 | 14 | 1 | AAQ45287 | EST polymorphic DN |
| c1476 | 12.8 | 1.2 | 18 | 1 | AAQ67186 | Human biallelic ma | c1549 | 12.4 | 1.1 | 14 | 1 | AAQ45287 | Human relA hammerh |
| c1477 | 12.8 | 1.2 | 18 | 1 | AAQ67186 | Human biallelic ma | c1550 | 12.4 | 1.1 | 14 | 1 | AAQ45287 | Human relA hammerh |
| c1478 | 12.8 | 1.2 | 18 | 1 | AAQ67186 | Human OB gene sequ | c1551 | 12.4 | 1.1 | 15 | 1 | AAQ45287 | Human ICAM hammerh |
| c1479 | 12.8 | 1.2 | 18 | 1 | AAQ67186 | Human OB DNA PCR p | c1552 | 12.4 | 1.1 | 15 | 1 | AAQ45287 | HLA-DR typing prob |
| c1480 | 12.8 | 1.2 | 18 | 1 | AAQ67186 | Human TNFalpha ant | c1553 | 12.4 | 1.1 | 15 | 1 | AAQ45287 | Vader transposon 5 |
| c1481 | 12.8 | 1.2 | 18 | 1 | AAQ67186 | Human TNFalpha ant | c1554 | 12.4 | 1.1 | 15 | 1 | AAQ45287 | HLA allele, HLA-DR |
| c1482 | 12.8 | 1.2 | 18 | 1 | AAQ67186 | Human TNFalpha ant | c1555 | 12.4 | 1.1 | 15 | 1 | AAQ45287 | HLA allele, HLA-DR |
| c1483 | 12.8 | 1.2 | 18 | 1 | AAQ67186 | Escherichia coli H | c1556 | 12.4 | 1.1 | 15 | 1 | AAQ45287 | BrB-2 gene antisense |
| c1484 | 12.8 | 1.2 | 18 | 1 | AAQ67186 | PCR primer Syk-M f | c1557 | 12.4 | 1.1 | 15 | 1 | AAQ45287 | JunB gene antisense |
| c1485 | 12.8 | 1.2 | 18 | 1 | AAQ67186 | Shrimp white spot | c1558 | 12.4 | 1.1 | 15 | 1 | AAQ45287 | Probe F67DR70 used |
| c1486 | 12.8 | 1.2 | 18 | 1 | AAQ67186 | SNP specific upper | c1559 | 12.4 | 1.1 | 15 | 1 | AAQ45287 | Oligonucleotide se |
| c1487 | 12.8 | 1.2 | 18 | 1 | AAQ67186 | Primer PC2 to ampl | c1560 | 12.4 | 1.1 | 15 | 1 | AAQ45287 | Oligonucleotide se |
| c1488 | 12.8 | 1.2 | 18 | 1 | AAQ67186 | Cytochrome P-450 (| c1561 | 12.4 | 1.1 | 15 | 1 | AAQ45287 | Tag sequence of a |
| c1489 | 12.8 | 1.2 | 18 | 1 | AAQ67186 | Cytochrome P-450 (| c1562 | 12.4 | 1.1 | 15 | 1 | AAQ45287 | Tag sequence of a |
| c1490 | 12.8 | 1.2 | 18 | 1 | AAQ67186 | Human phosphophol | c1563 | 12.4 | 1.1 | 15 | 1 | AAQ45287 | Substrate for ham |
| c1491 | 12.8 | 1.2 | 18 | 1 | AAQ67186 | Human Ob gene STS | c1564 | 12.4 | 1.1 | 15 | 1 | AAQ45287 | |
| c1492 | 12.8 | 1.2 | 18 | 1 | AAQ67186 | | c1565 | 12.4 | 1.1 | 15 | 1 | AAQ45287 | |
| c1493 | 12.8 | 1.2 | 18 | 1 | AAQ67186 | | c1566 | 12.4 | 1.1 | 15 | 1 | AAQ45287 | |

| | | | | | | | | | | | | | |
|-------|------|-----|----|---|-----------|--------------------|-------|------|-----|----|---|----------|--------------------|
| c1567 | 12.4 | 1.1 | 15 | 1 | AAZ64408 | Substrate for ham | 1640 | 12.4 | 1.1 | 17 | 1 | ABN07679 | Human GDMPL-1 17-m |
| c1568 | 12.4 | 1.1 | 15 | 1 | AAF92685 | HLA-DR typing prob | c1641 | 12.4 | 1.1 | 17 | 1 | ABN07800 | Human GDMPL-1 17-m |
| 1569 | 12.4 | 1.1 | 15 | 1 | AAF95031 | Mutant capture oli | c1642 | 12.4 | 1.1 | 17 | 1 | ABN07801 | Human GDMPL-1 17-m |
| c1570 | 12.4 | 1.1 | 15 | 1 | AAF60455 | Oligonucleotide c1 | c1643 | 12.4 | 1.1 | 17 | 1 | ABN07802 | Human GDMPL-1 17-m |
| c1571 | 12.4 | 1.1 | 15 | 1 | AAF81000 | PTGS2 allele speci | c1644 | 12.4 | 1.1 | 17 | 1 | ABN07803 | Human GDMPL-1 17-m |
| 1572 | 12.4 | 1.1 | 15 | 1 | AAF46502 | IGFBP2 oligonucleo | c1645 | 12.4 | 1.1 | 17 | 1 | ABN08111 | Human GDMPL-1 17-m |
| c1573 | 12.4 | 1.1 | 15 | 1 | AAF46504 | IGFBP2 oligonucleo | c1646 | 12.4 | 1.1 | 17 | 1 | ABN08112 | Human GDMPL-1 17-m |
| c1574 | 12.4 | 1.1 | 15 | 1 | AAF49043 | IGF-I oligonucleot | c1647 | 12.4 | 1.1 | 17 | 1 | ABN08113 | Human GDMPL-1 17-m |
| 1575 | 12.4 | 1.1 | 15 | 1 | AAF51980 | IGF-I oligonucleot | c1648 | 12.4 | 1.1 | 17 | 1 | ABN08114 | Human GDMPL-1 17-m |
| 1576 | 12.4 | 1.1 | 15 | 1 | AAF51981 | IGF-I oligonucleot | c1649 | 12.4 | 1.1 | 17 | 1 | ABN08393 | Human GDMPL-1 17-m |
| c1577 | 12.4 | 1.1 | 15 | 1 | AAF53299 | IGF-I oligonucleot | c1650 | 12.4 | 1.1 | 17 | 1 | ABN08394 | Human GDMPL-1 17-m |
| c1578 | 12.4 | 1.1 | 15 | 1 | AAF53300 | IGF-I oligonucleot | c1651 | 12.4 | 1.1 | 17 | 1 | ABN08659 | Human GDMPL-1 17-m |
| c1579 | 12.4 | 1.1 | 15 | 1 | ABX01316 | Hepatitis C virus | c1652 | 12.4 | 1.1 | 17 | 1 | ABN08659 | GAPDH cDNA PCR pri |
| c1580 | 12.4 | 1.1 | 15 | 1 | ABX01461 | Hepatitis C virus | c1653 | 12.4 | 1.1 | 17 | 1 | ABN08659 | Human ERG hammarhe |
| 1581 | 12.4 | 1.1 | 15 | 1 | ABK41344 | Human eIF2Bgamma r | c1654 | 12.4 | 1.1 | 17 | 1 | ABK17554 | Human ERG hammarhe |
| 1582 | 12.4 | 1.1 | 15 | 1 | ABK31940 | Human colon cancer | c1655 | 12.4 | 1.1 | 17 | 1 | ABK17718 | Human ERG hammarhe |
| c1583 | 12.4 | 1.1 | 15 | 1 | ABK32012 | Human colon cancer | c1656 | 12.4 | 1.1 | 17 | 1 | ABK17723 | Human ERG hammarhe |
| c1584 | 12.4 | 1.1 | 15 | 1 | ABK32522 | Human pancreatic c | c1657 | 12.4 | 1.1 | 17 | 1 | ABK17724 | Human ERG hammarhe |
| c1585 | 12.4 | 1.1 | 15 | 1 | ABZ76549 | Lactobacillus brev | c1658 | 12.4 | 1.1 | 17 | 1 | ABK18431 | Human ERG hammarhe |
| 1586 | 12.4 | 1.1 | 15 | 1 | AAV14166 | Probe HBP21 for g | c1659 | 12.4 | 1.1 | 17 | 1 | ABK18608 | Human ERG G-cleave |
| 1587 | 12.4 | 1.1 | 16 | 1 | AAV14166 | Complementary huma | c1660 | 12.4 | 1.1 | 17 | 1 | ABK19084 | Human ERG DNazyme |
| c1588 | 12.4 | 1.1 | 16 | 1 | AAV48906 | PCR primer for mar | c1661 | 12.4 | 1.1 | 17 | 1 | ABK19427 | Human ERG DNazyme |
| c1589 | 12.4 | 1.1 | 16 | 1 | AAV57828 | PCR primer for mar | c1662 | 12.4 | 1.1 | 17 | 1 | ABK26199 | Increased starch p |
| c1590 | 12.4 | 1.1 | 16 | 1 | AAV36683 | Human HLA-A/HLA-B | c1663 | 12.4 | 1.1 | 17 | 1 | ABK26200 | Increased starch p |
| 1591 | 12.4 | 1.1 | 16 | 1 | AAV32000 | Interphotoreceptor | c1664 | 12.4 | 1.1 | 17 | 1 | ABT34415 | Tumour suppression |
| c1592 | 12.4 | 1.1 | 16 | 1 | AAV46246 | Probe hybridising | c1665 | 12.4 | 1.1 | 17 | 1 | ABT35404 | Tumour suppression |
| 1593 | 12.4 | 1.1 | 16 | 1 | AAV36573 | Human inflammatory | c1666 | 12.4 | 1.1 | 17 | 1 | ABT35974 | Tumour suppression |
| c1594 | 12.4 | 1.1 | 16 | 1 | AAH91937 | Human 5-lipoxygasa | c1667 | 12.4 | 1.1 | 17 | 1 | ABT36096 | Tumour suppression |
| c1595 | 12.4 | 1.1 | 16 | 1 | ABT11146 | Human proteasome a | c1668 | 12.4 | 1.1 | 17 | 1 | ABT36562 | Tumour suppression |
| c1596 | 12.4 | 1.1 | 16 | 1 | ABK41462 | Human familial bip | c1669 | 12.4 | 1.1 | 17 | 1 | ABT37233 | Tumour suppression |
| 1597 | 12.4 | 1.1 | 16 | 1 | ACA58253 | HLA-DR beta sub-ty | c1670 | 12.4 | 1.1 | 17 | 1 | ABT37801 | Tumour suppression |
| c1598 | 12.4 | 1.1 | 17 | 1 | AAQ26112 | HLA-DR beta sub-ty | c1671 | 12.4 | 1.1 | 17 | 1 | ABT39985 | Tumour suppression |
| c1599 | 12.4 | 1.1 | 17 | 1 | AAQ26233 | HLA-DR beta sub-ty | c1672 | 12.4 | 1.1 | 17 | 1 | ACA06427 | NFKB sub-unit modu |
| c1600 | 12.4 | 1.1 | 17 | 1 | AAQ26331 | HLA-DR beta sub-ty | c1673 | 12.4 | 1.1 | 17 | 1 | ABZ60277 | Human K-Ras DNazym |
| c1601 | 12.4 | 1.1 | 17 | 1 | AAQ47606 | Human D HUMDUR/C | c1674 | 12.4 | 1.1 | 17 | 1 | ABZ60283 | Human K-Ras DNazym |
| c1602 | 12.4 | 1.1 | 17 | 1 | AAV71613 | Probe HBP50 for g | c1675 | 12.4 | 1.1 | 17 | 1 | ABZ61269 | Human H-Ras DNazym |
| c1603 | 12.4 | 1.1 | 17 | 1 | AAV714173 | Human EGF-R target | c1676 | 12.4 | 1.1 | 17 | 1 | ABZ61967 | Human H-Ras DNazym |
| 1604 | 12.4 | 1.1 | 17 | 1 | AAV97635 | Human c-fos target | c1677 | 12.4 | 1.1 | 17 | 1 | ABZ64762 | Human HER2 DNazyme |
| 1605 | 12.4 | 1.1 | 17 | 1 | AAV95304 | Human c-fos target | c1678 | 12.4 | 1.1 | 17 | 1 | ABZ64765 | Human HER2 DNazyme |
| 1606 | 12.4 | 1.1 | 17 | 1 | AAV95305 | Human c-fos target | c1679 | 12.4 | 1.1 | 17 | 1 | ABZ64766 | Human HER2 DNazyme |
| 1607 | 12.4 | 1.1 | 17 | 1 | AAV96425 | Potato citrate syn | c1680 | 12.4 | 1.1 | 17 | 1 | ABZ64806 | Human HER2 DNazyme |
| c1608 | 12.4 | 1.1 | 17 | 1 | AAV48869 | Brb-2 gene antise | c1681 | 12.4 | 1.1 | 17 | 1 | ABZ64876 | Human HER2 DNazyme |
| 1609 | 12.4 | 1.1 | 17 | 1 | AAV20398 | Integrin alpha 6 s | c1682 | 12.4 | 1.1 | 17 | 1 | ABZ64877 | Human HER2 DNazyme |
| 1610 | 12.4 | 1.1 | 17 | 1 | AAV91019 | Human C-raf target | c1683 | 12.4 | 1.1 | 17 | 1 | ABZ64901 | Human HER2 DNazyme |
| 1611 | 12.4 | 1.1 | 17 | 1 | AAV91020 | Human C-raf target | c1684 | 12.4 | 1.1 | 17 | 1 | ABZ64966 | Human HER2 DNazyme |
| c1612 | 12.4 | 1.1 | 17 | 1 | AAV91021 | PCR primer used to | c1685 | 12.2 | 1.1 | 18 | 1 | AAV16025 | PCR primer for Hum |
| 1613 | 12.4 | 1.1 | 17 | 1 | AAV91021 | Hammerhead ribozym | c1686 | 12.2 | 1.1 | 18 | 1 | AAV16025 | PCR primer for Hum |
| 1614 | 12.4 | 1.1 | 17 | 1 | AAV91021 | Hammerhead ribozym | c1687 | 12.2 | 1.1 | 18 | 1 | AAV16025 | PCR primer D-F use |
| 1615 | 12.4 | 1.1 | 17 | 1 | AAV91021 | Hammerhead ribozym | c1688 | 12.2 | 1.1 | 18 | 1 | AAV16025 | Murine Sox2 gene p |
| 1616 | 12.4 | 1.1 | 17 | 1 | AAV91021 | Hammerhead ribozym | c1689 | 12.2 | 1.1 | 18 | 1 | AAV16025 | Reverse transcript |
| c1617 | 12.4 | 1.1 | 17 | 1 | AAV91021 | Hammerhead ribozym | c1690 | 12.2 | 1.1 | 21 | 1 | AAV16025 | Oligonucleotide-na |
| c1618 | 12.4 | 1.1 | 17 | 1 | AAV91021 | Hammerhead ribozym | | | | 22 | 1 | AAV16025 | |
| c1619 | 12.4 | 1.1 | 17 | 1 | AAV91021 | Hammerhead ribozym | | | | | | | |
| 1620 | 12.4 | 1.1 | 17 | 1 | AAV91021 | Hammerhead ribozym | | | | | | | |
| 1621 | 12.4 | 1.1 | 17 | 1 | AAV91021 | Hammerhead ribozym | | | | | | | |
| c1622 | 12.4 | 1.1 | 17 | 1 | AAV91021 | Hammerhead ribozym | | | | | | | |
| 1623 | 12.4 | 1.1 | 17 | 1 | AAV91021 | Hammerhead ribozym | | | | | | | |
| c1624 | 12.4 | 1.1 | 17 | 1 | AAV91021 | Hammerhead ribozym | | | | | | | |
| 1625 | 12.4 | 1.1 | 17 | 1 | AAV91021 | Hammerhead ribozym | | | | | | | |
| 1626 | 12.4 | 1.1 | 17 | 1 | AAV91021 | Hammerhead ribozym | | | | | | | |
| 1627 | 12.4 | 1.1 | 17 | 1 | AAV91021 | Hammerhead ribozym | | | | | | | |
| c1628 | 12.4 | 1.1 | 17 | 1 | AAV91021 | Hammerhead ribozym | | | | | | | |
| 1629 | 12.4 | 1.1 | 17 | 1 | AAV91021 | Hammerhead ribozym | | | | | | | |
| c1630 | 12.4 | 1.1 | 17 | 1 | AAV91021 | Hammerhead ribozym | | | | | | | |
| c1631 | 12.4 | 1.1 | 17 | 1 | AAV91021 | Hammerhead ribozym | | | | | | | |
| c1632 | 12.4 | 1.1 | 17 | 1 | AAV91021 | Hammerhead ribozym | | | | | | | |
| c1633 | 12.4 | 1.1 | 17 | 1 | AAV91021 | Hammerhead ribozym | | | | | | | |
| c1634 | 12.4 | 1.1 | 17 | 1 | AAV91021 | Hammerhead ribozym | | | | | | | |
| 1635 | 12.4 | 1.1 | 17 | 1 | AAV91021 | Hammerhead ribozym | | | | | | | |
| 1636 | 12.4 | 1.1 | 17 | 1 | AAV91021 | Hammerhead ribozym | | | | | | | |
| 1637 | 12.4 | 1.1 | 17 | 1 | AAV91021 | Hammerhead ribozym | | | | | | | |
| 1638 | 12.4 | 1.1 | 17 | 1 | AAV91021 | Hammerhead ribozym | | | | | | | |
| 1639 | 12.4 | 1.1 | 17 | 1 | AAV91021 | Hammerhead ribozym | | | | | | | |

ALIGNMENTS

RESULT 1
 AAQ75728/c
 ID AAQ75728 standard; DNA; 21 BP.
 XX
 AC AAQ75728;
 XX
 XX
 DT 04-AUG-1995 (first entry)
 XX
 DE Reverse transcription primer used in cDNA analysis technique.
 XX
 XX Analysis; gene expression; reverse transcription; primer; cDNA;
 KW aggregate; restriction enzyme; ss.
 XX
 XX Synthetic.
 OS
 PN JP06303997-A.
 XX

PD 01-NOV-1994.
 XX
 PF 16-APR-1993; 93JP-0112515.
 XX
 PR 16-APR-1993; 93JP-0112515.
 XX
 PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX
 XX WPI; 1995-018287/03.
 DR
 XX
 XX Analysis of cDNA and gene expression - by amplification of mRNA
 PT followed by digestion with restriction enzymes
 PT
 XX Disclosure; Page 8; 11pp; Japanese.
 PS
 XX A method for the analysis of cDNA comprises (a) preparing an
 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
 CC and a plural type of labelled reverse transcription primers
 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
 CC template for each reverse transcription primer; (b) digesting each of
 CC the prepared aggregates of the double-stranded cDNAs with restriction
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
 CC separate lanes. The method can be used to analyse gene expression
 CC rapidly and easily.
 XX
 XX Sequence 21 BP; 3 A; 0 C; 0 G; 18 T; 0 other;
 SQ
 Query Match 1.9%; Score 21; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 44;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1080 TATTAAAAAATAAAAAAAAAA 1100
 DB 21 TATTAAAAAATAAAAAAAAAA 1
 RESULT 2
 AAA71444/c
 ID AAA71444 standard; DNA; 30 BP.
 AC AAA71444;
 XX
 XX
 DT 01-DEC-2000 (first entry)
 XX
 DE Human megisin promoter PCR primer SEQ ID NO: 11.
 XX
 KW Promoter; megisin; human; protein isolation; screening. PCR primer; ss.
 XX
 OS Homo sapiens.
 XX
 XX WO200043528-A1.
 PN
 XX 27-JUL-2000.
 PD
 XX
 XX 25-JAN-2000; 2000WO-JP00350.
 PF
 XX
 XX 25-JAN-1999; 99JP-0015667.
 PR
 XX (KURO)/ KUROKAWA K.
 PA (MIYA)/ MIYATA T.
 XX
 XX Miyata T;
 PI
 XX
 XX WPI; 2000-543257/49.
 DR
 XX
 XX DNA for promoter region of megisin useful for screening proteins -
 PT
 XX Example 5; Page 38; 45pp; Japanese.
 PS
 XX This invention describes a novel DNA sequence (I) representing a
 CC promoter region having part or all of a specific base sequence. The
 CC invention also describes (1) a vector containing (I); (2) a cell
 CC transformed by the above vector; and (3) protein produced using (I). (I)

CC is useful for screening and isolating proteins (especially transcription
 CC factors). AAA71434-A71469 represent PCR primers used in the method
 CC described in the invention.
 XX
 SQ Sequence 30 BP; 6 A; 10 C; 5 G; 9 T; 0 other;
 Query Match 1.9%; Score 21; DB 1; Length 30;
 Best Local Similarity 82.8%; Pred. No. 65;
 Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 266 GAGCACCTTCAGAAAGTTGTTGAAACTTG 294
 DB 30 GAGCACCTTCAGATAGGAGCTGAAACTTG 2
 RESULT 3
 AAH38447
 ID AAH38447 standard; DNA; 25 BP.
 XX
 AC AAH38447;
 XX
 DT 14-AUG-2001 (first entry)
 XX
 DE SNP specific SNPE primer SEQ ID 1243.
 XX
 KW Single nucleotide polymorphism; SNP; single nucleotide primer extension;
 KW SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;
 KW Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;
 KW polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
 KW acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
 KW inflammation; forensic investigation; paternity analysis; primer; ss.
 XX
 OS Homo sapiens.
 XX
 XX WO200129262-A2.
 PN
 XX 26-APR-2001.
 PD
 XX
 PF 13-OCT-2000; 2000WO-US28436.
 XX
 PR 15-OCT-1999; 99US-0160096.
 XX
 XX (ORCH-) ORCHID BIOSCIENCES INC.
 PA
 XX Picoult-Newburg L, Pohl M;
 XX
 XX WPI; 2001-290930/30.
 DR
 XX New genotyping oligonucleotide, useful for detecting the presence,
 PT absence or identity of single polynucleotide polymorphism in a nucleic
 PT acid sample -
 XX
 XX Claim 1; Page 56; 83pp; English.
 PS
 XX Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
 CC primer extension (SNPE) primers, and the sequences of regions flanking
 CC sites of single nucleotide polymorphisms SNPs. The present invention
 CC includes kits for determining the presence or absence of a SNP, using the
 CC oligonucleotides of the invention. The PCR primers are used to amplify a
 CC SNP flanking sequence, the SNPE primer is used as a genotyping primer.
 CC The oligonucleotides are useful for genotyping a nucleic acid sample by
 CC performing a single-nucleotide primer extension reaction. The
 CC oligonucleotides are useful for determining the presence, absence or
 CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to
 CC assess by association analysis the genotype of an individual or group of
 CC individuals, having a pathological phenotypic trait suspected of being
 CC caused by one or more SNPs. Phenotypic traits include diseases e.g.
 CC agammaglobulinaemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular
 CC dystrophy, familial hypercholesterolaemia, polycystic kidney disease,
 CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
 CC traits also include symptoms of or susceptibility to multifactorial
 CC disease of which a component is or may be genetic such as autoimmune
 CC diseases, including, rheumatoid arthritis, multiple sclerosis.

CC inflammation, cancer, nervous system diseases and infection by pathogenic
 CC microorganism. The method is also useful in forensic investigations and
 CC paternity analysis. The present sequence represents a single nucleotide
 CC primer extension (SNPE) primer specific for a human SNP containing DNA
 CC sequence.

XX Sequence 25 BP; 6 A; 2 C; 13 G; 4 T; 0 other;

Query Match 1.8%; Score 20.2; DB 1; Length 25;

Best Local Similarity 88.0%; Pred. No. 74;

Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 991 TTGGAAGTCTGAGGCTGAGGAATGG 1015

DB 1 TTGGGAGGCTGAGGCTGAGGAATGG 25

RESULT 4

AAQ75581/c

ID AAQ75581 standard; DNA; 20 BP.

XX AC

XX AAQ75581;

XX 04-AUG-1995 (first entry)

DE Reverse transcription primer used in cDNA analysis technique.

XX Analysis; gene expression; reverse transcription; primer; cDNA;
 KW aggregate; restriction enzyme; ss.

XX Synthetic.

XX JP06303997-A.

XX 01-NOV-1994.

XX 16-APR-1993; 93JP-0112515.

XX 16-APR-1993; 93JP-0112515.

XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

XX WPI; 1995-018287/03.

XX Analysis of cDNA and gene expression - by amplification of mRNA
 PT followed by digestion with restriction enzymes

XX Disclosure; Page 5; 11pp; Japanese.

CC A method for the analysis of cDNA comprises (a) preparing an
 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
 CC and a plural type of labelled reverse transcription primers
 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
 CC template for each reverse transcription primer; (b) digesting each of
 CC the prepared aggregates of the double-stranded cDNAs with restriction
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
 CC separate lanes. The method can be used to analyse gene expression
 CC rapidly and easily.

XX Sequence 20 BP; 2 A; 0 C; 0 G; 18 T; 0 other;

Query Match 1.8%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 63;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1081 ATTAAAAA1100

DB 20 ATTAAAAA1100

XX Analysis; gene expression; reverse transcription; primer; cDNA;
 KW aggregate; restriction enzyme; ss.
 XX Synthetic.
 XX JP06303997-A.
 XX 01-NOV-1994.
 XX 16-APR-1993; 93JP-0112515.
 XX 16-APR-1993; 93JP-0112515.

RESULT 5

AAQ75727/c

ID AAQ75727 standard; DNA; 21 BP.

XX AAQ75727;

XX AC

XX 04-AUG-1995 (first entry)

XX DE

XX Reverse transcription primer used in cDNA analysis technique.

XX Analysis; gene expression; reverse transcription; primer; cDNA;

XX aggregate; restriction enzyme; ss.

XX Synthetic.

XX JP06303997-A.

XX 01-NOV-1994.

XX 16-APR-1993; 93JP-0112515.

XX 16-APR-1993; 93JP-0112515.

XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

XX WPI; 1995-018287/03.

XX Analysis of cDNA and gene expression - by amplification of mRNA

XX followed by digestion with restriction enzymes

XX Disclosure; Page 8; 11pp; Japanese.

XX A method for the analysis of cDNA comprises (a) preparing an

XX aggregate of double-stranded cDNAs by using an aggregate of mRNAs

XX and a plural type of labelled reverse transcription primers

XX (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the

XX template for each reverse transcription primer; (b) digesting each of

XX the prepared aggregates of the double-stranded cDNAs with restriction

XX enzyme and; (c) electrophoresing the digested aggregate of cDNAs in

XX separate lanes. The method can be used to analyse gene expression

XX rapidly and easily.

XX Sequence 21 BP; 2 A; 0 C; 1 G; 18 T; 0 other;

Query Match 1.8%; Score 20; DB 1; Length 21;

Best Local Similarity 100.0%; Pred. No. 66;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1081 ATTAAAAA1100

DB 20 ATTAAAAA1100

XX Analysis; gene expression; reverse transcription; primer; cDNA;

XX aggregate; restriction enzyme; ss.

XX Synthetic.

XX JP06303997-A.

XX 01-NOV-1994.

XX 16-APR-1993; 93JP-0112515.

XX 16-APR-1993; 93JP-0112515.

XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

XX WPI; 1995-018287/03.

XX Analysis of cDNA and gene expression - by amplification of mRNA

XX followed by digestion with restriction enzymes

XX Disclosure; Page 8; 11pp; Japanese.

XX A method for the analysis of cDNA comprises (a) preparing an

XX aggregate of double-stranded cDNAs by using an aggregate of mRNAs

XX and a plural type of labelled reverse transcription primers

XX (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the

XX template for each reverse transcription primer; (b) digesting each of

XX the prepared aggregates of the double-stranded cDNAs with restriction

XX enzyme and; (c) electrophoresing the digested aggregate of cDNAs in

XX separate lanes. The method can be used to analyse gene expression

XX rapidly and easily.

XX Sequence 20 BP; 2 A; 0 C; 0 G; 18 T; 0 other;

Query Match 1.8%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 63;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1081 ATTAAAAA1100

DB 20 ATTAAAAA1100

XX Analysis; gene expression; reverse transcription; primer; cDNA;

XX aggregate; restriction enzyme; ss.

XX Synthetic.

XX JP06303997-A.

XX 01-NOV-1994.

XX 16-APR-1993; 93JP-0112515.

XX 16-APR-1993; 93JP-0112515.

PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX
 XX WPI; 1995-018287/03.
 XX
 XX Analysis of cDNA and gene expression - by amplification of mRNA
 PT followed by digestion with restriction enzymes
 XX
 XX Disclosure; Page 8; 11pp; Japanese.
 XX
 XX A method for the analysis of cDNA comprises (a) preparing an
 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
 CC and a plural type of labelled reverse transcription primers
 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
 CC template for each reverse transcription primer; (b) digesting each of
 CC the prepared aggregates of the double-stranded cDNAs with restriction
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
 CC separate lanes..The method can be used to analyse gene expression
 CC rapidly and easily.
 XX
 XX Sequence 21 BP; 2 A; 0 C; 0 G; 19 T; 0 other;
 SQ

Query Match 1.8%; Score 20; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 66;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 0;

QY 1081 ATTAAAAA1100
 DB 20 ATTAAAAA1100

RESULT 7
 AAQ75730/c
 ID AAQ75730 standard; DNA; 21 BP.
 XX
 XX AC AAQ75730;
 XX
 XX DT 04-AUG-1995 (first entry)
 XX
 XX DE Reverse transcription primer used in cDNA analysis technique.
 XX
 XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
 KW aggregate; restriction enzyme; ss.
 XX
 XX OS Synthetic.
 XX
 XX PN JP06303997-A.
 XX
 XX PD 01-NOV-1994.
 XX
 XX PF 16-APR-1993; 93JP-0112515.
 XX
 XX PR 16-APR-1993; 93JP-0112515.
 XX
 XX PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX
 XX DR WPI; 1995-018287/03.
 XX
 XX PT Analysis of cDNA and gene expression - by amplification of mRNA
 PT followed by digestion with restriction enzymes
 XX
 XX PS Disclosure; Page 8; 11pp; Japanese.
 XX
 XX A method for the analysis of cDNA comprises (a) preparing an
 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
 CC and a plural type of labelled reverse transcription primers
 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
 CC template for each reverse transcription primer; (b) digesting each of
 CC the prepared aggregates of the double-stranded cDNAs with restriction
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
 CC separate lanes..The method can be used to analyse gene expression
 CC rapidly and easily.
 XX
 XX Sequence 21 BP; 2 A; 1 C; 0 G; 18 T; 0 other;
 SQ

Query Match 1.8%; Score 20; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 66;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 0;

QY 1081 ATTAAAAA1100
 DB 20 ATTAAAAA1100

RESULT 8
 AAV71936/c
 ID AAV71936 standard; DNA; 27 BP.
 XX
 XX AC AAV71936;
 XX
 XX DT 18-FEB-1999 (first entry)
 XX
 XX DE Anchored poly T RT-PCR primer.
 XX
 XX KW Normalised; cDNA library; mRNA cloning; reverse transcription;
 KW immobilise; screening; hybridisation; nucleic acid amplification;
 KW expression pattern; drug development; PCR primer; RT-PCR; ss.
 XX
 XX OS Synthetic.
 XX
 XX PN WO9851789-A2.
 XX
 XX PD 19-NOV-1998.
 XX
 XX PF 13-MAY-1998; 98WO-DK00186.
 XX
 XX PR 27-MAR-1998; 98DK-0000432.
 PR 13-MAY-1997; 97DK-0000547.
 PR 19-MAY-1997; 97US-0871030.
 XX
 XX PA (DISP-) DISPLAY SYSTEMS BIOTECH APS.
 XX
 XX PI Warthoe PR;
 XX
 XX DR WPI; 1999-009772/01.
 XX
 XX PT Preparation of normalised, subdivided cDNA libraries from mRNA - by
 PT reverse transcription and amplification, used to screen for new
 PT genes and interacting proteins, potential drugs, and for diagnosis
 XX
 XX PS Example 1; Page 29; 71pp; English.
 XX
 XX CC The invention relates to preparation of a normalised, subdivided library
 CC of amplified cDNA from the coding regions of mRNA in a sample. The
 CC method involves reverse transcription, with at least one cDNA primer of
 CC formula 5'-Con1-dTn2-Vn3-Nn4 to form first stand cDNA where Con1 = any
 CC sequence of 1-100 nucleotides; dT = deoxythymidyl; n2 is at least 1; n3
 CC and n4 are both 0, or n3 is 1 and n4 is at least 1; followed by second
 CC strand cDNA synthesis using the first strand as template and a second
 CC cDNA primer of a similar formula, in the presence of DNA polymerase I (or
 CC its Klenow fragment) and amplification of double-stranded cDNA with a set
 CC of amplification primers. Comparison of cDNA in the prepared library with
 CC a database (a computer-generated list of molecular weights of restricted
 CC DNA fragments of known sequence) is used to determine presence of an
 CC expressed protein in a cell, also to detect changes in such expression
 CC (particularly for diagnosis of disease). Surfaces (chip) having
 CC amplified cDNA stably immobilised on it, obtained by a similar method,
 CC are used to screen for genes of a particular family, by hybridisation
 CC with nucleic acid from the family (to identify new genes) and to detect
 CC differences in expression patterns between cells. The polypeptides
 CC expressed by the libraries can be used for drug development. Sequences
 CC AAV71935 to AAV71946 represent primers used to exemplify the method of
 CC the invention.
 XX
 XX SQ Sequence 27 BP; 0 A; 1 C; 1 G; 25 T; 0 other;
 SQ

Query Match 1.8%; Score 19.6; DB 1; Length 27;

Best Local Similarity 84.6%; Pred. No. 1e+02;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1075 GCAACTATTAAAAA 1100
DB 27 GCAAAAAA 2

RESULT 9
ABK52620/C
ID ABK52620 standard; DNA; 27 BP.
XX AC ABK52620;
XX DT 27-AUG-2002 (first entry)
XX DE Minority genome method VFA-MUT-11 DNA sequence.
XX KW Minority genome method; viral quasi-species; majority genome;
XX KW Genetic diagnosis; viral infection; human immune deficiency virus;
XX KW hepatitis B; hepatitis C; antiviral therapy; ss.
XX OS Unidentified.
XX PH Key Location/Qualifiers
FT misc_difference 1
FT /*tag= a
FT /label= unknown
FT /note= "C6 aminolinker sequence"
XX PN W200183815-Al.
XX PD 08-NOV-2001.
XX PF 27-APR-2001; 2001WO-ES00165.
XX PR 27-APR-2000; 2000ES-0001068.
XX PA (CNSJ) CONSEJO SUPERIOR INVESTIGACIONES CIENTIF.
XX PI Arias Esteban A, Baranowski E, Briones Llorente C, Domingo Solans E;
PI Escarnis Homs C, Gomez Castilla J, Martin Ruiz-jarabo C;
PI Parro Garcia V;
XX WP1; 2002-147445/19.
XX DR Detecting minority genomes in viral quasi-species, useful for
XX PT identifying mutants responsible for drug resistance and to
XX PT individualise therapy -
XX PS Example 1; Page 53; 107pp; Spanish.
XX CC The present invention relates to a new method for detecting minority
XX CC genomes, present at less than 50%, in a population of nucleic acids of
XX CC a viral quasi-species and having at least one mutation with respect to
XX CC the majority genome. The invention can be used for genetic diagnosis of
XX CC viral infections, especially human immune deficiency virus and
XX CC hepatitis B or C, particularly to detect memory minority genomes that are
XX CC implicated in failure of antiviral therapy, so the method may make
XX CC possible design of therapies customised for individual patients. The
XX CC present nucleic acid sequence represents the VFA-MUT-11 DNA sequence that
XX CC was used in the methods of the invention.
XX SQ Sequence 27 BP; 2 A; 4 C; 2 G; 18 T; 1 other;

Query Match 1.8%; Score 19.6; DB 1; Length 27;
Best Local Similarity 84.6%; Pred. No. 1e+02;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1073 AAGCAACTATTAAAAA 1098
DB 27 ACGGAGGATTAAAAA 2

Best Local Similarity 84.6%; Pred. No. 1e+02;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1075 GCAACTATTAAAAA 1100
DB 27 GCAAAAAA 2

RESULT 10
AAQ75724/C
ID AAQ75724 standard; DNA; 21 BP.
XX AC AAQ75724;
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX KW aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-0112515.
XX PR 16-APR-1993; 93JP-0112515.
XX PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WP1; 1995-018287/03.
XX PT Analysis of cDNA and gene expression - by amplification of mRNA
XX PT followed by digestion with restriction enzymes
XX PS Disclosure; Page 8; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an
XX CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
XX CC and a plural type of labelled reverse transcription primers
XX CC (GENSEQ files AAQ75547-Q7598) and using the aggregate of mRNAs as the
XX CC template for each reverse transcription primer; (b) digesting each of
XX CC the prepared aggregates of the double-stranded cDNAs with restriction
XX CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
XX CC separate lanes. The method can be used to analyse gene expression
XX CC rapidly and easily.
XX SQ Sequence 21 BP; 4 A; 0 C; 0 G; 17 T; 0 other;

Query Match 1.8%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 85;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1080 TATTAAAAA 1100
DB 21 TTTAAAAA 1

RESULT 11
AAQ75732/C
ID AAQ75732 standard; DNA; 21 BP.
XX AC AAQ75732;
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX KW aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX PD 01-NOV-1994.

```
PF 16-APR-1993; 93JP-0112515.
XX
PR 16-APR-1993; 93JP-0112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA
PT followed by digestion with restriction enzymes
XX
XX Disclosure; Page 8; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC and a plural type of labelled reverse transcription primers
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
CC template for each reverse transcription primer; (b) digesting each of
CC the prepared aggregates of the double-stranded cDNAs with restriction
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC separate lanes. The method can be used to analyse gene expression
CC rapidly and easily.
XX
SQ Sequence 21 BP; 3 A; 1 C; 0 G; 17 T; 0 other;
Query Match 1.8%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 85;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1080 TATTAAAAA 1100
Db 21 TGTAAAAA 1

RESULT 12
AAQ75760/c
ID AAQ75760 standard; DNA; 21 BP.
XX
AC AAQ75760;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; Gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-0112515.
XX
XX 16-APR-1993; 93JP-0112515.
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA
PT followed by digestion with restriction enzymes
XX
XX Disclosure; Page 7; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC and a plural type of labelled reverse transcription primers
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
CC template for each reverse transcription primer; (b) digesting each of
CC the prepared aggregates of the double-stranded cDNAs with restriction
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC separate lanes. The method can be used to analyse gene expression
CC rapidly and easily.
XX
SQ Sequence 21 BP; 3 A; 1 C; 0 G; 17 T; 0 other;
Query Match 1.8%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 85;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1080 TATTAAAAA 1100
Db 21 TGTAAAAA 1

RESULT 13
AAQ75696/c
ID AAQ75696 standard; DNA; 21 BP.
XX
AC AAQ75696;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; Gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-0112515.
XX
XX 16-APR-1993; 93JP-0112515.
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA
PT followed by digestion with restriction enzymes
XX
XX Disclosure; Page 7; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC and a plural type of labelled reverse transcription primers
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
CC template for each reverse transcription primer; (b) digesting each of
CC the prepared aggregates of the double-stranded cDNAs with restriction
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC separate lanes. The method can be used to analyse gene expression
CC rapidly and easily.
XX
SQ Sequence 21 BP; 2 A; 1 C; 0 G; 18 T; 0 other;
Query Match 1.8%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 85;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1080 TATTAAAAA 1100
Db 21 TATGAAAAA 1

RESULT 14
AAQ75712/c
ID AAQ75712 standard; DNA; 21 BP.
XX
AC AAQ75712;
XX
```

```
CC separate lanes. The method can be used to analyse gene expression
CC rapidly and easily.
XX
SQ Sequence 21 BP; 2 A; 1 C; 0 G; 18 T; 0 other;
Query Match 1.8%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 85;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1080 TATTAAAAA 1100
Db 21 TATGAAAAA 1

RESULT 13
AAQ75696/c
ID AAQ75696 standard; DNA; 21 BP.
XX
AC AAQ75696;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; Gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-0112515.
XX
XX 16-APR-1993; 93JP-0112515.
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA
PT followed by digestion with restriction enzymes
XX
XX Disclosure; Page 7; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC and a plural type of labelled reverse transcription primers
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
CC template for each reverse transcription primer; (b) digesting each of
CC the prepared aggregates of the double-stranded cDNAs with restriction
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC separate lanes. The method can be used to analyse gene expression
CC rapidly and easily.
XX
SQ Sequence 21 BP; 2 A; 1 C; 0 G; 18 T; 0 other;
Query Match 1.8%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 85;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1080 TATTAAAAA 1100
Db 21 TATGAAAAA 1

RESULT 14
AAQ75712/c
ID AAQ75712 standard; DNA; 21 BP.
XX
AC AAQ75712;
XX
```

```

DT 04-AUG-1995 (first entry)
XX Reverse transcription primer used in cDNA analysis technique.
DE Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
KW Synthetic.
XX
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-0112515.
XX
XX 16-APR-1993; 93JP-0112515.
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA
XX followed by digestion with restriction enzymes
XX
XX Disclosure; Page 7; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an
XX aggregate of double-stranded cDNAs by using an aggregate of mRNAs
XX and a plural type of labelled reverse transcription primers
XX (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
XX template for each reverse transcription primer; (b) digesting each of
XX the prepared aggregates of the double-stranded cDNAs with restriction
XX enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
XX separate lanes. The method can be used to analyse gene expression
XX rapidly and easily.
XX
XX Sequence 21 BP; 2 A; 0 C; 1 G; 18 T; 0 other;
SQ
XX
XX Query Match 1.8%; Score 19.4; DB 1; Length 21;
XX Best Local Similarity 95.2%; Pred. No. 85;
XX Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1080 TATTAAAAA 1100
XX |||||
XX Db 21 TACTAAAAA 1
XX
XX RESULT 15
XX AAQ75720/c
XX ID AAQ75720 standard; DNA; 21 BP.
XX
XX AC AAQ75720;
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-0112515.
XX
XX 16-APR-1993; 93JP-0112515.
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Query Match 1.8%; Score 19.4; DB 1; Length 21;
XX Best Local Similarity 95.2%; Pred. No. 85;
XX Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1080 TATTAAAAA 1100
XX |||||
XX Db 21 TACTAAAAA 1
XX
XX RESULT 15
XX AAQ75720/c
XX ID AAQ75720 standard; DNA; 21 BP.
XX
XX AC AAQ75720;
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-0112515.
XX
XX 16-APR-1993; 93JP-0112515.
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Query Match 1.8%; Score 19.4; DB 1; Length 21;
XX Best Local Similarity 95.2%; Pred. No. 85;
XX Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1080 TATTAAAAA 1100
XX |||||
XX Db 21 TACTAAAAA 1
XX
XX RESULT 16
XX AAQ75680/c
XX ID AAQ75680 standard; DNA; 21 BP.
XX
XX AC AAQ75680;
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-0112515.
XX
XX 16-APR-1993; 93JP-0112515.
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA
XX followed by digestion with restriction enzymes
XX
XX Disclosure; Page 7; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an
XX aggregate of double-stranded cDNAs by using an aggregate of mRNAs
XX and a plural type of labelled reverse transcription primers
XX (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
XX template for each reverse transcription primer; (b) digesting each of
XX the prepared aggregates of the double-stranded cDNAs with restriction
XX enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
XX separate lanes. The method can be used to analyse gene expression
XX rapidly and easily.
XX
XX Sequence 21 BP; 2 A; 0 C; 1 G; 17 T; 0 other;
SQ
XX
XX Query Match 1.8%; Score 19.4; DB 1; Length 21;
XX Best Local Similarity 95.2%; Pred. No. 85;
XX Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1080 TATTAAAAA 1100
XX |||||
XX Db 21 TCTTAAAAA 1
XX
XX RESULT 16
XX AAQ75680/c
XX ID AAQ75680 standard; DNA; 21 BP.
XX
XX AC AAQ75680;
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-0112515.
XX
XX 16-APR-1993; 93JP-0112515.
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA
XX followed by digestion with restriction enzymes
XX
XX Disclosure; Page 7; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an
XX aggregate of double-stranded cDNAs by using an aggregate of mRNAs
XX and a plural type of labelled reverse transcription primers
XX (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
XX template for each reverse transcription primer; (b) digesting each of
XX the prepared aggregates of the double-stranded cDNAs with restriction
XX enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
XX separate lanes. The method can be used to analyse gene expression
XX rapidly and easily.
XX
XX Sequence 21 BP; 2 A; 0 C; 1 G; 19 T; 0 other;
SQ
XX
XX Query Match 1.8%; Score 19.4; DB 1; Length 21;
XX Best Local Similarity 95.2%; Pred. No. 85;

```

OS Synthetic.

XX JP06303997-A.

XX

XX 01-NOV-1994.

XX

XX 16-APR-1993; 93JP-0112515.

XX

XX 16-APR-1993; 93JP-0112515.

XX

XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

XX

XX WPI; 1995-018287/03.

XX

XX Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes

XX

XX Disclosure; Page 6; 11pp; Japanese.

XX

XX A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in separate lanes. The method can be used to analyse gene expression rapidly and easily.

XX

XX Sequence 21 BP; 2 A; 0 C; 1 G; 18 T; 0 other;

SQ

Query Match 1.8%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 85;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1080 TATTAAAAAIAAAAAAAAAA 1100
||| |||||||
DB 21 TATCAAAAAAAAAAAAAAAAAA 1

RESULT 19

ABK12409

ID ID ABK12409 standard; DNA; 24 BP.

XX AC ABK12409;

XX

DT 18-JUN-2002 (first entry)

XX

DE RT-PCR primer #1 for cDNA encoding polypeptide-laminin B210.67.

XX

KW Polypeptide-laminin B210.67; embryo development teratogenesis;
KW cytotstatic; reverse transcriptase-PCR; RT-PCR; primer; ss.
XX Unidentified.
OS

XX CNL328013-A.

PX PN

XX PD 26-DEC-2001.

XX

PF 14-JUN-2000; 2000CN-0116514.

XX

XX 14-JUN-2000; 2000CN-0116514.

XX

PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.

XX

XX Mao Y, Xie Y;

DR WPI; 2002-270054/32.

XX

XX Polypeptide-laminin B210.67, useful for treating diseases such as
PT embryo development teratogenesis -
XX Example 2; Page 18 (disclosure); 33pp; Chinese.

```
XX The present invention relates to the isolation of polypeptide-laminin
CC B210.67, and the polynucleotide encoding it. Also described is
CC the process for preparing the protein by DNA recombination. The
CC polypeptide is useful for treating diseases such as embryo
CC development teratogenesis. The present sequence for reverse
CC transcriptase (RT)-PCR primer #1 is used with RT-PCR primer #2
CC (ABK12410) for isolating cDNA encoding polypeptide-laminin B210.67.
XX Sequence 24 BP; 19 A; 2 C; 0 G; 3 T; 0 other;
SQ
Query Match 1.8%; Score 19.4; DB 1; Length 24;
Best Local Similarity 95.2%; Pred. No. 98;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1080 TATTAAAAA 1100
Db 3 TCTTAAAAA 23
RESULT 20
AAI66361/c
ID AAI66361 standard; DNA; 24 BP.
XX AC AAI66361;
XX DT 23-JAN-2002 (first entry)
XX DE Human phosphatidylinositol-3 kinase 35 cDNA PCR primer #2.
XX KW Human; phosphatidylinositol-3 kinase 35; PTINS-3 kinase 35; cancer;
XX KW haemopathy; development disorder; HIV infection; immunological disease;
XX KW inflammation; gene therapy; PCR primer; ss.
XX OS Homo sapiens.
XX PN WO200175014-A2.
XX PD 11-OCT-2001.
XX PF 16-MAR-2001; 2001WO-CN00328.
XX PR 17-MAR-2000; 2000CN-0114973.
XX PA (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
XX PI Mao Y, Xie Y;
XX WPI; 2002-025836/03.
XX DE New human phosphatidylinositol-3 (PTDINS3) kinase 35 for diagnosing and
PT treating malignant tumor, hemopathy, human immunodeficiency virus
PT infection, immunological diseases and various inflammations -
XX
XX Example 2; Page 12; 34pp; Chinese.
XX The present invention provides the protein and coding sequences of human
CC phosphatidylinositol-3 (PTDINS-3) kinase 35. The sequences can be used in
CC the treatment of cancer, haemopathy, HIV infection, development
CC disorders, immunological diseases and inflammation. The present sequence
CC is a PCR primer for the coding sequence of the invention.
XX
XX Sequence 24 BP; 3 A; 0 C; 1 G; 20 T; 0 other;
SQ
Query Match 1.8%; Score 19.4; DB 1; Length 24;
Best Local Similarity 95.2%; Pred. No. 98;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1080 TATTAAAAA 1100
Db 24 TCTTAAAAA 4
```

RESULT 21

```
ABK86170/c
ID ABK86170 standard; DNA; 25 BP.
XX AC ABK86170;
XX DT 24-SEP-2002 (first entry)
XX DE Oligo dT primer #3 used in method to study gene expression.
XX KW Oligo dT primer; gene expression analysis; primer; ss.
XX OS Synthetic.
XX PN WO200236828-A2.
XX PD 10-MAY-2002.
XX PF 01-NOV-2001; 2001WO-US45401.
XX PR 01-NOV-2000; 2000US-244933P.
XX PA (GENO-) GENOMIC SOLUTIONS INC.
XX PI Kane MD, Dombkowski AA, Nagel AC;
XX WPI; 2002-508123/54.
XX PT Identifying and characterizing gene expression in samples, for
PT identifying mRNAs expressed at different levels, comprises employing an
PT identifier having a oligo-dT primer of a specific sequence and a
PT detectable marker at its 5' end -
XX
XX Example 2; Page 21; 45pp; English.
XX The invention relates to systems for identification and characterisation
CC of gene expression in one or more samples, comprising an identifier having
CC a specific oligo-dT primer sequence, where the identifier comprises a
CC detectable marker at its 5' end. The system is useful for identifying any
CC or all genes expressed in a given in vivo or in vitro RNA sample, as well
CC as the relative differences in mRNA between 2 or more samples, where
CC desired, for supporting discovery of new genes, and for identifying mRNAs
CC that are expressed at different levels between 2 or more samples. The new
CC system or method addresses limitations of prior methods by comprising
CC compositions and systems that incorporate new strategies where molecular
CC or biochemical assay compositions and systems are linked to DNA or RNA
CC sequence databases for optimal resource efficiency in assaying gene
CC expression. The system has the following advantages over existing
CC methods: (a) prior sequence information or clone library construction is
CC not needed to enable the assay; (b) provides immediate sequence
CC information in addition to information concerning changes or differences
CC in mRNA level, to determine mRNA expression level and mRNA identification
CC in one assay; (c) generates cDNA fragments from all mRNAs present in the
CC sample for subsequent investigation by common molecular biology
CC techniques; and (d) does not require prior knowledge of the sequence of
CC the genome of the organism under investigation and can be employed in
CC organisms lacking significant genomic sequence information. The present
CC sequence represents an oligo dT primer used in the method of the
CC invention.
XX
XX Sequence 25 BP; 0 A; 0 C; 2 G; 23 T; 0 other;
SQ
Query Match 1.7%; Score 19.2; DB 1; Length 25;
Best Local Similarity 87.5%; Pred. No. 11e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1077 AACTATTAAAAA 1100
Db 24 AACCAAAAAA 1
RESULT 22
ABX79828/c
```

ID ABX79828 standard; cDNA; 27 BP.
 AC ABX79828;
 XX 17-APR-2003 (first entry)
 XX EST polymorphic DNA repeat polynucleotide #153.
 DE EST; expressed sequence tag; ss; polymorphic repeat; tandem repeat;
 XX polymorphic marker prediction of ubiquitous simple sequences; POMPOUS;
 KW Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;
 KW Haw River syndrome; Huntington's disease; fragile-X syndrome;
 KW Friedrich's ataxia; myotonic dystrophy; hyperandrogenaemia;
 KW spinal atrophy; bulbar atrophy; spinocerebellar ataxia.
 XX Homo sapiens.
 OS
 XX US6472154-B1.
 PN 29-OCT-2002.
 PD 31-DEC-1999; 99US-0475947.
 XX 31-DEC-1999; 99US-0475947.
 XX (TEXA) UNIV TEXAS SYSTEM.
 PA Garner HR, Wren JD, Minna JD, Fondon JW;
 XX WPI; 2003-208816/20.
 DR Identifying a candidate polymorphic repeat within a coding sequence,
 XX for understanding or treating genetic disease, comprises detecting
 PT tandem repeats in a target coding sequence and scoring the repeats for
 PT polymorphic probability -
 XX Examples; Column 717; 588pp; English.
 PS
 XX The invention discloses a method for identifying a candidate polymorphic
 CC repeat within a coding sequence (expressed sequence tag, EST), which
 CC comprises detecting tandem repeats in a target coding sequence, scoring
 CC the repeats for polymorphic probability and generating a dataset
 CC correlating the repeats with polymorphic probability to identify a
 CC candidate polymorphic repeat. The computational methods (polymorphic
 CC marker prediction of ubiquitous simple sequences, POMPOUS, and Rep-X) are
 CC useful for identifying and detecting candidate polymorphic repeats in
 CC human genes, which can be used to understand, treat or eliminate genetic
 CC diseases, predispositions or adverse drug-treatment reactions. Examples
 CC of diseases linked to nucleotide repeats are Machado-Joseph, Haw River
 CC syndrome, Huntington's disease, fragile-X syndrome, Friedrich's ataxia,
 CC myotonic dystrophy, hyperandrogenaemia, spinal and bulbar atrophy and
 CC spinocerebellar ataxia. The sequences presented in ABX79676-ABX80022 are
 CC the polymorphic repeats identified for a search of human ESTs.
 XX
 SQ Sequence 27 BP; 1 A; 0 C; 0 G; 26 T; 0 other;
 Query Match 1.7%; Score 19.2; DB 1; Length 27;
 Best Local Similarity 87.5%; Pred. No. 1.2e+02;
 Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1077 AACTATTAAAAA 1100
 DB 27 AACTAAAAA 4
 RESULT 23
 ID AAQ75552/c
 XX AAQ75552 standard; DNA; 19 BP.
 AC AAQ75552;
 XX 04-AUG-1995 (first entry)
 DT Analysis of cDNA and gene expression - by amplification of mRNA
 PT WPI; 1995-018287/03.
 XX Analysis of cDNA and gene expression - by amplification of mRNA

DE Reverse transcription primer used in cDNA analysis technique.
 XX Analysis; Gene expression; reverse transcription; primer; cDNA;
 KW aggregate; restriction enzyme; ss.
 XX Synthetic.
 OS
 XX JP06303997-A.
 PN 01-NOV-1994.
 PD 16-APR-1993; 93JP-0112515.
 XX 16-APR-1993; 93JP-0112515.
 PR 16-APR-1993; 93JP-0112515.
 XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 PA WPI; 1995-018287/03.
 DR Analysis of cDNA and gene expression - by amplification of mRNA
 PT followed by digestion with restriction enzymes
 XX Disclosure; Page 5; ilpp; Japanese.
 PS
 XX A method for the analysis of cDNA comprises (a) preparing an
 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
 CC and a plural type of labelled reverse transcription primers
 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
 CC template for each reverse transcription primer; (b) digesting each of
 CC the prepared aggregates of the double-stranded cDNAs with restriction
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
 CC separate lanes. The method can be used to analyse gene expression
 CC rapidly and easily.
 XX
 SQ Sequence 19 BP; 2 A; 0 C; 0 G; 17 T; 0 other;
 Query Match 1.7%; Score 19; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 90;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1082 TTAATAAAAAAAAAA 1100
 DB 19 TTAATAAAAAAAAAA 1
 RESULT 24
 ID AAQ75580/c
 XX AAQ75580 standard; DNA; 20 BP.
 AC AAQ75580;
 XX 04-AUG-1995 (first entry)
 DT Reverse transcription primer used in cDNA analysis technique.
 XX Analysis; Gene expression; reverse transcription; primer; cDNA;
 KW aggregate; restriction enzyme; ss.
 XX Synthetic.
 OS
 XX JP06303997-A.
 PN 01-NOV-1994.
 PD 16-APR-1993; 93JP-0112515.
 XX 16-APR-1993; 93JP-0112515.
 PR (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 PA WPI; 1995-018287/03.
 DR Analysis of cDNA and gene expression - by amplification of mRNA
 PT Analysis of cDNA and gene expression - by amplification of mRNA

```
PT followed by digestion with restriction enzymes
XX
XX Disclosure; Page 5; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC and a plural type of labelled reverse transcription primers
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
CC template for each reverse transcription primer; (b) digesting each of
CC the prepared aggregates of the double-stranded cDNAs with restriction
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC separate lanes. The method can be used to analyse gene expression
CC rapidly and easily.
XX
SQ Sequence 20 BP; 3 A; 0 C; 0 G; 17 T; 0 other;
Query Match 1.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1082 TTAATAAAAAAAAAAAAAAAAA 1100
Db 19 TTAATAAAAAAAAAAAAAAAAA 1

RESULT 26
AAQ75579/c
ID AAQ75579 standard; DNA; 20 BP.
AC AAQ75579;
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-0112515.
XX
XX 16-APR-1993; 93JP-0112515.
XX
XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA
XX followed by digestion with restriction enzymes
XX
XX Disclosure; Page 5; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an
XX aggregate of double-stranded cDNAs by using an aggregate of mRNAs
XX and a plural type of labelled reverse transcription primers
XX (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
XX template for each reverse transcription primer; (b) digesting each of
XX the prepared aggregates of the double-stranded cDNAs with restriction
XX enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
XX separate lanes. The method can be used to analyse gene expression
XX rapidly and easily.
XX
XX Sequence 20 BP; 2 A; 0 C; 1 G; 17 T; 0 other;
Query Match 1.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1082 TTAATAAAAAAAAAAAAAAAAA 1100
Db 19 TTAATAAAAAAAAAAAAAAAAA 1

RESULT 27
AAQ75723/c
ID AAQ75723 standard; DNA; 21 BP.
AC AAQ75723;
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX
```



```
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-0112515.
XX
PR 16-APR-1993; 93JP-0112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA
PT followed by digestion with restriction enzymes
XX
PS Disclosure; Page 8; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC and a plural type of labelled reverse transcription primers
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
CC template for each reverse transcription primer; (b) digesting each of
CC the prepared aggregates of the double-stranded cDNAs with restriction
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC separate lanes. The method can be used to analyse gene expression
CC rapidly and easily.
XX
SQ Sequence 21 BP; 3 A; 0 C; 1 G; 17 T; 0 other;
XX
Query Match 1.7%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1082 TTAATAAAAAAAAAAAAAA 1100
DB 19 TTAATAAAAAAAAAAAAAA 1
XX
RESULT 28
AAQ75725/c
ID AAQ75725 standard; DNA; 21 BP.
XX
AC AAQ75725;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
XX JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-0112515.
XX
PR 16-APR-1993; 93JP-0112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA
PT followed by digestion with restriction enzymes
XX
PS Disclosure; Page 8; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC and a plural type of labelled reverse transcription primers
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
CC template for each reverse transcription primer; (b) digesting each of
CC the prepared aggregates of the double-stranded cDNAs with restriction
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC separate lanes. The method can be used to analyse gene expression
CC rapidly and easily.
XX
SQ Sequence 21 BP; 3 A; 0 C; 1 G; 17 T; 0 other;
XX
Query Match 1.7%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1082 TTAATAAAAAAAAAAAAAA 1100
DB 19 TTAATAAAAAAAAAAAAAA 1
XX
RESULT 28
AAQ75725/c
ID AAQ75725 standard; DNA; 21 BP.
XX
AC AAQ75725;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
XX JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-0112515.
XX
PR 16-APR-1993; 93JP-0112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA
PT followed by digestion with restriction enzymes
XX
PS Disclosure; Page 8; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC and a plural type of labelled reverse transcription primers
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
CC template for each reverse transcription primer; (b) digesting each of
CC the prepared aggregates of the double-stranded cDNAs with restriction
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC separate lanes. The method can be used to analyse gene expression
CC rapidly and easily.
XX
SQ Sequence 21 BP; 3 A; 0 C; 1 G; 17 T; 0 other;
XX
Query Match 1.7%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1082 TTAATAAAAAAAAAAAAAA 1100
DB 19 TTAATAAAAAAAAAAAAAA 1
XX
RESULT 30
AAQ75731/c
```

```
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
CC template for each reverse transcription primer; (b) digesting each of
CC the prepared aggregates of the double-stranded cDNAs with restriction
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC separate lanes. The method can be used to analyse gene expression
CC rapidly and easily.
XX
SQ Sequence 21 BP; 3 A; 0 C; 0 G; 18 T; 0 other;
XX
Query Match 1.7%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1082 TTAATAAAAAAAAAAAAAA 1100
DB 19 TTAATAAAAAAAAAAAAAA 1
XX
RESULT 29
AAQ75726/c
ID AAQ75726 standard; DNA; 21 BP.
XX
AC AAQ75726;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
XX JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-0112515.
XX
PR 16-APR-1993; 93JP-0112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA
PT followed by digestion with restriction enzymes
XX
PS Disclosure; Page 8; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC and a plural type of labelled reverse transcription primers
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
CC template for each reverse transcription primer; (b) digesting each of
CC the prepared aggregates of the double-stranded cDNAs with restriction
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC separate lanes. The method can be used to analyse gene expression
CC rapidly and easily.
XX
SQ Sequence 21 BP; 3 A; 1 C; 0 G; 17 T; 0 other;
XX
Query Match 1.7%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1082 TTAATAAAAAAAAAAAAAA 1100
DB 19 TTAATAAAAAAAAAAAAAA 1
XX
RESULT 30
AAQ75731/c
```



```
SQ Sequence 21 BP; 2 A; 2 C; 0 G; 17 T; 0 other;
Query Match      1.7%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1082 TTAATAAAAAAAAAAAAAA 1100
DB 19 TTAATAAAAAAAAAAAAAA 1

RESULT 33
AAQ75719/c
ID AAQ75719 standard; DNA; 21 BP.
XX AC AAQ75719;
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX KW Analysis; Gene expression; reverse transcription; primer; cDNA;
XX KW aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX XX JP06303997-A.
XX XX 01-NOV-1994.
XX PF 16-APR-1993; 93JP-0112515.
XX PR 16-APR-1993; 93JP-0112515.
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX PT Analysis of cDNA and gene expression - by amplification of mRNA
XX PT followed by digestion with restriction enzymes
XX PS Disclosure; Page 8; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an
XX CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
XX CC and a plural type of labelled reverse transcription primers
XX CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
XX CC template for each reverse transcription primer; (b) digesting each of
XX CC the prepared aggregates of the double-stranded cDNAs with restriction
XX CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
XX CC separate lanes. The method can be used to analyse gene expression
XX CC rapidly and easily.
XX SQ Sequence 21 BP; 2 A; 0 C; 1 G; 18 T; 0 other;
Query Match      1.7%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1082 TTAATAAAAAAAAAAAAAA 1100
DB 19 TTAATAAAAAAAAAAAAAA 1

RESULT 35
AAQ75722/c
ID AAQ75722 standard; DNA; 21 BP.
XX AC AAQ75722;
XX XX 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX KW Analysis; Gene expression; reverse transcription; primer; cDNA;
XX KW aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX XX JP06303997-A.
XX XX 01-NOV-1994.
XX PF 16-APR-1993; 93JP-0112515.
XX PR 16-APR-1993; 93JP-0112515.
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX PT Analysis of cDNA and gene expression - by amplification of mRNA
XX PT followed by digestion with restriction enzymes
```

XX PS Disclosure; Page 8; 11pp; Japanese.

CC A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in separate lanes. The method can be used to analyse gene expression rapidly and easily.

XX SQ Sequence 21 BP; 2 A; 1 C; 1 G; 17 T; 0 other;

Query Match 1.7%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1082 TTAATAAAAAAAAAAAAAA 1100
|||||
Db 19 TTAATAAAAAAAAAAAAAA 1

RESULT 36
ABK86168/c
ID ABK86168 standard; DNA; 24 BP.
XX AC ABK86168;
XX DT 24-SEP-2002 (first entry)
XX DE Oligo dT primer #1 used in method to study gene expression.
XX KW Oligo dT primer; gene expression analysis; primer; ss.
XX OS Synthetic.
XX FN WO200236828-A2.
XX PD 10-MAY-2002.
XX PF 01-NOV-2001; 2001WO-US45401.
XX PR 01-NOV-2000; 2000US-244933P.
XX PA (GENO-) GENOMIC SOLUTIONS INC.
XX PI Kane MD, Dombkowski AA, Nagel AC;
XX DR WPI; 2002-508123/54.
XX PT Identifying and characterizing gene expression in samples, for identifying mRNAs expressed at different levels, comprises employing an identifier having an oligo-dT primer of a specific sequence and a detectable marker at its 5' end -
XX PS Disclosure; Page 11; 45pp; English.

CC The invention relates to systems for identification and characterisation of gene expression in one or more samples, comprising an identifier having a specific oligo-dT primer sequence, where the identifier comprises a detectable marker at its 5' end. The system is useful for identifying any or all genes expressed in a given in vivo or in vitro RNA sample, as well as the relative differences in mRNA between 2 or more samples, where that are expressed at different levels of new genes, and for identifying mRNAs that are expressed at different levels between 2 or more samples. The new system or method addresses limitations of prior methods by comprising compositions and systems that incorporate new strategies where molecular or biochemical assay compositions and systems are linked to DNA or RNA sequence databases for optimal resource efficiency in assaying gene expression. The system has the following advantages over existing methods: (a) prior sequence information or clone library construction is not needed to enable the assay; (b) provides immediate sequence information in addition to information concerning changes or differences

CC not needed to enable the assay; (b) provides immediate sequence information in addition to information concerning changes or differences in mRNA level, to determine mRNA expression level and mRNA identification in one assay; (c) generates cDNA fragments from all mRNAs present in the sample for subsequent investigation by common molecular biology techniques; and (d) does not require prior knowledge of the sequence of the genome of the organism under investigation and can be employed in organisms lacking significant genomic sequence in formation. The present sequence represents an oligo dT primer used in the method of the invention.

XX SQ Sequence 24 BP; 3 A; 1 C; 0 G; 20 T; 0 other;

Query Match 1.7%; Score 19; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1082 TTAATAAAAAAAAAAAAAA 1100
|||||
Db 22 TTAATAAAAAAAAAAAAAA 4

RESULT 37
ABK86169
ID ABK86169 standard; DNA; 24 BP.
XX AC ABK86169;
XX DT 24-SEP-2002 (first entry)
XX DE Oligo dT primer #2 used in method to study gene expression.
XX KW Oligo dT primer; gene expression analysis; primer; ss.
XX OS Synthetic.
XX FN WO200236828-A2.
XX PD 10-MAY-2002.
XX PF 01-NOV-2001; 2001WO-US45401.
XX PR 01-NOV-2000; 2000US-244933P.
XX PA (GENO-) GENOMIC SOLUTIONS INC.
XX PI Kane MD, Dombkowski AA, Nagel AC;
XX DR WPI; 2002-508123/54.
XX PT Identifying and characterizing gene expression in samples, for identifying mRNAs expressed at different levels, comprises employing an identifier having an oligo-dT primer of a specific sequence and a detectable marker at its 5' end -
XX PS Disclosure; Page 11; 45pp; English.

CC The invention relates to systems for identification and characterisation of gene expression in one or more samples, comprising an identifier having a specific oligo-dT primer sequence, where the identifier comprises a detectable marker at its 5' end. The system is useful for identifying any or all genes expressed in a given in vivo or in vitro RNA sample, as well as the relative differences in mRNA between 2 or more samples, where that are expressed at different levels of new genes, and for identifying mRNAs that are expressed at different levels between 2 or more samples. The new system or method addresses limitations of prior methods by comprising compositions and systems that incorporate new strategies where molecular or biochemical assay compositions and systems are linked to DNA or RNA sequence databases for optimal resource efficiency in assaying gene expression. The system has the following advantages over existing methods: (a) prior sequence information or clone library construction is not needed to enable the assay; (b) provides immediate sequence information in addition to information concerning changes or differences

CC in mRNA level, to determine mRNA expression level and mRNA identification
 CC in one assay; (c) generates cDNA fragments from all mRNAs present in the
 CC sample for subsequent investigation by common molecular biology
 CC techniques; and (d) does not require prior knowledge of the sequence of
 CC the genome of the organism under investigation and can be employed in
 CC organisms lacking significant genomic sequence information. The present
 CC sequence represents an oligo dT primer used in the method of the
 CC invention.

XX SQ Sequence 24 BP; 20 A; 0 C; 1 G; 3 T; 0 other;
 Query Match 1.7%; Score 19; DB 1; Length 24;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1082 TTAATAAAAAAAAAAAAAA 1100
 |||||
 Db 3 TTAATAAAAAAAAAAAAAA 21

RESULT 39
 AAV71935/c
 ID AAV71935 standard; DNA; 27 BP.

XX AC AAV71935;

XX DT 18-FEB-1999 (first entry)

XX DE Anchored poly T RT-PCR primer.

XX KW Normalised; cDNA library; mRNA cloning; reverse transcription;
 KW immobilise; screening; hybridisation; nucleic acid amplification;
 KW expression pattern; drug development; PCR primer; RT-PCR; ss.

XX OS Synthetic.

XX PN WO9851789-A2.

XX PD 19-NOV-1998.

XX PF 13-MAY-1998; 98WO-DK00186.

XX PR 27-MAR-1998; 98DK-0000432.

XX PR 13-MAY-1997; 97DK-0000547.

XX PR 19-MAY-1997; 97US-0871030.

XX PA (DISP-) DISPLAY SYSTEMS BIOTECH APS.

XX PI Warthoe PR;

XX DR WPI; 1999-009772/01.

XX PT Preparation of normalised, subdivided cDNA libraries from mRNA - by
 PT reverse transcription and amplification, used to screen for new
 PT genes and interacting proteins, potential drugs, and for diagnosis
 XX Example 1; Page 29; 71pp; English.

XX The invention relates to preparation of a normalised, subdivided library
 CC of amplified cDNA from the coding regions of mRNA in a sample. The
 CC method involves reverse transcription, with at least one cDNA primer of
 CC formula 5'-Con1-dTn2-Vn3-Nn4 to form first strand cDNA where Con1 = any
 CC sequence of 1-100 nucleotides; dT = deoxythymidyl; n2 is at least 1; n3
 CC and n4 are both 0, or n3 is 1 and n4 is at least 1; followed by second
 CC strand cDNA synthesis using the first strand as template and a second
 CC cDNA primer of a similar formula, in the presence of DNA polymerase I (or
 CC its Klenow fragment) and amplification of double-stranded cDNA with a set
 CC of amplification primers. Comparison of cDNA in the prepared library with
 CC a database (a computer-generated list of molecular weights of restricted
 CC DNA fragments of known sequence) is used to determine presence of an
 CC expressed protein in a cell, also to detect changes in such expression
 CC (particularly for diagnosis of disease). Surfaces (chip) having
 CC amplified cDNA stably immobilised on it, obtained by a similar method,

CC are used to screen for genes of a particular family, by hybridisation
 CC with nucleic acid from the family (to identify new genes) and to detect
 CC differences in expression patterns between cells. The polypeptides
 CC expressed by the libraries can be used for drug development. Sequences
 CC AAV71935 to AAV71946 represent primers used to exemplify the method of
 CC the invention.

XX SQ Sequence 27 BP; 2 A; 0 C; 0 G; 25 T; 0 other;

Query Match 1.7%; Score 19; DB 1; Length 27;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1082 TTAATAAAAAAAAAAAAAA 1100
 |||||
 Db 27 TTAATAAAAAAAAAAAAAA 9

RESULT 39
 ABK65992/c
 ID ABK65992 standard; DNA; 27 BP.

XX AC ABK65992;

XX DT 02-JUL-2002 (first entry)

XX DE Human gene specific PCR primer #80.

XX KW Primer; ss; DNA microarray; differential expression analysis; human.

XX OS Homo sapiens.

XX PN US6352829-B1.

XX PD 05-MAR-2002.

XX PF 05-JAN-1999; 99US-0225928.

XX PR 21-MAY-1997; 97US-0859998.

XX PA (CLON-) CLONTECH LAB INC.

XX PI Chenchik A, Johhadze G, Bibilashvili R;

XX DR WPI; 2002-314699/35.

XX PT Producing sub-population of labeled nucleic acids, useful for analysing
 PT differences in RNA profiles between several different physiological
 PT sources, using set of distinct gene specific primers

XX Example 3; SEQ ID No 80; 11pp; English.

XX The invention relates to producing a sub-population of labeled nucleic
 CC acids (NAS) comprising contacting a NA sample from a physiological
 CC source, with a pool of 50 distinct gene specific primers under suitable
 CC conditions to enzymatically generate sub-population of NAS, where
 CC each gene specific primer has a sequence complementary to a distinct
 CC mRNA, and each labeled NA is generated using a single gene specific
 CC primer. The method is useful for producing a sub-population of labeled
 CC NAS which is useful for analysing the differences in the RNA profiles
 CC between several different physiological sources, where the method
 CC comprises producing subpopulation of labeled NAS for the different
 CC physiological sources, comprising the populations for each physiological
 CC source to identify differences in the population, where the comparison
 CC is preferably performed by hybridising the labeled NAS for each of the
 CC distinct physiological sources to an array of probe NAS stably
 CC associated with the surface of a substrate to produce a hybridisation
 CC pattern for each of the sources, and comparing the patterns for each of
 CC the sources, where differential gene expression assays are
 CC utilised in differential expression analysis of diseased a normal
 CC tissue e.g. neoplastic a normal tissue, or different tissue or
 CC subissue types. The present sequence is a human gene specific PCR
 CC primer used in the method of the invention.

XX Identifying extendible primers for use in identification, or
PT classification of a nucleic acid of an organism, allele or gene such as
PT class 1/2 HUA comprises identifying all possible nucleotide sequences
PT of specific length -
XX
PS Claim 14; Page 47; 66pp; English.
XX
CC The present invention provides a method for identifying a set of
CC extendible primers which can be used in the identification, typing and
CC classification of genes. This can then be used to predict protein
CC sequence and structure, in organ donation to match the organ with the
CC receiver, and to identify bacteria in a sample. The method can be used to
CC type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC particular.
XX
SQ Sequence 25 BP; 3 A; 4 C; 1 G; 17 T; 0 other;

Query Match 1.7%; Score 18.6; DB 1; Length 25;
Best Local Similarity 84.0%; Pred. No. 1.4e+02;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1072 AAGCACTATTAAAAA 1096
DB 25 AAGGAGGTATCAAAAAA 1

RESULT 43
AAX78723/c
ID AAX78723 standard; DNA; 26 BP.
XX
AC AAX78723;
XX
DT 03-SEP-1999 (first entry)
XX
DE Human pancreatic PA153 EST-specific clone primer 12.
XX
KW Pancreatic disease; PA153; human; cytostatic; detection; antigen;
KW anti-PA153; antagonist; therapy; treatment; tumour; metastasis;
KW gene therapy; EST; expressed sequence tag; primer; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
XX WO9931274-A2.
XX
PD 24-JUN-1999.
XX
PF 11-DEC-1998; 98WO-US26441.
XX
PR 15-DEC-1997; 97US-0990568.
XX
PA (ABBO) ABBOTT LAB.
XX
PI Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN;
PI Gordon J, Granados EN, Hodges SC, Klass MR, Kratochvil JD;
PI Roberts-Rapp L, Russell JC, Stroupe SD;
XX
XX WPI; 1999-405041/34.
XX
XX PA153 cDNA transcribed from pancreatic tissue
PT
PS Example 2; Page 121; 123pp; English.
XX
CC This invention describes novel contiguous and partially overlapping
CC cDNA sequences and their encoded polypeptides, designated PA153,
CC transcribed from human pancreatic tissue and which have cytostatic
CC activity. The PA153 polynucleotides, proteins and antibodies are all
CC useful in methods of detection. Detection of PA153 polynucleotide,
CC antigens or anti-PA153 antibodies in a sample is indicative of
CC pancreatic disease. PA153 antibodies (antagonists) can also be used in
CC vivo for therapeutic use, e.g. treatment of pancreatic disease, tumours
CC or metastases. Antisense PA153 polynucleotides can be used in gene

CC therapy of pancreatic diseases. AAX78712-X78725 represent primers used
CC in the method of the invention.
XX
SQ Sequence 26 BP; 0 A; 0 C; 1 G; 25 T; 0 other;

Query Match 1.7%; Score 18.6; DB 1; Length 26;
Best Local Similarity 84.0%; Pred. No. 1.5e+02;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1076 CAACCTATTAAAAA 1100
DB 26 CAAAAA 2

RESULT 44
AAX07466/c
ID AAX07466 standard; cDNA; 26 BP.
XX
AC AAX07466;
XX
DT 08-JUN-1999 (first entry)
XX
DE Human BS124 specific EST clone oligonucleotide.
XX
KW BS124; breast; cancer; detection; diagnosis; prevention; treatment;
KW EST; ss.
XX
OS Synthetic.
XX
PN WO9859049-A1.
XX
PD 30-DEC-1998.
XX
PF 19-JUN-1998; 98WO-US12862.
XX
PR 20-JUN-1997; 97US-0879354.
XX
PA (ABBO) ABBOTT LAB.
XX
PI Billing-medel PA, Cohen M, Colpitts TL, Friedman PN;
PI Gordon J, Granados EN, Hodges SC, Klass MR, Kratochvil JD;
PI Russell JC, Scheffel CP, Stroupe SD, Yu H;
XX
XX WPI; 1999-105623/09.
XX
PT New isolated BS124 polynucleotides and polypeptides - used for
PT detecting, diagnosing, preventing or treating diseases or conditions
PT of the breast, such as breast cancer
XX
PS Disclosure, Page 97; 125pp; English.
XX
CC The sequence is that of an oligonucleotide used in the isolation of a
CC BS124-specific EST clone. It is useful for detecting, diagnosing,
CC staging, preventing or treating, or determining predisposition to
CC diseases or conditions of the breast, such as breast cancer.
XX
SQ Sequence 26 BP; 0 A; 0 C; 1 G; 25 T; 0 other;

Query Match 1.7%; Score 18.6; DB 1; Length 26;
Best Local Similarity 84.0%; Pred. No. 1.5e+02;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1076 CAACCTATTAAAAA 1100
DB 26 CAAAAA 2

RESULT 45
AAQ75597/c
ID AAQ75597 standard; DNA; 20 BP.
XX
XX AAQ75597;
AC
XX

DT 04-AUG-1995 (first entry)
 XX Reverse transcription primer used in cDNA analysis technique.
 DE Analysis: gene expression; reverse transcription; primer; cDNA;
 KW aggregate; restriction enzyme; ss.
 XX Synthetic.
 OS
 XX JP06303997-A.
 PN
 XX 01-NOV-1994.
 PD
 XX 16-APR-1993; 93JP-0112515.
 PF
 XX 16-APR-1993; 93JP-0112515.
 PR
 XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 PA
 XX WPI; 1995-018287/03.
 DR
 XX Analysis of cDNA and gene expression - by amplification of mRNA
 PT followed by digestion with restriction enzymes
 XX Disclosure; Page 5; 11pp; Japanese.
 PS
 XX A method for the analysis of cDNA comprises (a) preparing an
 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
 CC and a plural type of labelled reverse transcription primers
 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
 CC template for each reverse transcription primer; (b) digesting each of
 CC the prepared aggregates of the double-stranded cDNAs with restriction
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
 CC separate lanes. The method can be used to analyse gene expression
 CC rapidly and easily.
 XX
 SQ Sequence 20 BP; 1 A; 1 C; 0 G; 18 T; 0 other;
 Query Match 1.7%; Score 18.4; DB 1; Length 20;
 Best Local Similarity 95.0%; Pred. No. 1.2e+02;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1081 ATTAAAAA 1100
 Db 20 ATGAAAAA 1
 RESULT 46
 AAQ75584/c
 ID AAQ75584 standard; DNA; 20 BP.
 XX
 AC AAQ75584;
 XX
 DT 04-AUG-1995 (first entry)
 XX Reverse transcription primer used in cDNA analysis technique.
 DE Analysis: gene expression; reverse transcription; primer; cDNA;
 KW aggregate; restriction enzyme; ss.
 XX Synthetic.
 OS
 XX JP06303997-A.
 PN
 XX 01-NOV-1994.
 PD
 XX 16-APR-1993; 93JP-0112515.
 PF
 XX 16-APR-1993; 93JP-0112515.
 PR
 XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 PA
 XX WPI; 1995-018287/03.
 DR
 XX Analysis of cDNA and gene expression - by amplification of mRNA
 PT followed by digestion with restriction enzymes
 XX Disclosure; Page 5; 11pp; Japanese.
 PS
 XX A method for the analysis of cDNA comprises (a) preparing an
 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
 CC and a plural type of labelled reverse transcription primers
 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
 CC template for each reverse transcription primer; (b) digesting each of
 CC the prepared aggregates of the double-stranded cDNAs with restriction
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
 CC separate lanes. The method can be used to analyse gene expression
 CC rapidly and easily.
 XX
 SQ Sequence 20 BP; 1 A; 1 C; 0 G; 18 T; 0 other;
 Query Match 1.7%; Score 18.4; DB 1; Length 20;
 Best Local Similarity 95.0%; Pred. No. 1.2e+02;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1081 ATTAAAAA 1100
 Db 20 ATGAAAAA 1
 RESULT 46
 AAQ75584/c
 ID AAQ75584 standard; DNA; 20 BP.
 XX
 AC AAQ75584;
 XX
 DT 04-AUG-1995 (first entry)
 XX Reverse transcription primer used in cDNA analysis technique.
 DE Analysis: gene expression; reverse transcription; primer; cDNA;
 KW aggregate; restriction enzyme; ss.
 XX Synthetic.
 OS
 XX JP06303997-A.
 PN
 XX 01-NOV-1994.
 PD
 XX 16-APR-1993; 93JP-0112515.
 PF
 XX 16-APR-1993; 93JP-0112515.
 PR
 XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 PA
 XX WPI; 1995-018287/03.
 DR

XX Analysis of cDNA and gene expression - by amplification of mRNA
 PT followed by digestion with restriction enzymes
 XX Disclosure; Page 5; 11pp; Japanese.
 PS
 XX A method for the analysis of cDNA comprises (a) preparing an
 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
 CC and a plural type of labelled reverse transcription primers
 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
 CC template for each reverse transcription primer; (b) digesting each of
 CC the prepared aggregates of the double-stranded cDNAs with restriction
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
 CC separate lanes. The method can be used to analyse gene expression
 CC rapidly and easily.
 XX
 SQ Sequence 20 BP; 2 A; 0 C; 0 G; 18 T; 0 other;
 Query Match 1.7%; Score 18.4; DB 1; Length 20;
 Best Local Similarity 95.0%; Pred. No. 1.2e+02;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1080 TATTAAAA 1099
 Db 20 TATAAAAA 1

RESULT 47
 AAQ75585/c
 ID AAQ75585 standard; DNA; 20 BP.
 XX
 AC AAQ75585;
 XX
 DT 04-AUG-1995 (first entry)
 XX Reverse transcription primer used in cDNA analysis technique.
 DE Analysis: gene expression; reverse transcription; primer; cDNA;
 KW aggregate; restriction enzyme; ss.
 XX Synthetic.
 OS
 XX JP06303997-A.
 PN
 XX 01-NOV-1994.
 PD
 XX 16-APR-1993; 93JP-0112515.
 PF
 XX 16-APR-1993; 93JP-0112515.
 PR
 XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 PA
 XX WPI; 1995-018287/03.
 DR
 XX Analysis of cDNA and gene expression - by amplification of mRNA
 PT followed by digestion with restriction enzymes
 XX Disclosure; Page 5; 11pp; Japanese.
 PS
 XX A method for the analysis of cDNA comprises (a) preparing an
 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
 CC and a plural type of labelled reverse transcription primers
 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
 CC template for each reverse transcription primer; (b) digesting each of
 CC the prepared aggregates of the double-stranded cDNAs with restriction
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
 CC separate lanes. The method can be used to analyse gene expression
 CC rapidly and easily.
 XX
 SQ Sequence 20 BP; 1 A; 0 C; 0 G; 19 T; 0 other;
 Query Match 1.7%; Score 18.4; DB 1; Length 20;
 Best Local Similarity 95.0%; Pred. No. 1.2e+02;


```
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1081 ATTAAAAA1100
Db 20 AATAAAAA1

RESULT 48
AAQ75589/c
ID AAQ75589 standard; DNA; 20 BP.
XX
AC AAQ75589;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-0112515.
XX
PR 16-APR-1993; 93JP-0112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA
PT followed by digestion with restriction enzymes
XX
PS Disclosure; Page 5; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC and a plural type of labelled reverse transcription primers
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
CC template for each reverse transcription primer; (b) digesting each of
CC the prepared aggregates of the double-stranded cDNAs with restriction
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC separate lanes. The method can be used to analyse gene expression
CC rapidly and easily.
XX
SQ Sequence 20 BP; 1 A; 1 C; 0 G; 18 T; 0 other;

Query Match 1.7%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.2e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1081 ATTAAAAA1100
Db 20 ACTAAAAA1

RESULT 49
AAQ75577/c
ID AAQ75577 standard; DNA; 20 BP.
XX
AC AAQ75577;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-0112515.
XX
PR 16-APR-1993; 93JP-0112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA
PT followed by digestion with restriction enzymes
XX
PS Disclosure; Page 5; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC and a plural type of labelled reverse transcription primers
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
CC template for each reverse transcription primer; (b) digesting each of
CC the prepared aggregates of the double-stranded cDNAs with restriction
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC separate lanes. The method can be used to analyse gene expression
CC rapidly and easily.
XX
SQ Sequence 20 BP; 1 A; 1 C; 0 G; 18 T; 0 other;

Query Match 1.7%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.2e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1081 ATTAAAAA1100
Db 20 ACTAAAAA1

RESULT 50
AAQ75565/c
ID AAQ75565 standard; DNA; 20 BP.
XX
AC AAQ75565;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-0112515.
XX
PR 16-APR-1993; 93JP-0112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA
PT followed by digestion with restriction enzymes
XX
PS Disclosure; Page 5; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an
```

CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC and a plural type of labelled reverse transcription primers
CC (GENESEQ files AAQ75547-075798) and using the aggregate of mRNAs as the
CC template for each reverse transcription primer; (b) digesting each of
CC the prepared aggregates of the double-stranded cDNAs with restriction
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC separate lanes. The method can be used to analyse gene expression
CC rapidly and easily.

XX SQ Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 other;

Query Match 1.7%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.2e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1081 ATTAAAAAATAAAAAAAAAA 1100
DB 20 ATCAAAAAAAAAAAAAAAAAA 1

RESULT 51

AAQ75757/c
ID AAQ75757 standard; DNA; 21 BP.

AC AAQ75757;

XX 04-AUG-1995 (first entry)

XX Reverse transcription primer used in cDNA analysis technique.

XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.

XX Synthetic.

XX JP06303997-A.

XX 01-NOV-1994.

XX 16-APR-1993; 93JP-0112515.

XX 16-APR-1993; 93JP-0112515.

XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

XX WPI; 1995-018287/03.

XX Analysis of cDNA and gene expression - by amplification of mRNA
XX followed by digestion with restriction enzymes

XX Disclosure; Page 8; 11pp; Japanese.

XX A method for the analysis of cDNA comprises (a) preparing an
XX aggregate of double-stranded cDNAs by using an aggregate of mRNAs
XX and a plural type of labelled reverse transcription primers
XX (GENESEQ files AAQ75547-075798) and using the aggregate of mRNAs as the
XX template for each reverse transcription primer; (b) digesting each of
XX the prepared aggregates of the double-stranded cDNAs with restriction
XX enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
XX separate lanes. The method can be used to analyse gene expression
XX rapidly and easily.

XX Sequence 21 BP; 2 A; 1 C; 0 G; 18 T; 0 other;

Query Match 1.7%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 1.3e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1081 ATTAAAAAATAAAAAAAAAA 1100
DB 21 ATTGAAAAAAAAAAAAAAAAA 2

RESULT 52

AAQ75759/c
ID AAQ75759 standard; DNA; 21 BP.

XX AAQ75759;

XX 04-AUG-1995 (first entry)

XX Reverse transcription primer used in cDNA analysis technique.

XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.

XX Synthetic.

XX JP06303997-A.

XX 01-NOV-1994.

XX 16-APR-1993; 93JP-0112515.

XX 16-APR-1993; 93JP-0112515.

XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

XX WPI; 1995-018287/03.

XX Analysis of cDNA and gene expression - by amplification of mRNA
XX followed by digestion with restriction enzymes

XX Disclosure; Page 8; 11pp; Japanese.

XX A method for the analysis of cDNA comprises (a) preparing an
XX aggregate of double-stranded cDNAs by using an aggregate of mRNAs
XX and a plural type of labelled reverse transcription primers
XX (GENESEQ files AAQ75547-075798) and using the aggregate of mRNAs as the
XX template for each reverse transcription primer; (b) digesting each of
XX the prepared aggregates of the double-stranded cDNAs with restriction
XX enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
XX separate lanes. The method can be used to analyse gene expression
XX rapidly and easily.

XX Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 other;

Query Match 1.7%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 1.3e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1081 ATTAAAAAATAAAAAAAAAA 1100
DB 20 ATCAAAAAAAAAAAAAAAAAA 1

RESULT 53

AAQ75761/c
ID AAQ75761 standard; DNA; 21 BP.

XX AAQ75761;

XX 04-AUG-1995 (first entry)

XX Reverse transcription primer used in cDNA analysis technique.

XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.

XX Synthetic.

XX JP06303997-A.

XX 01-NOV-1994.

XX 16-APR-1993; 93JP-0112515.

CC and a plural type of labelled reverse transcription primers
 CC (GENESEQ files AAQ75547-075798) and using the aggregate of mRNAs as the
 CC template for each reverse transcription primer; (b) digesting each of
 CC the prepared aggregates of the double-stranded cDNAs with restriction
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
 CC separate lanes. The method can be used to analyse gene expression
 CC rapidly and easily.
 XX
 SQ Sequence 21 BP; 2 A; 1 C; 0 G; 18 T; 0 other;
 Query Match 1.7%; Score 18.4; DB 1; Length 21;
 Best Local Similarity 95.0%; Pred. No. 1.3e+02;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1080 TATTAAAAA 1099
 Db 20 TATAAAAAA 1
 RESULT 62
 AAQ75679/c
 ID AAQ75679 standard; DNA; 21 BP.
 XX
 AC AAQ75679;
 XX
 DT 04-AUG-1995 (first entry)
 XX
 DE Reverse transcription primer used in cDNA analysis technique.
 XX
 KW Analysis; gene expression; reverse transcription; primer; cDNA;
 XX aggregate; restriction enzyme; ss.
 XX Synthetic.
 OS JP06303997-A.
 PN JP06303997-A.
 PD 01-NOV-1994.
 XX
 PF 16-APR-1993; 93JP-0112515.
 XX
 PR 16-APR-1993; 93JP-0112515.
 XX
 PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX
 DT WPI; 1995-018287/03.
 XX
 DE Analysis of cDNA and gene expression - by amplification of mRNA
 XX followed by digestion with restriction enzymes
 XX Disclosure; Page 7; 11pp; Japanese.
 OS A method for the analysis of cDNA comprises (a) preparing an
 XX aggregate of double-stranded cDNAs by using an aggregate of mRNAs
 XX and a plural type of labelled reverse transcription primers
 XX (GENESEQ files AAQ75547-075798) and using the aggregate of mRNAs as the
 XX template for each reverse transcription primer; (b) digesting each of
 XX the prepared aggregates of the double-stranded cDNAs with restriction
 XX enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
 XX separate lanes. The method can be used to analyse gene expression
 XX rapidly and easily.
 XX
 SQ Sequence 21 BP; 1 A; 0 C; 1 G; 19 T; 0 other;
 Query Match 1.7%; Score 18.4; DB 1; Length 21;
 Best Local Similarity 95.0%; Pred. No. 1.3e+02;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1081 ATTAAAAA 1100
 Db 20 AATAAAAAA 1
 RESULT 63
 AAQ75682/c
 ID AAQ75682 standard; DNA; 21 BP.
 XX
 AC AAQ75682;
 XX
 DT 04-AUG-1995 (first entry)
 XX
 DE Reverse transcription primer used in cDNA analysis technique.
 XX
 KW Analysis; gene expression; reverse transcription; primer; cDNA;
 XX aggregate; restriction enzyme; ss.
 XX Synthetic.
 OS JP06303997-A.
 PN JP06303997-A.
 PD 01-NOV-1994.
 XX
 PF 16-APR-1993; 93JP-0112515.
 XX

AAQ75681/c
 ID AAQ75681 standard; DNA; 21 BP.
 XX
 AC AAQ75681;
 XX
 DT 04-AUG-1995 (first entry)
 XX
 DE Reverse transcription primer used in cDNA analysis technique.
 XX
 KW Analysis; gene expression; reverse transcription; primer; cDNA;
 XX aggregate; restriction enzyme; ss.
 XX Synthetic.
 OS JP06303997-A.
 PN JP06303997-A.
 PD 01-NOV-1994.
 XX
 PF 16-APR-1993; 93JP-0112515.
 XX
 PR 16-APR-1993; 93JP-0112515.
 XX
 PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX
 DT WPI; 1995-018287/03.
 XX
 DE Analysis of cDNA and gene expression - by amplification of mRNA
 XX followed by digestion with restriction enzymes
 XX Disclosure; Page 7; 11pp; Japanese.
 OS A method for the analysis of cDNA comprises (a) preparing an
 XX aggregate of double-stranded cDNAs by using an aggregate of mRNAs
 XX and a plural type of labelled reverse transcription primers
 XX (GENESEQ files AAQ75547-075798) and using the aggregate of mRNAs as the
 XX template for each reverse transcription primer; (b) digesting each of
 XX the prepared aggregates of the double-stranded cDNAs with restriction
 XX enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
 XX separate lanes. The method can be used to analyse gene expression
 XX rapidly and easily.
 XX
 SQ Sequence 21 BP; 1 A; 0 C; 0 G; 20 T; 0 other;
 Query Match 1.7%; Score 18.4; DB 1; Length 21;
 Best Local Similarity 95.0%; Pred. No. 1.3e+02;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1081 ATTAAAAA 1100
 Db 20 AATAAAAAA 1
 RESULT 64
 AAQ75682/c
 ID AAQ75682 standard; DNA; 21 BP.
 XX
 AC AAQ75682;
 XX
 DT 04-AUG-1995 (first entry)
 XX
 DE Reverse transcription primer used in cDNA analysis technique.
 XX
 KW Analysis; gene expression; reverse transcription; primer; cDNA;
 XX aggregate; restriction enzyme; ss.
 XX Synthetic.
 OS JP06303997-A.
 PN JP06303997-A.
 PD 01-NOV-1994.
 XX
 PF 16-APR-1993; 93JP-0112515.
 XX

PR 16-APR-1993; 93JP-0112515.
XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX WPI; 1995-018287/03.
XX Analysis of cDNA and gene expression - by amplification of mRNA
PT followed by digestion with restriction enzymes
XX Disclosure; Page 7; 11pp; Japanese.
XX A method for the analysis of cDNA comprises (a) preparing an
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC and a plural type of labelled reverse transcription primers
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
CC template for each reverse transcription primer; (b) digesting each of
CC the prepared aggregates of the double-stranded cDNAs with restriction
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC separate lanes. The method can be used to analyse gene expression
XX rapidly and easily.
XX Sequence 21 BP; 1 A; 1 C; 0 G; 19 T; 0 other;
XX Query Match 1.7%; Score 18.4; DB 1; Length 21;
XX Best Local Similarity 95.0%; Pred. No. 1.3e+02;
XX Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1081 ATTAAAAA 1100
DB 20 AATAAAAA 1
RESULT 65
AAQ75676/c
ID AAQ75676 standard; DNA; 21 BP.
XX AC AAQ75676;
XX 04-AUG-1995 (first entry)
XX Reverse transcription primer used in cDNA analysis technique.
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX Synthetic.
XX JP06303997-A.
XX 01-NOV-1994.
XX 16-APR-1993; 93JP-0112515.
XX 16-APR-1993; 93JP-0112515.
XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX WPI; 1995-018287/03.
XX Reverse transcription primer used in cDNA analysis technique.
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX Synthetic.
XX JP06303997-A.
XX 01-NOV-1994.
XX 16-APR-1993; 93JP-0112515.
XX 16-APR-1993; 93JP-0112515.
XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX WPI; 1995-018287/03.
XX Analysis of cDNA and gene expression - by amplification of mRNA
PT followed by digestion with restriction enzymes
XX Disclosure; Page 7; 11pp; Japanese.
XX A method for the analysis of cDNA comprises (a) preparing an
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC and a plural type of labelled reverse transcription primers
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
CC template for each reverse transcription primer; (b) digesting each of
CC the prepared aggregates of the double-stranded cDNAs with restriction
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC separate lanes. The method can be used to analyse gene expression
XX rapidly and easily.

XX SQ Sequence 21 BP; 3 A; 0 C; 0 G; 18 T; 0 other;
XX Query Match 1.7%; Score 18.4; DB 1; Length 21;
XX Best Local Similarity 95.0%; Pred. No. 1.3e+02;
XX Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1080 TATTA 1099
DB 20 TATTA 1
RESULT 66
AAQ75677/c
ID AAQ75677 standard; DNA; 21 BP.
XX AC AAQ75677;
XX 04-AUG-1995 (first entry)
XX Reverse transcription primer used in cDNA analysis technique.
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX Synthetic.
XX JP06303997-A.
XX 01-NOV-1994.
XX 16-APR-1993; 93JP-0112515.
XX 16-APR-1993; 93JP-0112515.
XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX WPI; 1995-018287/03.
XX Analysis of cDNA and gene expression - by amplification of mRNA
PT followed by digestion with restriction enzymes
XX Disclosure; Page 7; 11pp; Japanese.
XX A method for the analysis of cDNA comprises (a) preparing an
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC and a plural type of labelled reverse transcription primers
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
CC template for each reverse transcription primer; (b) digesting each of
CC the prepared aggregates of the double-stranded cDNAs with restriction
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC separate lanes. The method can be used to analyse gene expression
XX rapidly and easily.
XX Sequence 21 BP; 2 A; 0 C; 0 G; 19 T; 0 other;
XX Query Match 1.7%; Score 18.4; DB 1; Length 21;
XX Best Local Similarity 95.0%; Pred. No. 1.3e+02;
XX Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1080 TATTA 1099
DB 20 TATTA 1
RESULT 67
AAQ75629/c
ID AAQ75629 standard; DNA; 21 BP.
XX AC AAQ75629;
XX 04-AUG-1995 (first entry)
XX

QY 1081 ATTAAAAA1100
 PD |||||
 DB 20 ATCAAAAAA1

RESULT 70
 AAQ75634/c
 ID AAQ75634 standard; DNA; 21 BP.

XX AC AAQ75634;

XX 04-AUG-1995 (first entry)

XX Reverse transcription primer used in cDNA analysis technique.

XX Analysis; gene expression; reverse transcription; primer; cDNA;

XX aggregate; restriction enzyme; ss.

XX Synthetic.

XX JP06303997-A.

XX 01-NOV-1994.

XX 16-APR-1993; 93JP-0112515.

XX 16-APR-1993; 93JP-0112515.

XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

XX WPI; 1995-018287/03.

XX Analysis of cDNA and gene expression - by amplification of mRNA
 followed by digestion with restriction enzymes

XX Disclosure; Page 6; 11pp; Japanese.

XX A method for the analysis of cDNA comprises (a) preparing an
 aggregate of double-stranded cDNAs by using an aggregate of mRNAs
 and a plural type of labelled reverse transcription primers
 (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
 template for each reverse transcription primer; (b) digesting each of
 the prepared aggregates of the double-stranded cDNAs with restriction
 enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
 separate lanes. The method can be used to analyse gene expression
 rapidly and easily.

XX Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 other;

Query Match 1.7%; Score 18.4; DB 1; Length 21;
 Best Local Similarity 95.0%; Pred. No. 1.3e+02;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1081 ATTAAAAA1100
 PD |||||
 DB 20 ATCAAAAAA1

RESULT 71
 ABA93238
 ID ABA93238 standard; DNA; 22 BP.

XX AC ABA93238;

XX 18-APR-2002 (first entry)

XX Polya adaptor oligonucleotide SEQ ID NO:1.

XX Detection; comparative detection; adaptor; ss.

XX Synthetic.

XX JP2001333800-A.

XX 04-DEC-2001.
 XX 30-MAY-2000; 2000JP-0160324.
 XX 30-MAY-2000; 2000JP-0160324.
 XX (UNIT-) UNITECH CO LTD.
 XX WPI; 2002-135950/18.
 XX Comparative detection of the amounts of RNA and DNA -
 XX Disclosure; Page 9; 9pp; Japanese.

XX The present invention describes a method for the comparative detection
 of the amount of an RNA. The method comprises: (a) cDNAs obtained by
 transcribing respectively from at least two tissue RNAs are respectively
 fragmented by using a same restriction enzyme; (b) each different adaptor
 and a common adaptor are added to each of the cDNA fragments derived from
 the same or different tissues by the step (a); (c) the resultant adaptor-
 added cDNAs are mixed together; (d) an adaptor primer having the common
 sequence to said different adaptor and a gene-specific adaptor are used
 to amplify said adaptor-added cDNAs containing no region derived from
 polyadenylic acid of the mRNA before the addition of the adaptor among
 the adaptor-added cDNAs prepared by the step (b); (e) the ratios of the
 cDNA amounts are measured between the tissues; (f) the RNA is detected
 from the measured result; (g) each different adaptor and a common adaptor
 are added to each of the genomic DNA fragments derived from a same or
 different individuals; (h) the resultant adaptor-added genomic DNAs are
 mixed together; (i) the adaptor-added genomic DNAs are amplified by using
 an adaptor primer having the common sequence to the different adaptor and
 a sequence-specific adaptor; and (j) the ratios of the amplified amounts
 of the genomic DNAs are measured between the individuals. The method is
 used for the detection of the amounts of RNA and DNA. The present
 sequence represents an oligonucleotide which is used in the
 exemplification of the present invention.

XX Sequence 22 BP; 19 A; 1 C; 1 G; 1 T; 0 other;

Query Match 1.7%; Score 18.4; DB 1; Length 22;
 Best Local Similarity 95.0%; Pred. No. 1.3e+02;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1081 ATTAAAAA1100
 PD |||||
 DB 2 ATCAAAAAA21

RESULT 72
 ABV77669/c
 ID ABV77669 standard; DNA; 24 BP.

XX AC ABV77669;

XX 03-FEB-2003 (first entry)

XX Human zinc finger protein 9.79 PCR primer #1.

XX Human; zinc finger protein 9.79; cancer; HIV infection; cytostatic;
 anti-HIV; PCR; primer; ss.

XX Homo sapiens.

XX CN1343710-A.

XX 10-APR-2002.

XX 19-SEP-2000; 2000CN-0125246.

XX 19-SEP-2000; 2000CN-0125246.

XX (BODE-) BODE GENE DEV CO LTD SHANGHAI.

XX
PI Mao Y, Xie Y;
XX WPI; 2002-548879/59.
XX
XX A novel human zinc finger protein 9.79 polypeptide, useful for treating
XX several diseases e.g. cancer and HIV infection -
XX
XX Example 2; Page 16 (Disclosure); 31pp; Chinese.
XX
XX The present invention relates to human zinc finger protein 9.79 (see
XX ABP59011). The zinc finger protein is useful for treating several
XX diseases e.g. cancer and HIV infection. The present sequence is a PCR
XX primer, which was used in an example from the invention.
XX
XX Sequence 24 BP; 1 A; 2 C; 1 G; 20 T; 0 other;
SQ

Query Match 1.7%; Score 18.4; DB 1; Length 24;
Best Local Similarity 95.0%; Pred. No. 1.5e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1081 ATTAAAAA 1100
Db 23 ATGAAAAA 4

RESULT 73
AAH39959
ID AAH39959 standard; DNA; 25 BP.
XX
XX AAH39959;
XX
DT 14-AUG-2001 (first entry)
XX
DE SNP specific SNPE primer SEQ ID 2755.
XX
XX Single nucleotide polymorphism; SNP; single nucleotide primer extension;
XX SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;
XX Leech-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;
XX polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
XX acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
XX inflammation; forensic investigation; paternity analysis; primer; ss.
XX
XX Homo sapiens.
XX
XX WO200129262-A2.
XX
XX 26-APR-2001.
XX
XX 13-OCT-2000; 2000WO-US28436.
XX
XX 15-OCT-1999; 99US-0160096.
XX
XX (ORCH-) ORCHID BIOSCIENCES INC.
XX
XX Picoult-Newburg L, Pohl M;
XX
XX WPI; 2001-290930/30.
XX
XX New genotyping oligonucleotide, useful for detecting the presence,
XX absence or identity of single polynucleotide polymorphism in a nucleic
XX acid sample -
XX
XX Claim 1; Page 64; 83pp; English.
XX
XX Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
XX primer extension (SNPE) primers, and the sequences of regions flanking
XX sites of single nucleotide polymorphisms SNPs. The present invention
XX includes kits for determining the presence or absence of a SNP, using the
XX oligonucleotides of the invention. The PCR primers are used to amplify a
XX SNP flanking sequence, the SNPE primer is used as a genotyping primer.
XX The oligonucleotides are useful for genotyping a nucleic acid sample by
XX performing a single-nucleotide primer extension reaction. The

oligonucleotides are useful for determining the presence, absence or
identity of a SNP and for genotyping nucleic acid samples, for e.g. to
assess by association analysis the genotype of an individual or group of
individuals, having a pathological phenotypic trait suspected of being
caused by one or more SNPs. Phenotypic traits include diseases e.g.
agammaglobulinaemia, diabetes insipidus, Leech-Nyhan syndrome, muscular
dystrophy, familial hypercholesterolaemia, polycystic kidney disease,
osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
traits also include symptoms of or susceptibility to multifactorial
diseases of which a component is or may be genetic such as autoimmune
diseases including, rheumatoid arthritis, multiple sclerosis,
inflammation, cancer, nervous system diseases and infection by pathogenic
microorganism. The method is also useful in forensic investigations and
paternity analysis. The present sequence represents a single nucleotide
primer extension (SNPE) primer specific for a human SNP containing DNA
sequence.

XX
SQ Sequence 25 BP; 16 A; 2 C; 2 G; 5 T; 0 other;
Query Match 1.7%; Score 18.4; DB 1; Length 25;
Best Local Similarity 95.0%; Pred. No. 1.5e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1079 CTATTA 1098
Db 5 CTCTTA 24

RESULT 74
AAH76998/c
ID AAH76998 standard; DNA; 24 BP.
XX
XX AAH76998;
XX
DT 15-DEC-2001 (first entry)
XX
DE Human amyloid precursor protein 9 RT-PCR primer, SEQ ID NO:4.
XX
XX Human, amyloid precursor protein 9; recombinant production;
XX malignant tumour; cancer; blood disease; HIV infection;
XX human immunodeficiency virus; immune disorder; inflammatory condition;
XX cytostatic; anti-HIV; antiinflammatory; immunomodulator;
XX reverse transcription-PCR; RT-PCR primer; ss.
XX
XX Homo sapiens.
XX
XX WO200174878-A1.
XX
XX 11-OCT-2001.
XX
XX 23-MAR-2001; 2001WO-CN00391.
XX
XX 24-MAR-2000; 2000CN-0115106.
XX
XX (SHAN-) SHANGHAI BLOWNDOW GENE DEV INC.
XX
XX Mao Y, Xie Y;
XX
XX WPI; 2001-626386/72.
XX
XX New human amyloid precursor protein 9 and encoded polynucleotide,
XX applicable in diagnosis and treatment of cancer, hemopathy, human
XX immunodeficiency virus infection, immunological diseases and various
XX inflammations -
XX
XX Example 2; Page 16; 37pp; Chinese.
XX
XX The invention relates to human amyloid precursor protein 9 (AAG66809),
XX nucleic acids encoding it (AAH76996), and a method for the recombinant
XX production of amyloid precursor protein 9. The protein has a molecular
XX weight of 9 kD. The present invention additionally discloses an
XX antagonist of amyloid precursor protein 9 for therapeutic use, and an
XX antibody which specifically binds to amyloid precursor protein 9. Amyloid

XX OS Synthetic.

XX PN WO9732023-A1.

XX PD 04-SEP-1997.

XX PF 28-FEB-1997; 97WO-AU00124.

XX PR 01-MAR-1996; 96AU-0008386.

XX PA (FLOR-) FLORIGENE LTD.

XX PI Brugliera F, Holton TA, Michael MZ;

XX PX WPI; 1997-440691/41.

XX DR

XX PT Novel flavonoid 3'-hydroxylase(s) from flowering plants - and

XX PT corresponding DNA, used in the manipulation of pigmentation in

XX PT plants

XX PS Example 15; Page 59; 234pp; English.

XX CC Anchored poly(T) oligonucleotides polyT-anchA (AAT94667), polyT-anchC

XX CC (AAT94668) and polyT-anchG (AAT94669) are complementary to the upstream

XX CC region of a polyadenylation sequence. They were used to prime cDNA

XX CC synthesis from snapdragon (Antirrhinum majus) petal and leaf RNA,

XX CC and were also utilised in the PCR amplification of plant

XX CC cytochrome P450 sequences (see also AAT94670-73). A cDNA clone (see

XX CC AAT94657) encoding flavonoid 3' hydroxylase (see AAW35704) was isolated

XX CC using a differential display approach. This can be used to

XX CC manipulate the pigmentation of transgenic plants.

XX SQ

XX Query Match 1.6%; Score 18; DB 1; Length 18;

XX Best Local Similarity 100.0%; Pred. No. 1.3e+02;

XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX QY 1083 TAAAAAATAAAAA 1100

XX DB 18 TAAAAAATAAAAA 1

XX RESULT 78

XX AAX18372/c

XX ID AAX18372 standard; DNA; 18 BP.

XX AC AAX18372;

XX DT 11-MAY-1999 (first entry)

XX DE

XX RT-PCR primer of the invention SEQ ID 13.

XX KW RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.

XX OS Synthetic.

XX PN JP11032765-A.

XX PD 09-FEB-1999.

XX PF 18-JUL-1997; 97JP-0208312.

XX PR 18-JUL-1997; 97JP-0208312.

XX PA (TAKI) TAKARA SHUZO CO LTD.

XX DR WPI; 1999-183822/16.

XX PT Peptides having at least two new nucleotides - useful as primers in

XX PT RT-PCR

PS Disclosure; Page 11; 19pp; Japanese.

XX This sequence represents a primer of the invention. The invention relates

XX to sequences of at least two nucleotides of formula:

XX (X)m5'-(alpha)n-beta-N3'; or (X)m5'-(gamma)k-delta-N3'; where

XX X = a labelled compound and/or a nucleotide with voluntary sequence;

XX m = 0 or 1; alpha = thymine; n = natural number indicating the repetition

XX of alpha; beta, delta = V or N; V = adenine, guanine or cytosine;

XX N = adenine, guanine, cytosine or thymine; gamma = thymine;

XX k = natural number of 3 or over indicating the repetition of gamma, in

XX which thymine expressed by gamma is composed of 1/3 or less of adenine,

XX guanine and/or cytosine. The new nucleotides are useful as primers for

XX RT-PCR and determination of base sequences. The new sequences allow for

XX reproducible and highly efficient analysis of gene sequences.

XX SQ

XX Query Match 1.6%; Score 18; DB 1; Length 18;

XX Best Local Similarity 100.0%; Pred. No. 1.3e+02;

XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX QY 1082 TTAATAAAAAAAAAAAAA 1099

XX DB 18 TTAATAAAAAAAAAAAAA 1

XX RESULT 79

XX AAQ75553/c

XX ID AAQ75553 standard; DNA; 19 BP.

XX AC AAQ75553;

XX DT 04-AUG-1995 (first entry)

XX DE

XX Reverse transcription primer used in cDNA analysis technique.

XX KW Analysis; gene expression; reverse transcription; primer; cDNA;

XX KW aggregate; restriction enzyme; ss.

XX OS Synthetic.

XX PN JP06303997-A.

XX PD 01-NOV-1994.

XX PF 16-APR-1993; 93JP-0112515.

XX PR 16-APR-1993; 93JP-0112515.

XX PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

XX DR WPI; 1995-018287/03.

XX PT Analysis of cDNA and gene expression - by amplification of mRNA

XX PT followed by digestion with restriction enzymes

XX PS Disclosure; Page 5; 11pp; Japanese.

XX CC A method for the analysis of cDNA comprises (a) preparing an

XX CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs

XX CC and a plural type of labelled reverse transcription primers

XX CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the

XX CC template for each reverse transcription primer; (b) digesting each of

XX CC the prepared aggregates of the double-stranded cDNAs with restriction

XX CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in

XX CC separate lanes. The method can be used to analyse gene expression

XX CC rapidly and easily.

XX SQ

XX Query Match 1.6%; Score 18; DB 1; Length 19;

XX Best Local Similarity 100.0%; Pred. No. 1.4e+02;

XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1083 TAAAAAATAAAAAAAAAA 1100
DB 18 TAAAAAATAAAAAAAAAA 1

RESULT 80
AAQ75554/c
ID AAQ75554 standard; DNA; 19 BP.
XX
AC AAQ75554;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-0112515.
XX
PR 16-APR-1993; 93JP-0112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
PT WPI; 1995-018287/03.
XX
PS Analysis of cDNA and gene expression - by amplification of mRNA
PS followed by digestion with restriction enzymes
XX
SQ Sequence 19 BP; 1 A; 1 C; 0 G; 17 T; 0 other;
XX
Query Match 1.6%; Score 18; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAATAAAAAAAAAA 1100
DB 18 TAAAAAATAAAAAAAAAA 1

RESULT 81
AAQ75551/c
ID AAQ75551 standard; DNA; 19 BP.
XX
AC AAQ75551;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.

```

```

XX JP06303997-A.
XX 01-NOV-1994.
XX 16-APR-1993; 93JP-0112515.
XX 16-APR-1993; 93JP-0112515.
XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX WPI; 1995-018287/03.
XX Analysis of cDNA and gene expression - by amplification of mRNA
XX followed by digestion with restriction enzymes
XX Disclosure; Page 5; 11pp; Japanese.
XX A method for the analysis of cDNA comprises (a) preparing an
XX aggregate of double-stranded cDNAs by using an aggregate of mRNAs
XX and a plural type of labelled reverse transcription primers
XX (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
XX template for each reverse transcription primer; (b) digesting each of
XX the prepared aggregates of the double-stranded cDNAs with restriction
XX enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
XX separate lanes. The method can be used to analyse gene expression
XX rapidly and easily.
XX Sequence 19 BP; 1 A; 0 C; 1 G; 17 T; 0 other;
XX
Query Match 1.6%; Score 18; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAATAAAAAAAAAA 1100
DB 18 TAAAAAATAAAAAAAAAA 1

RESULT 82
AAQ49436/c
ID AAQ49436 standard; cDNA; 20 BP.
XX
AC AAQ49436;
XX
DT 25-MAR-2003 (updated)
DT 27-APR-1994 (first entry)
XX
DE Cytochrome P450 sequence amplification PCR primer polyT.
XX Transgenic plants; altered petal colour;
XX polymerase chain reaction; ss.
XX Synthetic.
XX WO9320206-A1.
XX 14-OCT-1993.
XX 25-MAR-1993; 93WO-AU00127.
XX 27-MAR-1992; 92AU-0001538.
XX 07-JAN-1993; 93AU-0006698.
XX (ITFL-) INT FLOWER DEV PTY LTD.
XX Cornish EC, Holton TA, Tanaka Y;
XX WPI; 1993-336914/42.
XX Nucleic acid isolate encoding flavonoid-3'-hydroxylase - is used to
XX create transgenic plants with altered petal colour
XX

```

PS Disclosure; Page 25; 86pp; English.

XX The sequence is that of a PCR primer which was used in polymerase

CC chain reactions for the amplification of cloned cytochrome P450

CC sequences.

CC (Updated on 25-MAR-2003 to correct PN field.)

XX SQ Sequence 20 BP; 1 A; 1 C; 1 G; 17 T; 0 other;

Query Match 1.6%; Score 18; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.4e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAATAAAAAAAAAA 1100

DB 18 TAAAAAATAAAAAAAAAA 1

RESULT 83

AA04916/c

ID AAT04916 standard; cDNA; 20 BP.

XX AC AAT04916;

XX 25-MAR-2003 (updated)

DT 15-MAY-1996 (first entry)

XX DE Mammalian stem cell factor (SCF) cDNA oligonucleotide primer 220-7.

XX KW Stem cell factor; progenitor; haematopoiesis; SCF; anaemia;

KW thrombocytopenia; leucopenia; AIDS; immunodeficiency; bone graft;

KW transplant; neoplasia; myelosuppression; bone marrow; ss.

XX OS Synthetic.

XX BP676470-A1.

XX 11-OCT-1995.

XX 04-OCT-1990; 95EP-0105391.

XX 01-OCT-1990; 90US-0589701.

PR 16-OCT-1989; 89US-0422383.

PR 11-JUN-1990; 90US-0537198.

PR 24-AUG-1990; 90US-0573616.

PR 28-SEP-1990; 90WO-US05548.

XX PA (AMGE-) AMGEN INC.

XX Rosselman RA, Martin FH, Suggs SV, Zsebo KM;

XX WPI; 1995-346090/45.

XX New stem cell factor polypeptide(s) - for stimulating the growth of

PT primitive progenitor cells, esp. for treating disorders involving

PT blood cells

XX Example 3; Fig 12C; 127pp; English.

XX AA04915-T04922 are oligonucleotide primers and probes used for the

CC amplification and sequencing of mammalian stem cell factor (SCF).

CC Non-naturally occurring SCF and C-terminally truncated polypeptides,

CC having amino acid sequences sufficiently duplicative of naturally

CC occurring SCF, stimulate growth of primitive progenitors such as

CC haematopoietic progenitor cells, neural stem cells and primordial

CC germ stem cells. The peptides can be used in a composition for

CC engraftment of bone marrow during transplantation, for enhancing

CC recovery after chemotherapy or radiation-induced bone marrow aplasia

CC or myelosuppression. They can also be used for treating neoplasia,

CC nerve damage, infertility, intestinal damage or myeloproliferative

CC disorders. Antibodies may be raised against the peptides for use in

CC detection or neutralisation of SCF in serum. SCF may be useful for

CC the treatment of AIDS and severe combined immunodeficiency (SCID);

CC states alone or in combination with other factors such as IL-7.

CC (Updated on 25-MAR-2003 to correct PF field.)

XX SQ Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 other;

Query Match 1.6%; Score 18; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.4e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAATAAAAAAAAAA 1100

DB 19 TAAAAAATAAAAAAAAAA 2

RESULT 84

AAQ75583/c

ID AAQ75583 standard; DNA; 20 BP.

XX AC AAQ75583;

XX 04-AUG-1995 (first entry)

DT Reverse transcription primer used in cDNA analysis technique.

DE Analysis; Gene expression; reverse transcription; primer; cDNA;

XX KW aggregate; restriction enzyme; ss.

XX OS Synthetic.

XX JF06303997-A.

XX 01-NOV-1994.

XX 16-APR-1993; 93JP-0112515.

XX 16-APR-1993; 93JP-0112515.

XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

XX WPI; 1995-018287/03.

XX Analysis of cDNA and gene expression - by amplification of mRNA

PT followed by digestion with restriction enzymes

XX PS Disclosure; Page 5; 11pp; Japanese.

XX A method for the analysis of cDNA comprises (a) preparing an

CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs

CC and a plural type of labelled reverse transcription primers

CC (GENESEQ files AAQ75547-075798) and using the aggregate of mRNAs as the

CC template for each reverse transcription primer; (b) digesting each of

CC the prepared aggregates of the double-stranded cDNAs with restriction

CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in

CC separate lanes. The method can be used to analyse gene expression

CC rapidly and easily.

XX SQ Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 other;

Query Match 1.6%; Score 18; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.4e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAATAAAAAAAAAA 1100

DB 18 TAAAAAATAAAAAAAAAA 1

RESULT 85

AAQ75586/c

ID AAQ75586 standard; DNA; 20 BP.

XX AC AAQ75586;

```

XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX KW aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-0112515.
XX PR 16-APR-1993; 93JP-0112515.
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX PT Analysis of cDNA and gene expression - by amplification of mRNA
XX PT followed by digestion with restriction enzymes
XX PS Disclosure; Page 5; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an
XX CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
XX CC and a plural type of labelled reverse transcription primers
XX CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
XX CC template for each reverse transcription primer; (b) digesting each of
XX CC the prepared aggregates of the double-stranded cDNAs with restriction
XX CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
XX CC separate lanes. The method can be used to analyse gene expression
XX CC rapidly and easily.
XX SQ Sequence 20 BP; 1 A; 1 C; 0 G; 18 T; 0 other;

Query Match 1.6%; Score 18; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAATAAAAAAAAAA 1100
DB 18 TAAAAAATAAAAAAAAAA 1

RESULT 86
AAQ75587/c
ID AAQ75587 standard; DNA; 20 BP.
XX AC AAQ75587;
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX KW aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-0112515.
XX PR 16-APR-1993; 93JP-0112515.
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX PT Analysis of cDNA and gene expression - by amplification of mRNA
XX PT followed by digestion with restriction enzymes
XX PS Disclosure; Page 5; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an
XX CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
XX CC and a plural type of labelled reverse transcription primers
XX CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
XX CC template for each reverse transcription primer; (b) digesting each of
XX CC the prepared aggregates of the double-stranded cDNAs with restriction
XX CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
XX CC separate lanes. The method can be used to analyse gene expression
XX CC rapidly and easily.
XX SQ Sequence 20 BP; 1 A; 1 C; 0 G; 18 T; 0 other;

Query Match 1.6%; Score 18; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAATAAAAAAAAAA 1100
DB 18 TAAAAAATAAAAAAAAAA 1

RESULT 86
AAQ75587/c
ID AAQ75587 standard; DNA; 20 BP.
XX AC AAQ75587;
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX KW aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-0112515.
XX PR 16-APR-1993; 93JP-0112515.
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX PT Analysis of cDNA and gene expression - by amplification of mRNA
XX PT followed by digestion with restriction enzymes
XX PS Disclosure; Page 5; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an
XX CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
XX CC and a plural type of labelled reverse transcription primers
XX CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
XX CC template for each reverse transcription primer; (b) digesting each of
XX CC the prepared aggregates of the double-stranded cDNAs with restriction
XX CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
XX CC separate lanes. The method can be used to analyse gene expression
XX CC rapidly and easily.
XX SQ Sequence 20 BP; 2 A; 1 C; 0 G; 17 T; 0 other;

Query Match 1.6%; Score 18; DB 1; Length 20;

```

```

DR WPI; 1995-018287/03.
XX Analysis of cDNA and gene expression - by amplification of mRNA
XX PT followed by digestion with restriction enzymes
XX PS Disclosure; Page 5; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an
XX CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
XX CC and a plural type of labelled reverse transcription primers
XX CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
XX CC template for each reverse transcription primer; (b) digesting each of
XX CC the prepared aggregates of the double-stranded cDNAs with restriction
XX CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
XX CC separate lanes. The method can be used to analyse gene expression
XX CC rapidly and easily.
XX SQ Sequence 20 BP; 1 A; 1 C; 1 G; 17 T; 0 other;

Query Match 1.6%; Score 18; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAATAAAAAAAAAA 1100
DB 18 TAAAAAATAAAAAAAAAA 1

RESULT 87
AAQ75588/c
ID AAQ75588 standard; DNA; 20 BP.
XX AC AAQ75588;
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX KW aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-0112515.
XX PR 16-APR-1993; 93JP-0112515.
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX PT Analysis of cDNA and gene expression - by amplification of mRNA
XX PT followed by digestion with restriction enzymes
XX PS Disclosure; Page 5; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an
XX CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
XX CC and a plural type of labelled reverse transcription primers
XX CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
XX CC template for each reverse transcription primer; (b) digesting each of
XX CC the prepared aggregates of the double-stranded cDNAs with restriction
XX CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
XX CC separate lanes. The method can be used to analyse gene expression
XX CC rapidly and easily.
XX SQ Sequence 20 BP; 2 A; 1 C; 0 G; 17 T; 0 other;

Query Match 1.6%; Score 18; DB 1; Length 20;

```

Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAATAAAAAAAAAA 1100
DB 18 TAAAAAATAAAAAAAAAA 1

RESULT 88

AAQ75590/c

ID AAQ75590 standard; DNA; 20 BP.

XX AC AAQ75590;
XX AC

XX 04-AUG-1995 (first entry)
XX DT

XX Reverse transcription primer used in cDNA analysis technique.

XX Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.

XX Synthetic.

XX OS

XX JP06303997-A.

XX PD 01-NOV-1994.

XX PF 16-APR-1993; 93JP-0112515.

XX PR 16-APR-1993; 93JP-0112515.

XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

XX WPI; 1995-018287/03.

XX DR

XX Analysis of cDNA and gene expression - by amplification of mRNA

XX followed by digestion with restriction enzymes

XX Disclosure; Page 5; 11pp; Japanese.

XX A method for the analysis of cDNA comprises (a) preparing an

XX aggregate of double-stranded cDNAs by using an aggregate of mRNAs

XX and a plural type of labelled reverse transcription primers

XX (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the

XX template for each reverse transcription primer; (b) digesting each of

XX the prepared aggregates of the double-stranded cDNAs with restriction

XX enzyme and; (c) electrophoresing the digested aggregate of cDNAs in

XX separate lanes. The method can be used to analyse gene expression

XX rapidly and easily.

XX Sequence 20 BP; 1 A; 2 C; 0 G; 17 T; 0 other;

XX Query Match 1.6%; Score 18; DB 1; Length 20;

XX Best Local Similarity 100.0%; Pred. No. 1.4e+02;

XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAATAAAAAAAAAA 1100

DB 18 TAAAAAATAAAAAAAAAA 1

RESULT 89

AAQ75575/c

ID AAQ75575 standard; DNA; 20 BP.

XX AC AAQ75575;
XX AC

XX 04-AUG-1995 (first entry)
XX DT

XX Reverse transcription primer used in cDNA analysis technique.

XX Analysis; gene expression; reverse transcription; primer; cDNA;

XX aggregate; restriction enzyme; ss.

XX Synthetic.

XX JP06303997-A.

XX PD 01-NOV-1994.

XX 16-APR-1993; 93JP-0112515.

XX 16-APR-1993; 93JP-0112515.

XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

XX WPI; 1995-018287/03.

XX Analysis of cDNA and gene expression - by amplification of mRNA

XX followed by digestion with restriction enzymes

XX Disclosure; Page 5; 11pp; Japanese.

XX

XX Synthetic.
XX OS

XX JP06303997-A.

XX PD 01-NOV-1994.

XX PF 16-APR-1993; 93JP-0112515.

XX PR 16-APR-1993; 93JP-0112515.

XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

XX WPI; 1995-018287/03.

XX DR

XX Analysis of cDNA and gene expression - by amplification of mRNA

XX followed by digestion with restriction enzymes

XX Disclosure; Page 5; 11pp; Japanese.

XX A method for the analysis of cDNA comprises (a) preparing an

XX aggregate of double-stranded cDNAs by using an aggregate of mRNAs

XX and a plural type of labelled reverse transcription primers

XX (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the

XX template for each reverse transcription primer; (b) digesting each of

XX the prepared aggregates of the double-stranded cDNAs with restriction

XX enzyme and; (c) electrophoresing the digested aggregate of cDNAs in

XX separate lanes. The method can be used to analyse gene expression

XX rapidly and easily.

XX Sequence 20 BP; 1 A; 0 C; 2 G; 17 T; 0 other;

XX Query Match 1.6%; Score 18; DB 1; Length 20;

XX Best Local Similarity 100.0%; Pred. No. 1.4e+02;

XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAATAAAAAAAAAA 1100

DB 18 TAAAAAATAAAAAAAAAA 1

RESULT 90

AAQ75576/c

ID AAQ75576 standard; DNA; 20 BP.

XX AC AAQ75576;
XX AC

XX 04-AUG-1995 (first entry)
XX DT

XX Reverse transcription primer used in cDNA analysis technique.

XX Analysis; gene expression; reverse transcription; primer; cDNA;

XX aggregate; restriction enzyme; ss.

XX Synthetic.

XX JP06303997-A.

XX PD 01-NOV-1994.

XX 16-APR-1993; 93JP-0112515.

XX 16-APR-1993; 93JP-0112515.

XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

XX WPI; 1995-018287/03.

XX Analysis of cDNA and gene expression - by amplification of mRNA

XX followed by digestion with restriction enzymes

XX Disclosure; Page 5; 11pp; Japanese.

XX

CC A method for the analysis of cDNA comprises (a) preparing an
 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
 CC and a plural type of labelled reverse transcription primers
 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
 CC template for each reverse transcription primer; (b) digesting each of
 CC the prepared aggregates of the double-stranded cDNAs with restriction
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
 CC separate lanes. The method can be used to analyse gene expression
 CC rapidly and easily.
 XX
 SQ Sequence 20 BP; 2 A; 0 C; 1 G; 17 T; 0 other;

Query Match 1.6%; Score 18; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAAAAAAAAAAAAA 1100
 |||||
 Db 18 TAAAAAAAAAAAAAAAAA 1

RESULT 91
 AAQ75578/c
 ID AAQ75578 standard; DNA; 20 BP.
 XX
 AC AAQ75578;

DT 04-AUG-1995 (first entry)

DE Reverse transcription primer used in cDNA analysis technique.

XX Analysis; gene expression; reverse transcription; primer; cDNA;
 KW aggregate; restriction enzyme; ss.
 XX
 OS Synthetic.

XX JP06303997-A.

PD 01-NOV-1994.

PF 16-APR-1993; 93JP-0112515.

XX 16-APR-1993; 93JP-0112515.

PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

DR WPI; 1995-018287/03.

PT Analysis of cDNA and gene expression - by amplification of mRNA
 followed by digestion with restriction enzymes

XX Disclosure; Page 5; 11pp; Japanese.

XX A method for the analysis of cDNA comprises (a) preparing an
 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
 CC and a plural type of labelled reverse transcription primers
 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
 CC template for each reverse transcription primer; (b) digesting each of
 CC the prepared aggregates of the double-stranded cDNAs with restriction
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
 CC separate lanes. The method can be used to analyse gene expression
 CC rapidly and easily.
 XX

SQ Sequence 20 BP; 1 A; 1 C; 1 G; 17 T; 0 other;

Query Match 1.6%; Score 18; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAAAAAAAAAAAAA 1100
 |||||
 Db 18 TAAAAAAAAAAAAAAAAA 1

RESULT 92
 AAQ7752/c
 ID AAQ7752 standard; DNA; 20 BP.
 XX
 AC AAQ7752;
 XX
 DT 07-DEC-1998 (first entry)
 XX
 DE Phosphorothioate oligonucleotide.
 XX
 KW Phosphorothioate; sulphurisation; heterocycle; automated synthesis;
 KW antisense; EDIH; Beaucage reagent; ss.
 XX
 OS Synthetic.

XX Key Location/Qualifiers

FT misc_feature 1..20

FT /tag= a

FT /note= "phosphorothioate internucleotide linkages"

XX PN WO9741130-A2.

XX PD 06-NOV-1997.

XX PF 29-APR-1997; 97WO-US07118.

XX PR 30-APR-1996; 96US-0641920.

XX PA (LOU) UNIV LOUISIANA STATE & AGRIC.

XX PB (MINU) UNIV MINNESOTA.

XX PI Barany G, Chen L, Hammer RP, Musier-Forsyth K, Xu Q;

XX DR WPI; 1997-549671/50.

XX Sulphurisation of phosphorus-containing compounds, e.g.
 PT oligonucleotide(s) - by contacting the compound with a
 PT di-sulphide-containing five-membered heterocycle

XX Example 7; Page 30; 51pp; English.

XX The present invention provides a method for sulphurising phosphorus-
 CC containing compounds. It comprises contacting the phosphorus-containing
 CC compound which a 1,2,4-dithiazolidine-2,5-dione compound or a
 CC 3-substituted-1,2,4-dithiazolin-5-one compound. The method is especially
 CC useful for incorporation of phosphorothioate linkages into biologically
 CC important molecules such as DNA, RNA and phosphopeptides. Molecules
 CC containing such linkages are useful e.g. as antisense compounds for
 CC inhibiting gene expression, as reagents for studying DNA-protein or RNA-
 CC protein interactions, or as catalytic RNA. The present sequence
 CC represents an oligonucleotide with phosphorothioate linkages prepared by
 CC the method of the invention.

XX SQ Sequence 20 BP; 1 A; 0 C; 0 G; 19 U; 0 other;

Query Match 1.6%; Score 18; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAAAAAAAAAAAAA 1100
 |||||
 Db 20 TAAAAAAAAAAAAAAAAA 3

RESULT 93

AAQ13753/c

ID AAQ13753 standard; DNA; 20 BP.

XX AAQ13753;

XX 27-JUL-2000 (first entry)

DE Stem cell factor universal oligonucleotide 220-7.
 XX Stem cell factor; SCF; haematopoietic progenitor cell; blood forming;
 KW primitive progenitor cell; haematopoietic disorder; syngeneic;
 KW allogeneic; autologous bone marrow transplant; gene therapy;
 KW transfection; haematopoietic stem cell; acute blood loss; neoplasia;
 KW cancer; ss.
 XX Synthetic.
 OS EP992579-A1.
 XX PN 12-APR-2000.
 XX PD 04-OCT-1990; 99EP-0122861.
 XX PF 16-OCT-1989; 89US-0422383.
 XX PR 11-JUN-1990; 90US-0537198.
 XX PR 24-AUG-1990; 90US-0573616.
 XX PR 28-SEP-1990; 90WO-US05548.
 XX PR 01-OCT-1990; 90US-0589701.
 XX PR 04-OCT-1990; 90EP-0310899.
 XX PA (AMGE-) AMGEN INC.
 XX PI Zsebo KM, Suggs SV, Bosselmann RA, Martin FH;
 XX WPI; 2000-259135/23.
 XX DR Production of hematopoietic cells suitable for administration to a
 PT subject using progenitor cells and expanding the cells using stem cell
 PT factor -
 XX Example 3; Fig 12C; 123pp; English.
 XX A method has been developed of making haematopoietic cells suitable for
 CC administration to a subject. The method comprises: (a) obtaining
 CC haematopoietic progenitor cells from a donor; and (b) expanding the
 CC cells by adding to the cells a haematopoietically effective dose of a
 CC polypeptide product having at least part of the primary structural
 CC confirmation and one or more of the biological properties of naturally
 CC occurring stem cell factor (SCF). The method is useful for stimulating
 CC primitive progenitor cells including early haematopoietic progenitor
 CC cells which are capable of maturing to erythroid, megakaryocyte,
 CC granulocyte, lymphocyte and macrophage cells. SCF results in absolute
 CC increases in haematopoietic cells of both myeloid and lymphoid lineages.
 CC SCF is useful for treating haematopoietic disorders. The method is
 CC useful for expanding early haematopoietic progenitors in syngeneic,
 CC allogeneic or autologous bone marrow transplant. SCF is useful for
 CC enhancing the efficiency of gene therapy based on transfecting the
 CC haematopoietic stem cells. SCF is also useful for combating the
 CC myelosuppressive effects of anti-HIV drugs such as AZT and for enhancing
 CC haematopoietic recovery after acute blood loss and as a boost to the
 CC immune system for fighting neoplasia (cancer). The present sequence
 CC represents a universal oligonucleotide which is used in an example from
 CC the present invention.
 XX Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 other;
 SQ Query Match 1.6%; Score 18; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1083 TAAAAAATAAAAAAAAAA 1100
 DB 19 TAAAAAATAAAAAAAAAA 2
 RESULT 94
 AAS10448/c
 ID AAS10448 standard; DNA; 20 BP.
 XX AC AAS10448;

XX 24-OCT-2001 (first entry)
 DT Human stem cell factor (SCF) cDNA universal PCR primer 220-7.
 XX Human; stem cell factor; SCF; haematopoietic progenitor cell;
 DE blood disorder; Hodgkin's disease; vitamin B12; folic acid deficiency;
 KW hypopigmentation disorder; viral disorder; AIDS; PCR primer; ss.
 KW Homo sapiens.
 OS US6248319-B1.
 XX PN 19-JUN-2001.
 XX PD 24-MAY-1995; 95US-0449653.
 XX PF 10-APR-1991; 91US-0684535.
 XX PR 25-NOV-1992; 92US-0982255.
 XX PR 16-OCT-1989; 89US-0422383.
 XX PR 11-JUN-1990; 90US-0537198.
 XX PR 24-AUG-1990; 90US-0573616.
 XX PR 01-OCT-1990; 90US-0589701.
 XX PR 21-DEC-1993; 93US-0172329.
 XX PA (ZSEB/) ZSEBO K M.
 PA (BOSS/) BOSSELMAN R A.
 PA (SUGG/) SUGGS S V.
 PA (WART/) MARTIN F H.
 XX PI Zsebo KM, Bosselmann RA, Suggs SV, Martin FH;
 XX WPI; 2001-407312/43.
 XX Increasing the number of early haematopoietic progenitor cells in the
 CC peripheral blood useful for the treatment of blood disorders including
 CC Hodgkin's disease comprises the administration of human stem cell
 CC factor -
 XX Example 3; Fig 12C; 210pp; English.
 XX The present sequence for universal PCR primer 220-7 is 1 of 19
 CC PCR primers (AAS10435-AAS10453) used to amplify various portions of
 CC the human SCF cDNA sequence. The sequence is described in an
 CC invention relating to novel stem cell factors, the polynucleotides
 CC encoding them and methods for producing the stem cell factors. The
 CC methods involve increasing the number of early haematopoietic progenitor
 CC cells in human peripheral blood by administering a haematopoietically
 CC effective human stem cell factor polypeptide. The methods are useful for
 CC the treatment of blood disorders, including myelofibrosis,
 CC myelocytosis, osteopetrosis, metastatic carcinoma, acute leukaemia,
 CC multiple myeloma, Hodgkin's disease, lymphoma, Gaucher's disease,
 CC Niemann-Pick disease, refractory anaemia, malaria, vitamin B12 and folic
 CC acid deficiency, hypopigmentation disorders i.e. piebaldism and viral
 CC induced disorders, including AIDS.
 XX Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 other;
 SQ Query Match 1.6%; Score 18; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1083 TAAAAAATAAAAAAAAAA 1100
 DB 19 TAAAAAATAAAAAAAAAA 2
 RESULT 95
 AAH41332/c
 ID AAH41332 standard; DNA; 20 BP.
 XX AC AAH41332;
 XX

DT 21-AUG-2001 (first entry)
 XX Universal stem cell factor (SCF) related oligonucleotide SEQ ID NO:33.
 DE Stem cell factor; SCF; stem cell factor receptor; blood cell disorder;
 XX gene therapy; PCR primer; mutagenesis; probe; ss.
 KW Synthetic.
 XX OS
 XX US6207454-B1.
 PN 27-MAR-2001.
 XX 31-DEC-1998; 98US-0224681.
 XX 21-DEC-1993; 93US-0172329.
 PR 24-MAY-1995; 95US-0049653.
 PR 12-JAN-1998; 98US-0005893.
 PR 25-NOV-1992; 92US-0982255.
 PR 16-OCT-1989; 89US-0422383.
 PR 11-JUN-1990; 90US-0537198.
 PR 24-AUG-1990; 90US-0573616.
 PR 01-OCT-1990; 90US-0589701.
 XX (AMGE-) AMGEN INC.
 PA Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
 PI WPI; 2001-366062/38.
 DR Enhancing efficiency of transfer of polynucleotide into a target
 PT mammalian cell in vitro, involves exposing cell that expresses a stem
 PT cell factor receptor to stem cell factor, and introducing
 PT polynucleotide into cell in vitro -
 XX Example 3; Fig 12C; 210pp; English.
 PS The present invention describes a method for enhancing (B) the
 CC efficiency of transfer of a polynucleotide (I) into a target mammalian
 CC cell (II) in vitro, comprising exposing (II) that expresses a stem cell
 CC factor (SCF) receptor to a biologically active SCF, its analogue or
 CC fragment, which induces cell proliferation, and introducing (I) to (II)
 CC in vitro. Exposure of SCF to (II) results in increased uptake of (I)
 CC into the cell. The method is useful for enhancing the efficiency of the
 CC transfer of a polynucleotide into a target mammalian cell in vitro.
 CC The method is useful in gene therapy techniques. AAH41301 to AAH41364
 CC and AAB98351 to AAB98390 represent sequences used in the exemplification
 CC of the present invention.
 XX SQ Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 other;
 Query Match 1.6%; Score 18; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1083 TAAAAA AAAAAAAAAA 1100
 Db 19 TAAAAA AAAAAAAAAA 2
 RESULT 96
 AAS04112/c
 ID AAS04112 standard; DNA; 20 BP.
 XX AAS04112;
 AC 29-AUG-2001 (first entry)
 XX Human SCF (stem cell factor) cDNA universal PCR primer 220-7.
 DE Human; stem cell factor; SCF; early haematopoietic progenitor cell;
 KW blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;
 KW anaemia; Kala azar; septicemia; malaria; hypopigmentation disorder;

KW PCR primer; ss.
 XX OS Homo sapiens.
 XX PN US6207417-B1.
 XX 27-MAR-2001.
 PD 07-JUN-1995; 95US-0482918.
 XX 21-DEC-1993; 93US-0172329.
 PR 16-OCT-1989; 89US-0422383.
 PR 11-JUN-1990; 90US-0537198.
 PR 24-AUG-1990; 90US-0573616.
 PR 01-OCT-1990; 90US-0589701.
 XX (ZSEB/) ZSEBO K M.
 PA (BOSS/) BOSSELMAN R A.
 PA (SUGG/) SUGGS S V.
 PA (MART/) MARTIN F H.
 XX Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
 PI WPI; 2001-298941/31.
 DR Novel nucleic acids encoding stem cell factor useful for treating
 PT disorders involving blood cells, e.g. leukaemia, splenomegaly, Hodgkin's
 PT disease, Kala azar, anaemia and septicemia -
 XX Example 3; Fig 12C; 209pp; English.
 PS The present sequence for universal PCR primer 220-7 is 1 of 8
 CC universal oligonucleotides (AAS04110-AAS04117) used in the
 CC isolation of the human SCF (stem cell factor) cDNA sequence. The
 CC present invention relates to novel stem cell factors
 CC (AAU02453-AAU02458, AAU02460, AAU02461) and the polynucleotides
 CC encoding them. SCF stimulate primitive progenitor cells including early
 CC haematopoietic progenitor cells. The invention also describes SCF
 CC peptides (AAU02462-AAU02481) and the oligonucleotides
 CC (AAS04081-AAS04117) used in the isolation of human and rat SCF
 CC sequences. The polynucleotide encoding SCF is useful for producing SCF
 CC and useful in gene therapy. It is useful for treating disorders
 CC involving blood cells such as myelofibrosis, metastatic carcinoma,
 CC acute leukaemia, multiple myeloma, Hodgkin's disease, lymphoma,
 CC Gaucher's disease, anaemia, congestive splenomegaly, Kala azar,
 CC sarcoidosis, military tuberculosis, disseminated fungus disease,
 CC fulminating septicemia, malaria, vitamin B12 and folic acid deficiency,
 CC pyridoxine deficiency, and hypopigmentation disorders such as
 CC piebaldism and vitiligo.
 XX SQ Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 other;
 Query Match 1.6%; Score 18; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1083 TAAAAA AAAAAAAAAA 1100
 Db 19 TAAAAA AAAAAAAAAA 2
 RESULT 97
 AAS04213/c
 ID AAS04213 standard; DNA; 20 BP.
 XX AAS04213;
 AC 29-AUG-2001 (first entry)
 XX Human SCF (stem cell factor) cDNA universal PCR primer 220-7.
 DE Human; stem cell factor; SCF; early haematopoietic progenitor cell;
 KW blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;

```

KW anaemia; kala azar; septicemia; malaria; hypopigmentation disorder;
KW PCR primer; ss.
XX
OS Homo sapiens.
XX
PN US6218148-B1.
XX
PD 17-APR-2001.
XX
PF 21-DEC-1993; 93US-0172329.
XX
PR 25-NOV-1992; 92US-0982255.
XX
PR 16-OCT-1989; 89US-0422383.
XX
PR 11-JUN-1990; 90US-0537198.
XX
PR 24-AUG-1990; 90US-0573616.
XX
PR 01-OCT-1990; 90US-0589701.
XX
PA (AMGE-) AMGEN INC.
XX
PI Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
XX WPI; 2001-281051/29.
XX
DR Isolated DNA sequence, encoding polypeptide product useful for
XX stimulating growth of early haematopoietic progenitor cells -
XX
XX Example 3; Fig 12C; 167pp; English.
XX
XX The present sequence for universal PCR primer 220-7 is 1 of 8
XX universal oligonucleotides (AAS04211-AAS04218) used in the
XX isolation of the human SCF (stem cell factor) cDNA sequence. The
XX present invention relates to novel stem cell factors
XX (AAU02761-AAU02767, AAU02770-AAU02775, AAU02797) and the polynucleotides
XX encoding them. SCF stimulate primitive progenitor cells including early
XX haematopoietic progenitor cells. The invention also describes SCF
XX peptides (AAU02777-AAU02794) and the oligonucleotides
XX (AAS04182-AAS04210) used in the isolation of human and rat SCF
XX sequences. The polynucleotide encoding SCF is useful for producing SCF
XX and useful in gene therapy. It is useful for treating disorders
XX involving blood cells such as myelofibrosis, metastatic carcinoma,
XX acute leukaemia, multiple myeloma, Hodgkin's disease, lymphoma,
XX Gaucher's disease, anaemia, congestive splenomegaly, kala azar,
XX sarcoidosis, military tuberculosis, disseminated fungus disease,
XX fulminating septicemia, malaria, vitamin B12 and folic acid deficiency,
XX pyridoxine deficiency, and hypopigmentation disorders such as
XX piebaldism and vitiligo.
XX
SQ Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 other;

Query Match 1.6%; Score 18; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAATAAAAAAAAAA 1100
Db 19 TAAAAAATAAAAAAAAAA 2

RESULT 98
AAH23890/c
ID AAH23890 standard; DNA; 20 BP.
XX
AC AAH23890;
XX
XX 07-AUG-2001 (first entry)
XX
DE Human SCF (stem cell factor) cDNA universal PCR primer 220-7.
XX
XX Human; stem cell factor; SCF; early haematopoietic progenitor cell;
KW blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;
KW anaemia; kala azar; septicemia; malaria; hypopigmentation disorder;
KW PCR primer; ss.
XX

```

```

OS Homo sapiens.
XX
PN US6204363-B1.
XX
PD 20-MAR-2001.
XX
PF 25-NOV-1992; 92US-0982255.
XX
PR 10-APR-1991; 91US-0684535.
XX
PR 16-OCT-1989; 89US-0422383.
XX
PR 11-JUN-1990; 90US-0537198.
XX
PR 24-AUG-1990; 90US-0573616.
XX
PR 01-OCT-1990; 90US-0589701.
XX
PA (AMGE-) AMGEN INC.
XX
PI Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
XX WPI; 2001-256683/26.
XX
DR New stem cell factor polypeptides and their analogs which stimulate
XX growth of early hematopoietic progenitors, useful for treating aplastic
XX anemia, carcinoma, multiple myeloma, vitiligo, kala azar, Hodgkin's
XX disease -
XX
XX Example 3; Fig 12C; 166pp; English.
XX
XX The present sequence for universal PCR primer 220-7 is 1 of 8
XX universal oligonucleotides (AAH23888-AAH23895) used in the
XX isolation of the human SCF (stem cell factor) cDNA sequence. The
XX present invention relates to novel stem cell factors
XX (AAB73561-AAB73568, AAB73571-AAB73576) and the polynucleotides
XX encoding them. SCF stimulate primitive progenitor cells including early
XX haematopoietic progenitor cells. The invention also describes SCF
XX peptides (AAB73578-AAB73597) and the oligonucleotides
XX (AAH23859-AAH23887) used in the isolation of human and rat SCF
XX sequences. The polynucleotide encoding SCF is useful for producing SCF
XX and useful in gene therapy. It is useful for treating disorders
XX involving blood cells such as myelofibrosis, metastatic carcinoma,
XX acute leukaemia, multiple myeloma, Hodgkin's disease, lymphoma,
XX Gaucher's disease, anaemia, congestive splenomegaly, kala azar,
XX sarcoidosis, military tuberculosis, disseminated fungus disease,
XX fulminating septicemia, malaria, vitamin B12 and folic acid deficiency,
XX pyridoxine deficiency, and hypopigmentation disorders such as
XX piebaldism and vitiligo.
XX
SQ Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 other;

Query Match 1.6%; Score 18; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAATAAAAAAAAAA 1100
Db 19 TAAAAAATAAAAAAAAAA 2

RESULT 99
AAF89092/c
ID AAF89092 standard; DNA; 20 BP.
XX
AC AAF89092;
XX
XX 13-JUL-2001 (first entry)
XX
DE Mammalian stem cell factor PCR primer SEQ ID NO: 33.
XX
XX Human; rat; mammal; stem cell factor; SCF; cell growth stimulation;
KW Gene therapy; haematopoietic disorder; aplastic anaemia; leukaemia;
KW neurological damage; intestinal damage; infertility; AIDS; SCID;
KW severe combined immunodeficiency; PCR primer; ss.
XX
XX Mammalia.

```

```

XX PN US6207802-B1.
XX XX
XX PD 27-MAR-2001.
XX XX
XX PF 09-NOV-1994; 94US-0336728.
XX XX
XX PR 25-NOV-1992; 92US-0982255.
XX PR 16-OCT-1989; 89US-0422383.
XX PR 11-JUN-1990; 90US-0537198.
XX PR 24-AUG-1990; 90US-0573616.
XX PR 01-OCT-1990; 90US-0589701.
XX XX
XX PA (AMGE-) AMGEN INC.
XX PI Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
XX XX
XX DR WPI; 2001-353108/37.
XX XX
XX PT Novel isolated non-human mammalian stem cell factor polypeptide
XX PT stimulating growth of early haematopoietic progenitor cells, useful for
XX PT treating aplastic anaemia, lymphoma, Letterer-Siwe disease, Kala azar,
XX PT sarcoidosis -
XX XX
XX PS Example 3; Fig 12C; 209pp; English.
XX XX
XX CC The present invention provides the protein and coding sequences of
XX CC mammalian stem cell factors (SCFs). These are capable of stimulating the
XX CC growth of early haematopoietic progenitor cells, neural stem cells and
XX CC primordial germ stem cells. The sequences are useful in the treatment of
XX CC leukaemias, haematopoietic disorders, aplastic anaemia, paroxysmal
XX CC nocturnal haemoglobinuria, malaria, pigmentation disorders, neurological
XX CC and intestinal damage, infertility, AIDS and severe combined
XX CC immunodeficiency (SCID). The present sequence is primer used to amplify
XX CC an SCF in the exemplification of the invention.
XX XX
XX SQ Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 other;
XX XX
XX Query Match 1.6%; Score 18; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 1.4e+02;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX XX
XX QY 1083 TAAAAAATAAAAAAAAAA 1100
XX DB ||||| ||||| ||||| ||||| |||||
XX 19 TAAAAAATAAAAAAAAAA 2
XX XX
XX RESULT 100
XX ABS73849/C
XX ID ABS73849 standard; DNA; 20 BP.
XX XX
XX AC ABS73849;
XX XX
XX DT 05-DEC-2002 (first entry)
XX XX
XX DE SCF universal oligonucleotide 220-7.
XX XX
XX KW Stem cell factor; SCF; blood-forming system; blood cell disorder;
XX KW haematopoietic system; metastatic carcinoma; acute leukaemia;
XX KW multiple myeloma; Hodgkin's disease; lymphoma; malaria; vitiligo;
XX KW refractory erythroblastic anaemia; lymphatic disease; cytostatic;
XX KW disseminated fungus disease; haematopoietic; tuberculostatic;
XX KW anticanceric; antifungal; antimalarial; dermatological; ss.
XX XX
XX OS Synthetic.
XX XX
XX EP1241258-A2.
XX XX
XX PD 18-SEP-2002.
XX XX
XX PF 04-OCT-1990; 2002EP-0008587.
XX XX
XX PR 16-OCT-1989; 89US-0422383.

```

```

PR 11-JUN-1990; 90US-0537198.
PR 24-AUG-1990; 90US-0573616.
PR 28-SEP-1990; 90WO-US05548.
PR 01-OCT-1990; 90US-0589701.
PR 04-OCT-1990; 90EP-0310899.
PR 04-OCT-1990; 95EP-0105391.
XX XX
XX PA (AMGE-) AMGEN INC.
XX XX
XX PI Zsebo KM, Suggs SV, Bosselman RA, Martin FH;
XX XX
XX DR WPI; 2002-684093/74.
XX XX
XX PT Production of a human stem cell factor (SCF) polypeptide for treating
XX PT disorders involving blood cells, such as leukaemia, comprises culturing
XX PT mammalian cells comprising non-human SCF promoter DNA linked to DNA
XX PT encoding the human SCF -
XX XX
XX PS Example 3; Fig 12C; 120pp; English.
XX XX
XX CC The present invention relates to novel stem cell factors (SCFs),
XX CC polynucleotide sequences encoding the SCFs, and methods of producing
XX CC them. SCFs are involved in the blood-forming (haematopoietic)
XX CC system in mammals, particularly humans. The method of the invention
XX CC is useful for the production of human SCF. The stem cell factors are
XX CC useful to treat disorders involving blood cells e.g. metastatic
XX CC carcinoma, acute leukaemia, multiple myeloma, Hodgkin's disease,
XX CC lymphoma, refractory erythroblastic anaemia, myeloid tuberculosis,
XX CC disseminated fungus disease, malaria, and vitiligo. The present
XX CC sequence representing a universal oligonucleotide for SCF DNA is
XX CC used in the examples of the present invention.
XX XX
XX SQ Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 other;
XX XX
XX Query Match 1.6%; Score 18; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 1.4e+02;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX XX
XX QY 1083 TAAAAAATAAAAAAAAAA 1100
XX DB ||||| ||||| ||||| ||||| |||||
XX 19 TAAAAAATAAAAAAAAAA 2
XX XX
XX RESULT 101
XX RAD35465/C
XX ID RAD35465 standard; DNA; 20 BP.
XX XX
XX AC RAD35465;
XX XX
XX DT 25-JUL-2002 (first entry)
XX XX
XX DE Rat SCF 5' cDNA amplifying PCR primer, 220-7.
XX XX
XX KW Rat; stem cell factor; SCF protein; leucopaenia; thrombocytopaenia;
XX KW anaemia; myelosuppression; nerve damage; myeloproliferative disorder;
XX KW infertility; neoplasia; myelofibrosis; myelocytosis; osteopetrosis;
XX KW metastatic carcinoma; acute leukaemia; multiple myeloma; sarcoidosis;
XX KW Hodgkin's disease; lymphoma; Gaucher's disease; Niemann-Pick disease;
XX KW Letterer-Siwe disease; refractory erythroblastic anaemia; Kala azar;
XX KW disseminated fungus disease; congestive splenomegaly; splenic pancytopenia;
XX KW acquired immune deficiency syndrome; Fulminating septicemia; piebaldism; AIDS;
XX KW pyridoxine deficiency; vitamin B12 deficiency; folic acid deficiency;
XX KW Diamond Blackfan anaemia; hypopigmentation disorder; vitiligo; PCR;
XX KW primer; ss.
XX XX
XX OS Rattus sp.
XX XX
XX EN US2002018763-A1.
XX XX
XX PD 14-FEB-2002.
XX XX
XX PF 12-JAN-1998; 98US-0005243.

```



```
DR WPI; 1995-018287/03.
XX Analysis of cDNA and gene expression - by amplification of mRNA
PT followed by digestion with restriction enzymes
XX
XX PS Disclosure; Page 7; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC and a plural type of labelled reverse transcription primers
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
CC template for each reverse transcription primer; (b) digesting each of
CC the prepared aggregates of the double-stranded cDNAs with restriction
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC separate lanes. The method can be used to analyse gene expression
CC rapidly and easily.
XX
SQ Sequence 21 BP; 1 A; 2 C; 1 G; 17 T; 0 other;

Query Match          1.6%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAA
Db 18 TAAAAA

RESULT 107
AAQ75700/c
ID AAQ75700 standard; DNA; 21 BP.
XX
AC AAQ75700;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-0112515.
XX
PR 16-APR-1993; 93JP-0112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-0112515.
XX
PR 16-APR-1993; 93JP-0112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA
PT followed by digestion with restriction enzymes
XX
XX PS Disclosure; Page 7; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC and a plural type of labelled reverse transcription primers
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
CC template for each reverse transcription primer; (b) digesting each of
CC the prepared aggregates of the double-stranded cDNAs with restriction
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC separate lanes. The method can be used to analyse gene expression
CC rapidly and easily.
XX
SQ Sequence 21 BP; 2 A; 2 C; 0 G; 17 T; 0 other;

Query Match          1.6%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAA
Db 18 TAAAAA

RESULT 108
AAQ75701/c
ID AAQ75701 standard; DNA; 21 BP.
XX
AC AAQ75701;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-0112515.
XX
PR 16-APR-1993; 93JP-0112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA
PT followed by digestion with restriction enzymes
XX
XX PS Disclosure; Page 7; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC and a plural type of labelled reverse transcription primers
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
CC template for each reverse transcription primer; (b) digesting each of
CC the prepared aggregates of the double-stranded cDNAs with restriction
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC separate lanes. The method can be used to analyse gene expression
CC rapidly and easily.
XX
SQ Sequence 21 BP; 1 A; 2 C; 0 G; 18 T; 0 other;

Query Match          1.6%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAA
Db 18 TAAAAA

RESULT 109
AAQ75702/c
ID AAQ75702 standard; DNA; 21 BP.
XX
AC AAQ75702;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
```

```
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAA
Db 18 TAAAAA

RESULT 108
AAQ75701/c
ID AAQ75701 standard; DNA; 21 BP.
XX
AC AAQ75701;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-0112515.
XX
PR 16-APR-1993; 93JP-0112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA
PT followed by digestion with restriction enzymes
XX
XX PS Disclosure; Page 7; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC and a plural type of labelled reverse transcription primers
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
CC template for each reverse transcription primer; (b) digesting each of
CC the prepared aggregates of the double-stranded cDNAs with restriction
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC separate lanes. The method can be used to analyse gene expression
CC rapidly and easily.
XX
SQ Sequence 21 BP; 1 A; 2 C; 0 G; 18 T; 0 other;

Query Match          1.6%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAA
Db 18 TAAAAA

RESULT 109
AAQ75702/c
ID AAQ75702 standard; DNA; 21 BP.
XX
AC AAQ75702;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
```



```

XX OS Synthetic.
XX PN JP06303997-A.
XX XX
XX PD 01-NOV-1994.
XX XX
XX PF 16-APR-1993; 93JP-0112515.
XX XX
XX PR 16-APR-1993; 93JP-0112515.
XX XX
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX XX
XX DR WPI; 1995-018287/03.
XX PT Analysis of cDNA and gene expression - by amplification of mRNA
XX PT followed by digestion with restriction enzymes
XX PS Disclosure; Page 7; 11pp; Japanese.
XX XX
XX CC A method for the analysis of cDNA comprises (a) preparing an
XX CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
XX CC and a plural type of labelled reverse transcription primers
XX CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
XX CC template for each reverse transcription primer; (b) digesting each of
XX CC the prepared aggregates of the double-stranded cDNAs with restriction
XX CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
XX CC separate lanes. The method can be used to analyse gene expression
XX CC rapidly and easily.
XX CC Sequence 21 BP; 1 A; 3 C; 0 G; 17 T; 0 other;
XX
XX Query Match 1.6%; Score 18; DB 1; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 1.5e+02;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1083 TAAAAAATAAAAAAAAAA 1100
XX |||||||
XX DB 18 TAAAAAATAAAAAAAAAA 1
XX
XX RESULT 110
XX AAQ75703/c
XX ID AAQ75703 standard; DNA; 21 BP.
XX XX
XX AC AAQ75703;
XX XX
XX DT 04-AUG-1995 (first entry)
XX XX
XX DE Reverse transcription primer used in cDNA analysis technique.
XX XX
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX KW aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX XX
XX PD 01-NOV-1994.
XX XX
XX PF 16-APR-1993; 93JP-0112515.
XX XX
XX PR 16-APR-1993; 93JP-0112515.
XX XX
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX XX
XX DR WPI; 1995-018287/03.
XX PT Analysis of cDNA and gene expression - by amplification of mRNA
XX PT followed by digestion with restriction enzymes
XX PS Disclosure; Page 7; 11pp; Japanese.
XX XX
XX CC A method for the analysis of cDNA comprises (a) preparing an
XX CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
XX CC and a plural type of labelled reverse transcription primers
XX CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
XX CC template for each reverse transcription primer; (b) digesting each of
XX CC the prepared aggregates of the double-stranded cDNAs with restriction
XX CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
XX CC separate lanes. The method can be used to analyse gene expression
XX CC rapidly and easily.
XX CC Sequence 21 BP; 1 A; 3 C; 0 G; 17 T; 0 other;
XX
XX Query Match 1.6%; Score 18; DB 1; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 1.5e+02;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1083 TAAAAAATAAAAAAAAAA 1100
XX |||||||
XX DB 18 TAAAAAATAAAAAAAAAA 1
XX
XX RESULT 110
XX AAQ75703/c
XX ID AAQ75703 standard; DNA; 21 BP.
XX XX
XX AC AAQ75703;
XX XX
XX DT 04-AUG-1995 (first entry)
XX XX
XX DE Reverse transcription primer used in cDNA analysis technique.
XX XX
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX KW aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX XX
XX PD 01-NOV-1994.
XX XX
XX PF 16-APR-1993; 93JP-0112515.
XX XX
XX PR 16-APR-1993; 93JP-0112515.
XX XX
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX XX
XX DR WPI; 1995-018287/03.
XX PT Analysis of cDNA and gene expression - by amplification of mRNA
XX PT followed by digestion with restriction enzymes
XX PS Disclosure; Page 7; 11pp; Japanese.
XX XX

```

```

CC A method for the analysis of cDNA comprises (a) preparing an
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC and a plural type of labelled reverse transcription primers
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
CC template for each reverse transcription primer; (b) digesting each of
CC the prepared aggregates of the double-stranded cDNAs with restriction
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC separate lanes. The method can be used to analyse gene expression
CC rapidly and easily.
CC Sequence 21 BP; 1 A; 0 C; 3 G; 17 T; 0 other;
XX
XX Query Match 1.6%; Score 18; DB 1; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 1.5e+02;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1083 TAAAAAATAAAAAAAAAA 1100
XX |||||||
XX DB 18 TAAAAAATAAAAAAAAAA 1
XX
XX RESULT 111
XX AAQ75704/c
XX ID AAQ75704 standard; DNA; 21 BP.
XX XX
XX AC AAQ75704;
XX XX
XX DT 04-AUG-1995 (first entry)
XX XX
XX DE Reverse transcription primer used in cDNA analysis technique.
XX XX
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX KW aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX XX
XX PD 01-NOV-1994.
XX XX
XX PF 16-APR-1993; 93JP-0112515.
XX XX
XX PR 16-APR-1993; 93JP-0112515.
XX XX
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX XX
XX DR WPI; 1995-018287/03.
XX XX
XX PT Analysis of cDNA and gene expression - by amplification of mRNA
XX PT followed by digestion with restriction enzymes
XX PS Disclosure; Page 7; 11pp; Japanese.
XX XX
XX CC A method for the analysis of cDNA comprises (a) preparing an
XX CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
XX CC and a plural type of labelled reverse transcription primers
XX CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
XX CC template for each reverse transcription primer; (b) digesting each of
XX CC the prepared aggregates of the double-stranded cDNAs with restriction
XX CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
XX CC separate lanes. The method can be used to analyse gene expression
XX CC rapidly and easily.
XX CC Sequence 21 BP; 2 A; 0 C; 2 G; 17 T; 0 other;
XX
XX Query Match 1.6%; Score 18; DB 1; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 1.5e+02;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1083 TAAAAAATAAAAAAAAAA 1100
XX |||||||
XX DB 18 TAAAAAATAAAAAAAAAA 1
XX
XX RESULT 110
XX AAQ75703/c
XX ID AAQ75703 standard; DNA; 21 BP.
XX XX
XX AC AAQ75703;
XX XX
XX DT 04-AUG-1995 (first entry)
XX XX
XX DE Reverse transcription primer used in cDNA analysis technique.
XX XX
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX KW aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX XX
XX PD 01-NOV-1994.
XX XX
XX PF 16-APR-1993; 93JP-0112515.
XX XX
XX PR 16-APR-1993; 93JP-0112515.
XX XX
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX XX
XX DR WPI; 1995-018287/03.
XX XX
XX PT Analysis of cDNA and gene expression - by amplification of mRNA
XX PT followed by digestion with restriction enzymes
XX PS Disclosure; Page 7; 11pp; Japanese.
XX XX
XX CC A method for the analysis of cDNA comprises (a) preparing an
XX CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
XX CC and a plural type of labelled reverse transcription primers
XX CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
XX CC template for each reverse transcription primer; (b) digesting each of
XX CC the prepared aggregates of the double-stranded cDNAs with restriction
XX CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
XX CC separate lanes. The method can be used to analyse gene expression
XX CC rapidly and easily.
XX CC Sequence 21 BP; 2 A; 0 C; 2 G; 17 T; 0 other;
XX
XX Query Match 1.6%; Score 18; DB 1; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 1.5e+02;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1083 TAAAAAATAAAAAAAAAA 1100
XX |||||||
XX DB 18 TAAAAAATAAAAAAAAAA 1
XX
XX RESULT 110
XX AAQ75703/c
XX ID AAQ75703 standard; DNA; 21 BP.
XX XX
XX AC AAQ75703;
XX XX
XX DT 04-AUG-1995 (first entry)
XX XX
XX DE Reverse transcription primer used in cDNA analysis technique.
XX XX
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX KW aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX XX
XX PD 01-NOV-1994.
XX XX
XX PF 16-APR-1993; 93JP-0112515.
XX XX
XX PR 16-APR-1993; 93JP-0112515.
XX XX
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX XX
XX DR WPI; 1995-018287/03.
XX XX
XX PT Analysis of cDNA and gene expression - by amplification of mRNA
XX PT followed by digestion with restriction enzymes
XX PS Disclosure; Page 7; 11pp; Japanese.
XX XX

```

```

RESULT 112
AAQ75705/c
ID AAQ75705 standard; DNA; 21 BP.
XX
XX AAQ75705;
AC
XX
XX 04-AUG-1995 (first entry)
DT
XX
XX Reverse transcription primer used in cDNA analysis technique.
DE
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX
XX JP06303997-A.
PN
XX
XX 01-NOV-1994.
PD
XX
XX 16-APR-1993; 93JP-0112515.
PF
XX
XX 16-APR-1993; 93JP-0112515.
PR
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
PA
XX
XX WPI; 1995-018287/03.
DR
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA
PT followed by digestion with restriction enzymes
XX
XX Disclosure; Page 7; 11pp; Japanese.
PS
XX
XX A method for the analysis of cDNA comprises (a) preparing an
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC and a plural type of labelled reverse transcription primers
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
CC template for each reverse transcription primer; (b) digesting each of
CC the prepared aggregates of the double-stranded cDNAs with restriction
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC separate lanes. The method can be used to analyse gene expression
CC rapidly and easily.
XX
XX Sequence 21 BP; 1 A; 0 C; 2 G; 18 T; 0 other;
SQ
Query Match 1.6%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred.No. 1.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAAAAAAAAAAAAA 1100
Db 18 TAAAAAAAAAAAAAAAAA 1

RESULT 113
AAQ75706/c
ID AAQ75706 standard; DNA; 21 BP.
XX
XX AAQ75706;
AC
XX
XX 04-AUG-1995 (first entry)
DT
XX
XX Reverse transcription primer used in cDNA analysis technique.
DE
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX
XX JP06303997-A.
PN
XX
XX 01-NOV-1994.
PD
XX
XX

```

```

PF 16-APR-1993; 93JP-0112515.
XX
XX 16-APR-1993; 93JP-0112515.
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
PA
XX
XX WPI; 1995-018287/03.
DR
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA
PT followed by digestion with restriction enzymes
XX
XX Disclosure; Page 7; 11pp; Japanese.
PS
XX
XX A method for the analysis of cDNA comprises (a) preparing an
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC and a plural type of labelled reverse transcription primers
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
CC template for each reverse transcription primer; (b) digesting each of
CC the prepared aggregates of the double-stranded cDNAs with restriction
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC separate lanes. The method can be used to analyse gene expression
CC rapidly and easily.
XX
XX Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 other;
SQ
Query Match 1.6%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred.No. 1.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAAAAAAAAAAAAA 1100
Db 18 TAAAAAAAAAAAAAAAAA 1

RESULT 114
AAQ75707/c
ID AAQ75707 standard; DNA; 21 BP.
XX
XX AAQ75707;
AC
XX
XX 04-AUG-1995 (first entry)
DT
XX
XX Reverse transcription primer used in cDNA analysis technique.
DE
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX
XX JP06303997-A.
PN
XX
XX 01-NOV-1994.
PD
XX
XX 16-APR-1993; 93JP-0112515.
PF
XX
XX 16-APR-1993; 93JP-0112515.
PR
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
PA
XX
XX WPI; 1995-018287/03.
DR
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA
PT followed by digestion with restriction enzymes
XX
XX Disclosure; Page 7; 11pp; Japanese.
PS
XX
XX A method for the analysis of cDNA comprises (a) preparing an
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC and a plural type of labelled reverse transcription primers
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
CC template for each reverse transcription primer; (b) digesting each of
CC the prepared aggregates of the double-stranded cDNAs with restriction
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC separate lanes. The method can be used to analyse gene expression
CC rapidly and easily.
XX
XX Sequence 21 BP; 1 A; 0 C; 2 G; 18 T; 0 other;
SQ
Query Match 1.6%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred.No. 1.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAAAAAAAAAAAAA 1100
Db 18 TAAAAAAAAAAAAAAAAA 1

RESULT 115
AAQ75708/c
ID AAQ75708 standard; DNA; 21 BP.
XX
XX AAQ75708;
AC
XX
XX 04-AUG-1995 (first entry)
DT
XX
XX Reverse transcription primer used in cDNA analysis technique.
DE
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX
XX JP06303997-A.
PN
XX
XX 01-NOV-1994.
PD
XX
XX

```

CC separte lanes. The method can be used to analyse gene expression
CC rapidly and easily.
XX
SQ Sequence 21 BP; 2 A; 0 C; 2 G; 17 T; 0 other;

Query Match 1.6%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAA...AAAAA 1100
Db 18 TAAAAA...AAAAA 1

RESULT 115
AAQ75708/c
ID AAQ75708 standard; DNA; 21 BP.
XX
AC AAQ75708;
XX
XX
XX
DT 04-AUG-1995 (first entry)
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
XX JP06303997-A.
XX
PD 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-0112515.
XX
XX 16-APR-1993; 93JP-0112515.
XX
XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA
XX followed by digestion with restriction enzymes
XX
XX Disclosure; Page 7; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an
XX aggregate of double-stranded cDNAs by using an aggregate of mRNAs
XX and a plural type of labelled reverse transcription primers
XX (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
XX template for each reverse transcription primer; (b) digesting each of
XX the prepared aggregates of the double-stranded cDNAs with restriction
XX enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
XX separte lanes. The method can be used to analyse gene expression
XX rapidly and easily.
XX
SQ Sequence 21 BP; 3 A; 0 C; 1 G; 17 T; 0 other;

Query Match 1.6%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAA...AAAAA 1100
Db 18 TAAAAA...AAAAA 1

RESULT 116
AAQ75709/c
ID AAQ75709 standard; DNA; 21 BP.
XX
AC AAQ75709;
XX
XX

DT 04-AUG-1995 (first entry)
XX Reverse transcription primer used in cDNA analysis technique.
DE
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX
XX JP06303997-A.
XX
PD 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-0112515.
XX
XX 16-APR-1993; 93JP-0112515.
XX
XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA
XX followed by digestion with restriction enzymes
XX
XX Disclosure; Page 7; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an
XX aggregate of double-stranded cDNAs by using an aggregate of mRNAs
XX and a plural type of labelled reverse transcription primers
XX (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
XX template for each reverse transcription primer; (b) digesting each of
XX the prepared aggregates of the double-stranded cDNAs with restriction
XX enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
XX separte lanes. The method can be used to analyse gene expression
XX rapidly and easily.
XX
SQ Sequence 21 BP; 2 A; 0 C; 1 G; 18 T; 0 other;

Query Match 1.6%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAA...AAAAA 1100
Db 18 TAAAAA...AAAAA 1

RESULT 117
AAQ75710/c
ID AAQ75710 standard; DNA; 21 BP.
XX
AC AAQ75710;
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX
XX JP06303997-A.
XX
PD 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-0112515.
XX
XX 16-APR-1993; 93JP-0112515.
XX
XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX

XX Analysis of cDNA and gene expression - by amplification of mRNA
PT followed by digestion with restriction enzymes
XX
XX Disclosure; Page 7; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC and a plural type of labelled reverse transcription primers
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
CC template for each reverse transcription primer; (b) digesting each of
CC the prepared aggregates of the double-stranded cDNAs with restriction
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC separate lanes. The method can be used to analyse gene expression
CC rapidly and easily.
XX
SQ Sequence 21 BP; 2 A; 1 C; 1 G; 17 T; 0 other;
Query Match 1.6%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1083 TAAAAAATAAAAAA 1100
| | | | | | | | | | | | | | | | | | | | | |
Db 18 TAAAAAATAAAAAA 1
RESULT 118
AAQ75715/c
ID AAQ75715 standard; DNA; 21 BP.
XX
AC AAQ75715;
XX
XX 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-0112515.
XX
PR 16-APR-1993; 93JP-0112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA
PT followed by digestion with restriction enzymes
XX
PS Disclosure; Page 8; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC and a plural type of labelled reverse transcription primers
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
CC template for each reverse transcription primer; (b) digesting each of
CC the prepared aggregates of the double-stranded cDNAs with restriction
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC separate lanes. The method can be used to analyse gene expression
CC rapidly and easily.
XX
SQ Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 other;
Query Match 1.6%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1083 TAAAAAATAAAAAA 1100
| | | | | | | | | | | | | | | | | | | | | |
Db 18 TAAAAAATAAAAAA 1
RESULT 120
AAQ75717/c
ID AAQ75717 standard; DNA; 21 BP.
XX
AC AAQ75717;
XX
XX 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1083 TAAAAAATAAAAAA 1100
| | | | | | | | | | | | | | | | | | | | | |
Db 18 TAAAAAATAAAAAA 1
RESULT 119
AAQ75716/c
ID AAQ75716 standard; DNA; 21 BP.
XX
AC AAQ75716;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-0112515.
XX
PR 16-APR-1993; 93JP-0112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA
PT followed by digestion with restriction enzymes
XX
PS Disclosure; Page 8; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC and a plural type of labelled reverse transcription primers
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
CC template for each reverse transcription primer; (b) digesting each of
CC the prepared aggregates of the double-stranded cDNAs with restriction
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC separate lanes. The method can be used to analyse gene expression
CC rapidly and easily.
XX
SQ Sequence 21 BP; 2 A; 1 C; 1 G; 17 T; 0 other;
Query Match 1.6%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1083 TAAAAAATAAAAAA 1100
| | | | | | | | | | | | | | | | | | | | | |
Db 18 TAAAAAATAAAAAA 1
RESULT 120
AAQ75717/c
ID AAQ75717 standard; DNA; 21 BP.
XX
AC AAQ75717;
XX
XX 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX

OS
XX
PN
XX
XX
PD
XX
PF
XX
PR
XX
XX
PA
XX
XX
DR
XX
PT
XX
PT
XX
PS
XX
XX
CC
CC
CC
CC
CC
CC
CC
CC
CC
CC
XX
SQ

Synthetic.
JP06303997-A.
01-NOV-1994.
16-APR-1993; 93JP-0112515.
16-APR-1993; 93JP-0112515.
(NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
WPI; 1995-018287/03.
Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes
Disclosure; Page 8; 11pp; Japanese.
A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in separate lanes. The method can be used to analyse gene expression rapidly and easily.
Sequence 21 BP; 1 A; 2 C; 1 G; 17 T; 0 other;
Query Match 1.6%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAAAAAAAAAAAAA 1100
|||
DB 18 TAAAAAAAAAAAAAAAAA 1

RESULT 122
AAQ75683/c
ID AAQ75683 standard; DNA; 21 BP.
XX
AC AAQ75683;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-0112515.
XX
PR 16-APR-1993; 93JP-0112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes
XX
PS Disclosure; Page 7; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in separate lanes. The method can be used to analyse gene expression rapidly and easily.
Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 other;
Query Match 1.6%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAAAAAAAAAAAAA 1100
|||
DB 18 TAAAAAAAAAAAAAAAAA 1

RESULT 121
AAQ75718/c
ID AAQ75718 standard; DNA; 21 BP.
XX
AC AAQ75718;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-0112515.
XX
PR 16-APR-1993; 93JP-0112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes
XX
PS Disclosure; Page 8; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an

OS
XX
PN
XX
XX
PD
XX
PF
XX
PR
XX
XX
PA
XX
XX
DR
XX
PT
XX
PT
XX
PS
XX
XX
CC
CC
CC
CC
CC
CC
CC
CC
CC
CC
XX
SQ

aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in separate lanes. The method can be used to analyse gene expression rapidly and easily.
Sequence 21 BP; 1 A; 2 C; 1 G; 17 T; 0 other;
Query Match 1.6%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAAAAAAAAAAAAA 1100
|||
DB 18 TAAAAAAAAAAAAAAAAA 1

RESULT 122
AAQ75683/c
ID AAQ75683 standard; DNA; 21 BP.
XX
AC AAQ75683;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-0112515.
XX
PR 16-APR-1993; 93JP-0112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes
XX
PS Disclosure; Page 7; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in separate lanes. The method can be used to analyse gene expression rapidly and easily.
Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 other;
Query Match 1.6%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAAAAAAAAAAAAA 1100
|||
DB 18 TAAAAAAAAAAAAAAAAA 1

RESULT 121
AAQ75718/c
ID AAQ75718 standard; DNA; 21 BP.
XX
AC AAQ75718;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-0112515.
XX
PR 16-APR-1993; 93JP-0112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes
XX
PS Disclosure; Page 8; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an

```

RESULT 123
AAQ75684/c
ID AAQ75684 standard; DNA; 21 BP.
XX AC AAQ75684;
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX KW aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-0112515.
XX PR 16-APR-1993; 93JP-0112515.
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX PT Analysis of cDNA and gene expression - by amplification of mRNA
    followed by digestion with restriction enzymes
XX PS Disclosure; Page 7; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an
    aggregate of double-stranded cDNAs by using an aggregate of mRNAs
    and a plural type of labelled reverse transcription primers
    (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
    template for each reverse transcription primer; (b) digesting each of
    the prepared aggregates of the double-stranded cDNAs with restriction
    enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
    separate lanes. The method can be used to analyse gene expression
    rapidly and easily.
XX SQ Sequence 21 BP; 2 A; 1 C; 0 G; 18 T; 0 other;
    Query Match 1.6%; Score 18; DB 1; Length 21;
    Best Local Similarity 100.0%; Pred. No. 1.5e+02;
    Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAA
Db 18 TAAAAA

RESULT 124
AAQ75685/c
ID AAQ75685 standard; DNA; 21 BP.
XX AC AAQ75685;
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX KW aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-0112515.

```

```

XX PR 16-APR-1993; 93JP-0112515.
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX PT Analysis of cDNA and gene expression - by amplification of mRNA
    followed by digestion with restriction enzymes
XX PS Disclosure; Page 7; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an
    aggregate of double-stranded cDNAs by using an aggregate of mRNAs
    and a plural type of labelled reverse transcription primers
    (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
    template for each reverse transcription primer; (b) digesting each of
    the prepared aggregates of the double-stranded cDNAs with restriction
    enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
    separate lanes. The method can be used to analyse gene expression
    rapidly and easily.
XX SQ Sequence 21 BP; 1 A; 1 C; 0 G; 19 T; 0 other;
    Query Match 1.6%; Score 18; DB 1; Length 21;
    Best Local Similarity 100.0%; Pred. No. 1.5e+02;
    Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAA
Db 18 TAAAAA

RESULT 125
AAQ75686/c
ID AAQ75686 standard; DNA; 21 BP.
XX AC AAQ75686;
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX KW aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-0112515.
XX PR 16-APR-1993; 93JP-0112515.
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX PT Analysis of cDNA and gene expression - by amplification of mRNA
    followed by digestion with restriction enzymes
XX PS Disclosure; Page 7; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an
    aggregate of double-stranded cDNAs by using an aggregate of mRNAs
    and a plural type of labelled reverse transcription primers
    (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
    template for each reverse transcription primer; (b) digesting each of
    the prepared aggregates of the double-stranded cDNAs with restriction
    enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
    separate lanes. The method can be used to analyse gene expression
    rapidly and easily.
XX SQ Sequence 21 BP; 1 A; 1 C; 0 G; 19 T; 0 other;
    Query Match 1.6%; Score 18; DB 1; Length 21;
    Best Local Similarity 100.0%; Pred. No. 1.5e+02;
    Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAA
Db 18 TAAAAA

```

```
CC rapidly and easily.
XX
SQ Sequence 21 BP; 1 A; 2 C; 0 G; 18 T; 0 other;

Query Match 1.6%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAATAAAAAAAAAA 1100
DB 18 TAAAAAATAAAAAAAAAA 1

RESULT 126
AAQ75687/c
ID AAQ75687 standard; DNA; 21 BP.
XX AC AAQ75687;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX
FN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-0112515.
XX
PR 16-APR-1993; 93JP-0112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA
followed by digestion with restriction enzymes
XX
PS Disclosure; Page 7; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an
aggregate of double-stranded cDNAs by using an aggregate of mRNAs
and a plural type of labelled reverse transcription primers
(GENESQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
template for each reverse transcription primer; (b) digesting each of
the prepared aggregates of the double-stranded cDNAs with restriction
enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
separate lanes. The method can be used to analyse gene expression
rapidly and easily.
XX
SQ Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 other;

Query Match 1.6%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAATAAAAAAAAAA 1100
DB 18 TAAAAAATAAAAAAAAAA 1

RESULT 127
AAQ75688/c
ID AAQ75688 standard; DNA; 21 BP.
XX AC AAQ75688;
XX
DT 04-AUG-1995 (first entry)
XX
```

```
XX Reverse transcription primer used in cDNA analysis technique.
DE
XX Analysis; gene expression; reverse transcription; primer; cDNA;
aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX
FN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-0112515.
XX
PR 16-APR-1993; 93JP-0112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA
followed by digestion with restriction enzymes
XX
PS Disclosure; Page 7; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an
aggregate of double-stranded cDNAs by using an aggregate of mRNAs
and a plural type of labelled reverse transcription primers
(GENESQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
template for each reverse transcription primer; (b) digesting each of
the prepared aggregates of the double-stranded cDNAs with restriction
enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
separate lanes. The method can be used to analyse gene expression
rapidly and easily.
XX
SQ Sequence 21 BP; 2 A; 1 C; 1 G; 17 T; 0 other;

Query Match 1.6%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAATAAAAAAAAAA 1100
DB 18 TAAAAAATAAAAAAAAAA 1

RESULT 128
AAQ75689/c
ID AAQ75689 standard; DNA; 21 BP.
XX AC AAQ75689;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX
FN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-0112515.
XX
PR 16-APR-1993; 93JP-0112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
```

PT Analysis of cDNA and gene expression - by amplification of mRNA
 PT followed by digestion with restriction enzymes
 PS Disclosure; Page 7; 11pp; Japanese.
 XX
 CC A method for the analysis of cDNA comprises (a) preparing an
 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
 CC and a plural type of labelled reverse transcription primers
 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
 CC template for each reverse transcription primer; (b) digesting each of
 CC the prepared aggregates of the double-stranded cDNAs with restriction
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
 CC separate lanes. The method can be used to analyse gene expression
 CC rapidly and easily.
 XX
 SQ Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 other;
 Query Match 1.6%; Score 18; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1083 TAAAAA1100
 DB 18 TAAAAA1100
 RESULT 129
 AAQ75690/c
 ID AAQ75690 standard; DNA; 21 BP.
 AC AAQ75690;
 XX
 DT 04-AUG-1995 (first entry)
 XX
 DE Reverse transcription primer used in cDNA analysis technique.
 DE Analysis; gene expression; reverse transcription; primer; cDNA;
 DE aggregate; restriction enzyme; ss.
 XX
 OS Synthetic.
 XX
 PN JP06303997-A.
 XX
 PD 01-NOV-1994.
 XX
 PF 16-APR-1993; 93JP-0112515.
 XX
 PR 16-APR-1993; 93JP-0112515.
 XX
 PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX
 DR WPI; 1995-018287/03.
 XX
 DE Reverse transcription primer used in cDNA analysis technique.
 DE Analysis; gene expression; reverse transcription; primer; cDNA;
 DE aggregate; restriction enzyme; ss.
 XX
 OS Synthetic.
 XX
 PN JP06303997-A.
 XX
 PD 01-NOV-1994.
 XX
 PF 16-APR-1993; 93JP-0112515.
 XX
 PR 16-APR-1993; 93JP-0112515.
 XX
 PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX
 DR WPI; 1995-018287/03.
 XX
 DE Analysis of cDNA and gene expression - by amplification of mRNA
 DE followed by digestion with restriction enzymes
 PS Disclosure; Page 7; 11pp; Japanese.
 XX
 CC A method for the analysis of cDNA comprises (a) preparing an
 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
 CC and a plural type of labelled reverse transcription primers
 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
 CC template for each reverse transcription primer; (b) digesting each of
 CC the prepared aggregates of the double-stranded cDNAs with restriction
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
 CC separate lanes. The method can be used to analyse gene expression
 CC rapidly and easily.
 XX
 SQ Sequence 21 BP; 1 A; 2 C; 1 G; 17 T; 0 other;
 Query Match 1.6%; Score 18; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAA1100
 DB 18 TAAAAA1100
 RESULT 130
 AAQ75671/c
 ID AAQ75671 standard; DNA; 21 BP.
 AC AAQ75671;
 XX
 DT 04-AUG-1995 (first entry)
 XX
 DE Reverse transcription primer used in cDNA analysis technique.
 DE Analysis; gene expression; reverse transcription; primer; cDNA;
 DE aggregate; restriction enzyme; ss.
 XX
 OS Synthetic.
 XX
 PN JP06303997-A.
 XX
 PD 01-NOV-1994.
 XX
 PF 16-APR-1993; 93JP-0112515.
 XX
 PR 16-APR-1993; 93JP-0112515.
 XX
 PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX
 DR WPI; 1995-018287/03.
 XX
 DE Analysis of cDNA and gene expression - by amplification of mRNA
 DE followed by digestion with restriction enzymes
 PS Disclosure; Page 7; 11pp; Japanese.
 XX
 CC A method for the analysis of cDNA comprises (a) preparing an
 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
 CC and a plural type of labelled reverse transcription primers
 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
 CC template for each reverse transcription primer; (b) digesting each of
 CC the prepared aggregates of the double-stranded cDNAs with restriction
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
 CC separate lanes. The method can be used to analyse gene expression
 CC rapidly and easily.
 XX
 SQ Sequence 21 BP; 1 A; 0 C; 2 G; 18 T; 0 other;
 Query Match 1.6%; Score 18; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1083 TAAAAA1100
 DB 18 TAAAAA1100
 RESULT 131
 AAQ75672/c
 ID AAQ75672 standard; DNA; 21 BP.
 AC AAQ75672;
 XX
 DT 04-AUG-1995 (first entry)
 XX
 DE Reverse transcription primer used in cDNA analysis technique.
 DE Analysis; gene expression; reverse transcription; primer; cDNA;
 DE aggregate; restriction enzyme; ss.
 XX
 OS Synthetic.

XX JP06303997-A.
 XX 01-NOV-1994.
 XX 16-APR-1993; 93JP-0112515.
 XX 16-APR-1993; 93JP-0112515.
 XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX WPI; 1995-018287/03.
 XX Analysis of cDNA and gene expression - by amplification of mRNA
 XX followed by digestion with restriction enzymes
 XX Disclosure; Page 7; 11pp; Japanese.
 XX A method for the analysis of cDNA comprises (a) preparing an
 XX aggregate of double-stranded cDNAs by using an aggregate of mRNAs
 XX and a plural type of labelled reverse transcription primers
 XX (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
 XX template for each reverse transcription primer; (b) digesting each of
 XX the prepared aggregates of the double-stranded cDNAs with restriction
 XX enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
 XX separate lanes. The method can be used to analyse gene expression
 XX rapidly and easily.
 XX Sequence 21 BP; 2 A; 0 C; 1 G; 18 T; 0 other;
 XX
 XX Query Match 1.6%; Score 18; DB 1; Length 21;
 XX Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 1083 TAAAAAATAAAAAAAAAA 1100
 XX 18 TAAAAAATAAAAAAAAAA 1
 XX
 XX RESULT 132
 XX AAQ75673/C
 XX ID AAQ75673 standard; DNA; 21 BP.
 XX AC AAQ75673;
 XX DT 04-AUG-1995 (first entry)
 XX DE Reverse transcription primer used in cDNA analysis technique.
 XX Analysis; gene expression; reverse transcription; primer; cDNA;
 XX aggregate; restriction enzyme; ss.
 XX Synthetic.
 XX JP06303997-A.
 XX 01-NOV-1994.
 XX 16-APR-1993; 93JP-0112515.
 XX 16-APR-1993; 93JP-0112515.
 XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX WPI; 1995-018287/03.
 XX Analysis of cDNA and gene expression - by amplification of mRNA
 XX followed by digestion with restriction enzymes
 XX Disclosure; Page 7; 11pp; Japanese.
 XX A method for the analysis of cDNA comprises (a) preparing an
 XX aggregate of double-stranded cDNAs by using an aggregate of mRNAs
 XX and a plural type of labelled reverse transcription primers
 XX (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
 XX template for each reverse transcription primer; (b) digesting each of
 XX the prepared aggregates of the double-stranded cDNAs with restriction
 XX enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
 XX separate lanes. The method can be used to analyse gene expression
 XX rapidly and easily.
 XX Sequence 21 BP; 2 A; 0 C; 1 G; 18 T; 0 other;
 XX
 XX Query Match 1.6%; Score 18; DB 1; Length 21;
 XX Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 1083 TAAAAAATAAAAAAAAAA 1100
 XX 18 TAAAAAATAAAAAAAAAA 1
 XX
 XX RESULT 132
 XX AAQ75673/C
 XX ID AAQ75673 standard; DNA; 21 BP.
 XX AC AAQ75673;
 XX DT 04-AUG-1995 (first entry)
 XX DE Reverse transcription primer used in cDNA analysis technique.
 XX Analysis; gene expression; reverse transcription; primer; cDNA;
 XX aggregate; restriction enzyme; ss.
 XX Synthetic.
 XX JP06303997-A.
 XX 01-NOV-1994.
 XX 16-APR-1993; 93JP-0112515.
 XX 16-APR-1993; 93JP-0112515.
 XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX WPI; 1995-018287/03.
 XX Analysis of cDNA and gene expression - by amplification of mRNA
 XX followed by digestion with restriction enzymes
 XX Disclosure; Page 7; 11pp; Japanese.
 XX A method for the analysis of cDNA comprises (a) preparing an
 XX aggregate of double-stranded cDNAs by using an aggregate of mRNAs

CC and a plural type of labelled reverse transcription primers
 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
 CC template for each reverse transcription primer; (b) digesting each of
 CC the prepared aggregates of the double-stranded cDNAs with restriction
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
 CC separate lanes. The method can be used to analyse gene expression
 CC rapidly and easily.
 CC Sequence 21 BP; 1 A; 0 C; 1 G; 19 T; 0 other;
 CC
 CC Query Match 1.6%; Score 18; DB 1; Length 21;
 CC Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 CC Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC QY 1083 TAAAAAATAAAAAAAAAA 1100
 CC 18 TAAAAAATAAAAAAAAAA 1
 CC
 CC RESULT 133
 CC AAQ75674/C
 CC ID AAQ75674 standard; DNA; 21 BP.
 CC AC AAQ75674;
 CC DT 04-AUG-1995 (first entry)
 CC DE Reverse transcription primer used in cDNA analysis technique.
 CC Analysis; gene expression; reverse transcription; primer; cDNA;
 CC aggregate; restriction enzyme; ss.
 CC Synthetic.
 CC JP06303997-A.
 CC 01-NOV-1994.
 CC 16-APR-1993; 93JP-0112515.
 CC 16-APR-1993; 93JP-0112515.
 CC (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 CC WPI; 1995-018287/03.
 CC Analysis of cDNA and gene expression - by amplification of mRNA
 CC followed by digestion with restriction enzymes
 CC Disclosure; Page 7; 11pp; Japanese.
 CC A method for the analysis of cDNA comprises (a) preparing an
 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
 CC and a plural type of labelled reverse transcription primers
 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
 CC template for each reverse transcription primer; (b) digesting each of
 CC the prepared aggregates of the double-stranded cDNAs with restriction
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
 CC separate lanes. The method can be used to analyse gene expression
 CC rapidly and easily.
 CC Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 other;
 CC
 CC Query Match 1.6%; Score 18; DB 1; Length 21;
 CC Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 CC Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC QY 1083 TAAAAAATAAAAAAAAAA 1100
 CC 18 TAAAAAATAAAAAAAAAA 1
 CC
 CC RESULT 134

AAQ30430/C
 ID AAQ30430 standard; DNA; 23 BP.
 AC AAQ30430;
 XX
 DT 25-MAR-2003 (updated)
 DT 07-DEC-1992 (first entry)
 XX
 DE Oligomer IL6803 for forming triplex with HUMIL6 target duplex.
 XX
 KW Human interleukin-6 gene; herpes simplex; AIDS; modified; HIV;
 KW RSV; HPV; malignancy; hepatitis; inflammation; ss.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT modified_base 1 /*tag= a
 FT /mod_base= OTHER
 FT /note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"
 FT modified_base 23
 FT /tag= b
 FT /mod_base= OTHER
 FT /note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"
 FT misc_feature 12..23
 FT /tag= c
 FT /label= inverted_polarity_region
 FT /note= "see comments"
 FT misc_feature 11..12
 FT /tag= d
 FT /note= "o-xyloso dimer synthon linkage"
 XX
 PN WO209705-A1.
 XX
 PD 11-JUN-1992.
 XX
 PF 25-NOV-1991; 91WO-US08811.
 XX
 PR 23-NOV-1990; 90US-0617907.
 PR 18-JAN-1991; 91US-0643382.
 PR 08-APR-1991; 91US-0683420.
 PR 17-APR-1991; 91US-0686544.
 PR 17-APR-1991; 91US-0686546.
 PR 17-APR-1991; 91US-0686547.
 PR 27-SEP-1991; 91US-0766733.
 XX
 PA (GILE-) GILEAD SCI INC.
 XX
 PI Froehler B, Krawczyk S, Matteucci MD, Milligan J;
 XX
 DR WPI; 1992-217083/26.
 XX
 FT New oligomers contg. modified bases - which form a triplex with
 FT G-C doublet in a DNA duplex, for treating and diagnosing HIV,
 FT hepatitis, herpes, malignancy and inflammation
 XX
 PS Claim 12; Page 71; 77pp; English.
 XX
 CC The synthetic oligomer is capable of forming a triplex at
 CC physiological pH with a purine rich target sequence by coupling
 CC into the major groove of the duplex. The specific target sequence
 CC of this oligomer is the human interleukin 6 gene untranslated
 CC sequence contg. a purine rich sequence concd. on one strand
 CC of the duplex. The oligomer, and others like it are useful in
 CC diagnosis and therapy of diseases characterised by specific DNA
 CC duplex targets, e.g. HPV, HIV, hepatitis B, herpes, malignant
 CC tumours and inflammation. The triple helices form under mild conditions
 CC thus assays may be carried out without subjecting the test specimen to
 CC harsh conditions. The oligomer contains an inverted polarity region
 CC formed from an o-xyloso dimer synthon. The linking gp. is o-xyloso
 CC (nucleotides have the 3' positions of xylose sugars linked via the o-
 CC xylene ring). Two nucleotides are coupled through a xylene residue
 CC to form the dimer synthon. This additional modifications may render

CC the oligomer stable to nuclease activity. The oligomer is able to
 CC inhibit gene expression, as verified by in vitro systems.
 CC See also AAQ25452-25501 and AAQ30296-448.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 23 BP; 2 A; 0 C; 0 G; 21 T; 0 other;
 Query Match 1.6%; Score 18; DB 1; Length 23;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1083 TAAAAAATAAAAAA 1100
 Db 23 TAAAAAATAAAAAA 6
 RESULT 135
 AAQ30431/C
 ID AAQ30431 standard; DNA; 23 BP.
 XX
 AC AAQ30431;
 XX
 DT 25-MAR-2003 (updated)
 DT 07-DEC-1992 (first entry)
 XX
 DE Oligomer IL6804 for forming triplex with HUMIL6 target duplex.
 XX
 KW Human interleukin-6 gene; herpes simplex; AIDS; modified; HIV;
 KW RSV; HPV; malignancy; hepatitis; inflammation; ss.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT modified_base 1 /*tag= a
 FT /mod_base= OTHER
 FT /note= "OTHER= N4 N4 ethanocytosine"
 FT modified_base 23
 FT /tag= b
 FT /mod_base= OTHER
 FT /note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"
 FT misc_feature 12..23
 FT /tag= c
 FT /label= inverted_polarity_region
 FT /note= "see comments"
 FT misc_feature 11..12
 FT /tag= d
 FT /note= "o-xyloso dimer synthon linkage"
 XX
 PN WO209705-A1.
 XX
 PD 11-JUN-1992.
 XX
 PF 25-NOV-1991; 91WO-US08811.
 XX
 PR 23-NOV-1990; 90US-0617907.
 PR 18-JAN-1991; 91US-0643382.
 PR 08-APR-1991; 91US-0683420.
 PR 17-APR-1991; 91US-0686544.
 PR 17-APR-1991; 91US-0686546.
 PR 17-APR-1991; 91US-0686547.
 PR 27-SEP-1991; 91US-0766733.
 XX
 PA (GILE-) GILEAD SCI INC.
 XX
 PI Froehler B, Krawczyk S, Matteucci MD, Milligan J;
 XX
 DR WPI; 1992-217083/26.
 XX
 FT New oligomers contg. modified bases - which form a triplex with
 FT G-C doublet in a DNA duplex, for treating and diagnosing HIV,
 FT hepatitis, herpes, malignancy and inflammation

comprising screening a DNA sample for the variant MLH1 or MSH2 gene where presence of the variant indicates presence of, or susceptibility to HNPCC; (2) a method of identifying mutants in splice donor or acceptor sites of a human MLH1 gene, comprising sequencing splice donor or acceptor sites of the gene with intronic primers for the human MLH1 gene and analysing the sequence to identify any mutants; (3) a method of identifying mutants in splice donor or acceptor sites of a human MSH2 gene, comprising sequencing splice donor or acceptor sites of the gene with intronic primers for the human MSH2 gene and analysing the sequence to identify any mutants; and (4) a transgenic model system for colorectal cancer comprising cells expressing the variant MLH1 or MSH2 gene. The MLH1 and MSH2 variants are used to diagnose or determine a patient's susceptibility to hereditary non-polypoidis colorectal cancer. ABL01648 to ABL01745 and ABL01746 to ABL01831 represent hMLH1 and hMSH2 gene fragments from the present invention. ABL01832 to ABL01839 represent mutagenic primers used in the exemplification of the present invention.

Sequence 23 BP; 21 A; 0 C; 1 G; 1 T; 0 other;

Query Match 1.6%; Score 18; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAA...AAAAA 1100
Db 2 TAAAAA...AAAAA 19

RESULT 137
AAV42215/c
ID AAV42215 standard; DNA; 25 BP.
XX AC AAV42215;
XX DT 16-OCT-1998 (first entry)
XX DE Sequencing primer used to exemplify the invention.
XX KW Incyte clone 1; fluorescent label; probe; primer; DNA sequencing; ss.
XX OS Synthetic.
XX PH Key Location/Qualifiers
FT modified_base 1 /tag= a
FT /note= "labelled with the donor carboxyfluorescein"
FT modified_base 7 /tag= b
FT /note= "optionally labelled with the acceptor 6-carboxyrhodamine"
FT modified_base 14 /tag= b
FT /note= "optionally labelled with the acceptor 6-carboxyrhodamine"
FT modified_base 17 /tag= b
FT /note= "optionally labelled with the acceptor 6-carboxyrhodamine"
FT modified_base 17 /tag= a
FT /note= "optionally labelled with the donor carboxyfluorescein"

WO9831834-A1.
23-JUL-1998.
12-DEC-1997; 97WO-US22914.
15-JAN-1997; 97US-0784162.
(INCY-) INCYTE PHARM INC.

Claim 12; Page 71; 77pp; English.

The synthetic oligomer is capable of forming a triplex at physiological pH with a purine rich target sequence by coupling into the major groove of the duplex. The specific target sequence of this oligomer is the human interleukin 6 gene untranslated sequence contg. a purine rich sequence concd. on one strand of the duplex. The oligomer, and others like it are useful in diagnosis and therapy of diseases characterised by specific DNA duplex targets, e.g. HPV, HER, HIV, hepatitis B, herpes, malignant tumours and inflammation. The triple helices form under mild conditions such assays may be carried out without subjecting the test specimen to harsh conditions. The oligomer contains an inverted polarity region formed from an o-xyloso dimer synthn. The linking gp. is o-xyloso (nucleotides have the 3'positions of xylose sugars linked via the o-xyloso ring). Two nucleotides are coupled through a xyloso residue to form the dimer synthn. This additional modification may render the oligomer stable to nuclease activity. The oligomer is able to inhibit gene expression, as verified by in vitro systems. See also AAQ25452-25501 and AAQ30226-448. (Updated on 25-MAR-2003 to correct PN field.)

Sequence 23 BP; 1 A; 1 C; 0 G; 21 T; 0 other;

Query Match 1.6%; Score 18; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAA...AAAAA 1100
Db 23 TAAAAA...AAAAA 6

RESULT 136
ABL01773
ID ABL01773 standard; DNA; 23 BP.
XX AC ABL01773;
XX DT 18-MAR-2002 (first entry)
XX DE Human MSH2 (hMSH2) intronic sequence SEQ ID NO:126.
XX KW Human; MLH1; MSH2; hMLH1; hMSH2; variant gene; diagnosis; HNPCC;
XX KW hereditary non-polypoidis colorectal cancer; ds.
XX OS Homo sapiens.
XX FN US2001049336-A1.
XX PD 22-NOV-2001.
XX PF 22-OCT-1999; 99US-0426548.
XX PR 22-OCT-1998; 98US-105180P.
XX PA (ROBB/) ROBBINS D.
XX PA (LING/) LIN-GOERKE J L.
XX PA (LING/) LING J C.
XX PI Robbins D, Lin-Goerke JL, Ling JC;
XX WPI; 2002-105577/14.
XX New variants of the human MLH1 and MSH2 genes for diagnosing or determining a predisposition for hereditary non-polypoidis colorectal cancer -
XX Disclosure; Page 4; 38pp; English.
XX The present invention describes a variant human MLH1 or MSH2 gene. Also described are: (1) a method for diagnosing or predicting susceptibility to hereditary non-polypoidis colorectal cancer (HNPCC),

XX Ju J;
PI XX
XX WPI; 1998-414127/35.
DR XX
XX Set of energy-transfer fluorescent labels with donor and acceptor at
PT different separations - useful for DNA sequencing allows use of
PT fewer analysing wavelengths or an increased throughput
PT XX
PS Example 1; Page 14; 30pp; English.

XX The present sequence exemplified the primer of the invention, and
CC is used to sequence Incyte clone 1 (AAV42737). The primer of the
CC invention is labelled with a set of at least 2 different fluorescent
CC labels. The set comprises an energy-transfer fluorescent label with at
CC least 1 each of a donor fluorophore and an acceptor fluorophore capable
CC of energy transfer, and separated by a distance x, and a second similar
CC fluorescent label in which the separation distance is y, x and y being
CC sufficiently different for the two fluorescent labels to produce
CC distinct fluorescent signals. Fluorescent labels are useful in
CC multicomponent analyses, e.g. as probes for fluorescent in situ
CC hybridisation or especially as primers for DNA sequencing.

XX Sequence 25 BP; 1 A; 1 C; 0 G; 23 T; 0 other;
SQ

Query Match 1.6%; Score 18; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+02; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 0;

Qy 1083 TAAAAAAAAAAAAAAA 1100
| | | | |
Db 24 TAAAAAAAAAAAAAAA 7

RESULT 138
AAX84259/c
ID AAX84259 standard; DNA; 25 BP.
XX
AC AAX84259;
XX
DT 08-SEP-1999 (first entry)
XX
DE PCR primer for human Nck associated protein 1 coding sequence.
XX
KW Nck associated protein 1; Napl; human; apoptosis; Alzheimer's disease;
KW therapy; PCR primer; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9931239-A1.
XX
PD 24-JUN-1999.
XX
PF 14-DEC-1998; 98WO-JF05646.
XX
PR 15-DEC-1997; 97JP-0363183.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
PA (SAKA/) SAKAKI Y.
XX
PI Sakaki Y;
XX
DR WPI; 1999-395181/33.

XX Protein inhibiting apoptosis, useful in the diagnosis and treatment
PT of Alzheimer's disease
PT
XX Disclosure; Page 76; 90pp; Japanese.

XX This sequence represents a PCR primer used to isolate DNA encoding the
CC human Nck associated protein 1 (Nap1) of the invention. Nap1 inhibits
CC apoptosis. The protein can be used in the investigation, diagnosis and
CC treatment.

```

Matches 17; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1082 TTAATAAAAAAAAAAAAAA 1100
Db :|||||
19 DKAAAAAAAAAAAAAAAAAAAA 1

RESULT 140
AAQ75744/c
ID AAQ75744 standard; DNA; 21 BP.
XX
AC AAQ75744;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
FN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-0112515.
XX
PR 16-APR-1993; 93JP-0112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA
PT followed by digestion with restriction enzymes
XX
PS Disclosure; Page 8; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC and a plural type of labelled reverse transcription primers
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
CC template for each reverse transcription primer; (b) digesting each of
CC the prepared aggregates of the double-stranded cDNAs with restriction
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC separate lanes. The method can be used to analyse gene expression
CC rapidly and easily.
XX
SQ Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 other;
WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA
PT followed by digestion with restriction enzymes
XX
PS Disclosure; Page 8; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC and a plural type of labelled reverse transcription primers
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
CC template for each reverse transcription primer; (b) digesting each of
CC the prepared aggregates of the double-stranded cDNAs with restriction
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC separate lanes. The method can be used to analyse gene expression
CC rapidly and easily.
XX
SQ Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 other;

Query Match 1.6%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1080 TATTAAAAAAAAAAAAAAAA 1100
Db :|||||
21 TACGAAAAAAAAAAAAAAAAAAAA 1

RESULT 141
AAQ75752/c
ID AAQ75752 standard; DNA; 21 BP.
XX
AC AAQ75752;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
FN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-0112515.
XX
PR 16-APR-1993; 93JP-0112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA
PT followed by digestion with restriction enzymes
XX
PS Disclosure; Page 9; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an

```

```

OS Synthetic.
XX
FN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-0112515.
XX
PR 16-APR-1993; 93JP-0112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA
PT followed by digestion with restriction enzymes
XX
PS Disclosure; Page 8; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC and a plural type of labelled reverse transcription primers
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
CC template for each reverse transcription primer; (b) digesting each of
CC the prepared aggregates of the double-stranded cDNAs with restriction
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC separate lanes. The method can be used to analyse gene expression
CC rapidly and easily.
XX
SQ Sequence 21 BP; 2 A; 1 C; 1 G; 17 T; 0 other;

Query Match 1.6%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1080 TATTAAAAAAAAAAAAAAAA 1100
Db :|||||
21 TCTGAAAAAAAAAAAAAAAAAAAA 1

RESULT 142
AAQ75792/c
ID AAQ75792 standard; DNA; 21 BP.
XX
AC AAQ75792;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
FN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-0112515.
XX
PR 16-APR-1993; 93JP-0112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA
PT followed by digestion with restriction enzymes
XX
PS Disclosure; Page 9; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an

```

CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
 CC and a plural type of labelled reverse transcription primers
 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
 CC template for each reverse transcription primer; (b) digesting each of
 CC the prepared aggregates of the double-stranded cDNAs with restriction
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
 CC separate lanes. The method can be used to analyse gene expression
 CC rapidly and easily.
 XX Sequence 21 BP; 1 A; 2 C; 0 G; 18 T; 0 other;
 SQ
 Query Match 1.6%; Score 17.8; DB 1; Length 21;
 Best Local Similarity 90.5%; Pred. NO. 1.6e+02;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1080 TATTAAAAA...AAAAA 1100
 DB 21 TAGGAAAAA...AAAAA 1
 RESULT 143
 AAQ75771/c
 ID AAQ75771 standard; DNA; 21 BP.
 AC AAQ75771;
 DT 04-AUG-1995 (first entry)
 DE Reverse transcription primer used in cDNA analysis technique.
 XX Analysis; gene expression; reverse transcription; primer; cDNA;
 XX aggregate; restriction enzyme; ss.
 XX Synthetic.
 XX JP06303997-A.
 XX 01-NOV-1994.
 XX 16-APR-1993; 93JP-0112515.
 XX 16-APR-1993; 93JP-0112515.
 XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX WPI; 1995-018287/03.
 XX Analysis of cDNA and gene expression - by amplification of mRNA
 XX followed by digestion with restriction enzymes
 XX Disclosure; Page 9; lipp; Japanese.
 XX A method for the analysis of cDNA comprises (a) preparing an
 XX aggregate of double-stranded cDNAs by using an aggregate of mRNAs
 XX and a plural type of labelled reverse transcription primers
 XX (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
 XX template for each reverse transcription primer; (b) digesting each of
 XX the prepared aggregates of the double-stranded cDNAs with restriction
 XX enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
 XX separate lanes. The method can be used to analyse gene expression
 XX rapidly and easily.
 XX Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 other;
 SQ
 Query Match 1.6%; Score 17.8; DB 1; Length 21;
 Best Local Similarity 90.5%; Pred. NO. 1.6e+02;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1079 CTATTAAAAA...AAAAA 1099
 DB 21 CTAGAAAAA...AAAAA 1

RESULT 144
 AAQ75776/c
 ID AAQ75776 standard; DNA; 21 BP.
 AC AAQ75776;
 DT 04-AUG-1995 (first entry)
 DE Reverse transcription primer used in cDNA analysis technique.
 XX Analysis; gene expression; reverse transcription; primer; cDNA;
 XX aggregate; restriction enzyme; ss.
 XX Synthetic.
 XX JP06303997-A.
 XX 01-NOV-1994.
 XX 16-APR-1993; 93JP-0112515.
 XX 16-APR-1993; 93JP-0112515.
 XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX WPI; 1995-018287/03.
 XX Analysis of cDNA and gene expression - by amplification of mRNA
 XX followed by digestion with restriction enzymes
 XX Disclosure; Page 9; lipp; Japanese.
 XX A method for the analysis of cDNA comprises (a) preparing an
 XX aggregate of double-stranded cDNAs by using an aggregate of mRNAs
 XX and a plural type of labelled reverse transcription primers
 XX (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
 XX template for each reverse transcription primer; (b) digesting each of
 XX the prepared aggregates of the double-stranded cDNAs with restriction
 XX enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
 XX separate lanes. The method can be used to analyse gene expression
 XX rapidly and easily.
 XX Sequence 21 BP; 1 A; 1 C; 0 G; 19 T; 0 other;
 SQ
 Query Match 1.6%; Score 17.8; DB 1; Length 21;
 Best Local Similarity 90.5%; Pred. NO. 1.6e+02;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1080 TATTAAAAA...AAAAA 1100
 DB 21 TAGGAAAAA...AAAAA 1
 RESULT 145
 AAQ75756/c
 ID AAQ75756 standard; DNA; 21 BP.
 AC AAQ75756;
 DT 04-AUG-1995 (first entry)
 DE Reverse transcription primer used in cDNA analysis technique.
 XX Analysis; gene expression; reverse transcription; primer; cDNA;
 XX aggregate; restriction enzyme; ss.
 XX Synthetic.
 XX JP06303997-A.
 XX 01-NOV-1994.
 XX 16-APR-1993; 93JP-0112515.

```

XX PR 16-APR-1993; 93JP-0112515.
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX PT Analysis of cDNA and gene expression - by amplification of mRNA
XX PT followed by digestion with restriction enzymes
XX PS Disclosure; Page 8; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an
XX CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
XX CC and a plural type of labelled reverse transcription primers
XX CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
XX CC template for each reverse transcription primer; (b) digesting each of
XX CC the prepared aggregates of the double-stranded cDNAs with restriction
XX CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
XX CC separate lanes. The method can be used to analyse gene expression
XX CC rapidly and easily.
XX SQ Sequence 21 BP; 3 A; 1 C; 0 G; 17 T; 0 other;
Query Match 1.6%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1080 TATTAAAAA 1100
DB 21 TTTGAAAAA 1
RESULT 146
AAQ75764/c
ID AAQ75764 standard; DNA; 21 BP.
AC AAQ75764;
XX 04-AUG-1995 (first entry)
XX Reverse transcription primer used in cDNA analysis technique.
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX Synthetic.
XX JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-0112515.
XX PR 16-APR-1993; 93JP-0112515.
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX PT Analysis of cDNA and gene expression - by amplification of mRNA
XX PT followed by digestion with restriction enzymes
XX PS Disclosure; Page 9; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an
XX CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
XX CC and a plural type of labelled reverse transcription primers
XX CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
XX CC template for each reverse transcription primer; (b) digesting each of
XX CC the prepared aggregates of the double-stranded cDNAs with restriction
XX CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
XX CC separate lanes. The method can be used to analyse gene expression
XX CC rapidly and easily.
XX SQ Sequence 21 BP; 3 A; 0 C; 1 G; 17 T; 0 other;
Query Match 1.6%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1080 TATTAAAAA 1100
DB 21 TTTGAAAAA 1
RESULT 146
AAQ75764/c
ID AAQ75764 standard; DNA; 21 BP.
AC AAQ75764;
XX 04-AUG-1995 (first entry)
XX Reverse transcription primer used in cDNA analysis technique.
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX Synthetic.
XX JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-0112515.
XX PR 16-APR-1993; 93JP-0112515.
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX PT Analysis of cDNA and gene expression - by amplification of mRNA
XX PT followed by digestion with restriction enzymes
XX PS Disclosure; Page 9; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an
XX CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
XX CC and a plural type of labelled reverse transcription primers
XX CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
XX CC template for each reverse transcription primer; (b) digesting each of
XX CC the prepared aggregates of the double-stranded cDNAs with restriction
XX CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
XX CC separate lanes. The method can be used to analyse gene expression

```

```

CC rapidly and easily.
XX SQ Sequence 21 BP; 2 A; 2 C; 0 G; 17 T; 0 other;
Query Match 1.6%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1080 TATTAAAAA 1100
DB 21 TTTGAAAAA 1
RESULT 147
AAQ75628/c
ID AAQ75628 standard; DNA; 21 BP.
XX AAQ75628;
XX 04-AUG-1995 (first entry)
XX Reverse transcription primer used in cDNA analysis technique.
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX Synthetic.
XX JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-0112515.
XX PR 16-APR-1993; 93JP-0112515.
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX PT Analysis of cDNA and gene expression - by amplification of mRNA
XX PT followed by digestion with restriction enzymes
XX PS Disclosure; Page 6; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an
XX CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
XX CC and a plural type of labelled reverse transcription primers
XX CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
XX CC template for each reverse transcription primer; (b) digesting each of
XX CC the prepared aggregates of the double-stranded cDNAs with restriction
XX CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
XX CC separate lanes. The method can be used to analyse gene expression
XX CC rapidly and easily.
XX SQ Sequence 21 BP; 3 A; 0 C; 1 G; 17 T; 0 other;
Query Match 1.6%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1080 TATTAAAAA 1100
DB 21 TTTGAAAAA 1
RESULT 148
AAQ75636/c
ID AAQ75636 standard; DNA; 21 BP.
XX AAQ75636;
XX 04-AUG-1995 (first entry)

```

XX Reverse transcription primer used in cDNA analysis technique.
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
XX JF06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-0112515.
XX
XX 16-APR-1993; 93JP-0112515.
XX
XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA
PT followed by digestion with restriction enzymes
XX
XX Disclosure; Page 6; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC and a plural type of labelled reverse transcription primers
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
CC template for each reverse transcription primer; (b) digesting each of
CC the prepared aggregates of the double-stranded cDNAs with restriction
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC separate lanes. The method can be used to analyse gene expression
CC rapidly and easily.
XX
XX Sequence 21 BP; 2 A; 1 C; 1 G; 17 T; 0 other;
SQ
Query Match 1.6%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1080 TATTAAAAA 1100
Db 21 TGTCAAAAAA 1
RESULT 149
AAQ75643/C
ID AAQ75643 standard; DNA; 21 BP.
XX
XX AAQ75643;
AC
XX
XX 04-AUG-1995 (first entry)
DT
XX
XX Reverse transcription primer used in cDNA analysis technique.
DE
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
XX Synthetic.
OS
XX
XX JF06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-0112515.
XX
XX 16-APR-1993; 93JP-0112515.
XX
XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA
PT followed by digestion with restriction enzymes
XX
XX Disclosure; Page 6; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC and a plural type of labelled reverse transcription primers
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
CC template for each reverse transcription primer; (b) digesting each of
CC the prepared aggregates of the double-stranded cDNAs with restriction
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC separate lanes. The method can be used to analyse gene expression
CC rapidly and easily.
XX
XX Sequence 21 BP; 2 A; 1 C; 1 G; 17 T; 0 other;
SQ
Query Match 1.6%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1080 TATTAAAAA 1100
Db 21 TGTCAAAAAA 1
RESULT 149
AAQ75643/C
ID AAQ75643 standard; DNA; 21 BP.
XX
XX AAQ75643;
AC
XX
XX 04-AUG-1995 (first entry)
DT
XX
XX Reverse transcription primer used in cDNA analysis technique.
DE
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
XX Synthetic.
OS
XX
XX JF06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-0112515.
XX
XX 16-APR-1993; 93JP-0112515.
XX
XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA
PT followed by digestion with restriction enzymes
XX
XX Disclosure; Page 6; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC and a plural type of labelled reverse transcription primers
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
CC template for each reverse transcription primer; (b) digesting each of
CC the prepared aggregates of the double-stranded cDNAs with restriction
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC separate lanes. The method can be used to analyse gene expression
CC rapidly and easily.
XX
XX Sequence 21 BP; 1 A; 0 C; 2 G; 18 T; 0 other;
SQ
Query Match 1.6%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

PT Analysis of cDNA and gene expression - by amplification of mRNA
PT followed by digestion with restriction enzymes
XX
XX Disclosure; Page 6; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC and a plural type of labelled reverse transcription primers
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
CC template for each reverse transcription primer; (b) digesting each of
CC the prepared aggregates of the double-stranded cDNAs with restriction
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC separate lanes. The method can be used to analyse gene expression
CC rapidly and easily.
XX
XX Sequence 21 BP; 1 A; 0 C; 2 G; 18 T; 0 other;
SQ

Query Match 1.6%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1079 CTATTAAAAA 1099
Db 21 CTCAAAAAA 1

RESULT 150
AAQ75616/C
ID AAQ75616 standard; DNA; 21 BP.
XX
XX AAQ75616;
AC
XX
XX 04-AUG-1995 (first entry)
DT
XX
XX Reverse transcription primer used in cDNA analysis technique.
DE
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
XX Synthetic.
OS
XX
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-0112515.
XX
XX 16-APR-1993; 93JP-0112515.
XX
XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA
PT followed by digestion with restriction enzymes
XX
XX Disclosure; Page 6; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC and a plural type of labelled reverse transcription primers
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
CC template for each reverse transcription primer; (b) digesting each of
CC the prepared aggregates of the double-stranded cDNAs with restriction
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC separate lanes. The method can be used to analyse gene expression
CC rapidly and easily.
XX
XX Sequence 21 BP; 1 A; 0 C; 2 G; 18 T; 0 other;
SQ

Query Match 1.6%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1080 TATTAAAAA 1100
 DB 21 TACCAAAAAA 1

RESULT 151
 AAQ75624/c
 ID AAQ75624 standard; DNA; 21 BP.
 AC AAQ75624;
 DT 04-AUG-1995 (first entry)
 DE Reverse transcription primer used in cDNA analysis technique.
 KW Analysis; gene expression; reverse transcription; primer; cDNA;
 KW aggregate; restriction enzyme; ss.
 OS Synthetic.
 XX JP06303997-A.
 XX 01-NOV-1994.
 XX 16-APR-1993; 93JP-0112515.
 XX 16-APR-1993; 93JP-0112515.
 XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX WPI; 1995-018287/03.
 XX Analysis of cDNA and gene expression - by amplification of mRNA
 XX followed by digestion with restriction enzymes
 XX Disclosure; Page 6; 11pp; Japanese.
 XX A method for the analysis of cDNA comprises (a) preparing an
 XX aggregate of double-stranded cDNAs by using an aggregate of mRNAs
 XX and a plural type of labelled reverse transcription primers
 XX (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
 XX template for each reverse transcription primer; (b) digesting each of
 XX the prepared aggregates of the double-stranded cDNAs with restriction
 XX enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
 XX separate lanes. The method can be used to analyse gene expression
 XX rapidly and easily.
 XX Sequence 21 BP; 2 A; 0 C; 2 G; 17 T; 0 other;
 XX WPI; 1995-018287/03.
 XX Analysis of cDNA and gene expression - by amplification of mRNA
 XX followed by digestion with restriction enzymes
 XX Disclosure; Page 6; 11pp; Japanese.
 XX A method for the analysis of cDNA comprises (a) preparing an
 XX aggregate of double-stranded cDNAs by using an aggregate of mRNAs
 XX and a plural type of labelled reverse transcription primers
 XX (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
 XX template for each reverse transcription primer; (b) digesting each of
 XX the prepared aggregates of the double-stranded cDNAs with restriction
 XX enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
 XX separate lanes. The method can be used to analyse gene expression
 XX rapidly and easily.
 XX Query Match 1.6%; Score 17.8; DB 1; Length 21;
 XX Best Local Similarity 90.5%; Pred. No. 1.6e+02;
 XX Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 XX QY 1080 TATTAAAAA 1100
 XX DB 21 TCTCAAAAAA 1

RESULT 152
 AAQ75664/c
 ID AAQ75664 standard; DNA; 21 BP.
 AC AAQ75664;
 DT 04-AUG-1995 (first entry)
 DE Reverse transcription primer used in cDNA analysis technique.
 KW Analysis; gene expression; reverse transcription; primer; cDNA;
 KW aggregate; restriction enzyme; ss.
 OS Synthetic.

XX JP06303997-A.
 XX 01-NOV-1994.
 XX 16-APR-1993; 93JP-0112515.
 XX 16-APR-1993; 93JP-0112515.
 XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX WPI; 1995-018287/03.
 XX Analysis of cDNA and gene expression - by amplification of mRNA
 XX followed by digestion with restriction enzymes
 XX Disclosure; Page 7; 11pp; Japanese.
 XX A method for the analysis of cDNA comprises (a) preparing an
 XX aggregate of double-stranded cDNAs by using an aggregate of mRNAs
 XX and a plural type of labelled reverse transcription primers
 XX (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
 XX template for each reverse transcription primer; (b) digesting each of
 XX the prepared aggregates of the double-stranded cDNAs with restriction
 XX enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
 XX separate lanes. The method can be used to analyse gene expression
 XX rapidly and easily.
 XX Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 other;
 XX Query Match 1.6%; Score 17.8; DB 1; Length 21;
 XX Best Local Similarity 90.5%; Pred. No. 1.6e+02;
 XX Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 XX QY 1080 TATTAAAAA 1100
 XX DB 21 TAGCAAAAAA 1

RESULT 153
 AAQ75648/c
 ID AAQ75648 standard; DNA; 21 BP.
 AC AAQ75648;
 DT 04-AUG-1995 (first entry)
 DE Reverse transcription primer used in cDNA analysis technique.
 KW Analysis; gene expression; reverse transcription; primer; cDNA;
 KW aggregate; restriction enzyme; ss.
 OS Synthetic.
 XX JP06303997-A.
 XX 01-NOV-1994.
 XX 16-APR-1993; 93JP-0112515.
 XX 16-APR-1993; 93JP-0112515.
 XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX WPI; 1995-018287/03.
 XX Analysis of cDNA and gene expression - by amplification of mRNA
 XX followed by digestion with restriction enzymes
 XX Disclosure; Page 6; 11pp; Japanese.
 XX A method for the analysis of cDNA comprises (a) preparing an
 XX aggregate of double-stranded cDNAs by using an aggregate of mRNAs

CC and a plural type of labelled reverse transcription primers
 CC (GENESEQ files AA075547-075798) and using the aggregate of mRNAs as the
 CC template for each reverse transcription primer; (b) digesting each of
 CC the prepared aggregates of the double-stranded cDNAs with restriction
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
 CC separate lanes. The method can be used to analyse gene expression
 CC rapidly and easily.
 XX
 SQ Sequence 21 BP; 1 A; 0 C; 1 G; 19 T; 0 other;

Query Match 1.6%; Score 17.8; DB 1; Length 21;
 Best Local Similarity 90.5%; Pred. No. 1.6e+02;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1080 TATTAAAAA...AAAAA 1100
 DB 21 TAACAAAAA...AAAAA 1

RESULT 154
 AAF32494/c
 ID AAF32494 standard; DNA; 21 BP.
 AC AAF32494;
 XX
 DT 19-APR-2001 (first entry)
 XX
 DE Human CD38 exon 4 PCR primer SEQ ID NO:9.
 XX
 KW Human; CD38; diabetes mellitus; detection; cyclic ADP-ribose; cADPR;
 KW PCR primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN JP2000316578-A.
 XX
 PD 21-NOV-2000.
 XX
 PF 12-MAY-1999; 99JP-0131955.
 XX
 PR 12-MAY-1999; 99JP-0131955.
 XX
 PA (BMLB-) BML KK.
 PA (KANE/) KANETSUKA A.
 PA (OKAM/) OKAMOTO H.
 XX
 DR WPI; 2001-128255/14.
 XX
 PT Detecting onset of diabetes mellitus comprises detecting specific gene
 PT mutations in the CD38 gene -
 XX
 PS Example; Page 6; 19pp; Japanese.
 XX

The present invention describes a method using a mutation in the CD38
 CC gene (involved in the production of cyclic ADP-ribose (cADPR)), to
 CC detect the onset of diabetes mellitus. The method is useful for
 CC detecting the onset of diabetes mellitus. The present sequence
 CC represents a PCR primer for human CD38, which is used in an example
 CC from the present invention.
 XX
 SQ Sequence 21 BP; 2 A; 10 C; 2 G; 7 T; 0 other;

Query Match 1.6%; Score 17.8; DB 1; Length 21;
 Best Local Similarity 90.5%; Pred. No. 1.6e+02;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 995 AAGTCGAGGCTGGAGATGG 1015
 DB 21 AAGACGAGGCTGGAGATGG 1

RESULT 155
 AAZ00877/c
 ID AAZ00877 standard; DNA; 24 BP.
 AC AAZ00877;
 XX
 DT 18-OCT-2001 (first entry)
 XX
 DE Human CCR4 related protein 31 PCR primer 2.
 XX
 KW Human; CCR4; cancer; HIV; Human immunodeficiency virus; infection;
 KW PCR primer; ss.

ID AAZ00877 standard; DNA; 24 BP.
 XX
 AC AAZ00877;
 XX
 DT 27-SEP-1999 (first entry)
 XX
 DE PCR primer PGRT32 for PGI coding sequence.
 XX
 KW PGI gene; biallelic marker; PCR primer; PGI-related biallelic marker;
 KW cancer; prostate cancer; diagnosis; therapy; prostate specific antigen;
 KW PSA; human; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO9932644-A2.
 XX
 PD 01-JUL-1999.
 XX
 PF 22-DEC-1998; 98WO-IB02133.
 XX
 PR 09-SEP-1998; 98US-0099658.
 PR 22-DEC-1997; 97US-0996306.
 XX
 PA (GEST) GENSET.
 XX
 PI Blumenfeld M, Bougueleret L, Chumakov I, Cohen D;
 XX
 DR WPI; 1999-405178/34.
 XX
 PT Use of a prostate cancer associated gene and biallelic markers
 PT derived from it
 XX
 PS Example 6; Page 42; 385pp; English.
 XX

The invention relates to a mammalian PGI gene and protein, and a set of
 CC PGI biallelic markers. The PGI polynucleotide and biallelic markers are
 CC used in a hybridisation assay, a sequencing assay, or in an
 CC allele-specific amplification assay for determining the identity of a
 CC nucleotide at a PGI-related biallelic marker. The methods can be used to
 CC detect and to assess the risk of developing cancer or prostate cancer.
 CC Early-stage diagnosis of prostate cancer relies on prostate specific
 CC antigen (PSA) dosage. However, the effectiveness of this is limited due
 CC to its inability to discriminate between malignant and non-malignant
 CC affections of the organ. A need exists for both a reliable diagnostic
 CC procedure which would enable early-stage diagnosis, and for preventative
 CC and curative treatments of the disease. The PGI gene can be used for
 CC detection of prostate cancer, and the risk of developing it in the
 CC future, and can also be used to determine therapies for the disease.
 XX
 SQ Sequence 24 BP; 3 A; 0 C; 1 G; 20 T; 0 other;

Query Match 1.6%; Score 17.8; DB 1; Length 24;
 Best Local Similarity 90.5%; Pred. No. 1.9e+02;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1080 TATTAAAAA...AAAAA 1100
 DB 23 TTTCAAAAAA...AAAAA 3

RESULT 156
 AAH75510/c
 ID AAH75510 standard; DNA; 24 BP.
 XX
 AC AAH75510;
 XX
 DT 18-OCT-2001 (first entry)
 XX
 DE Human CCR4 related protein 31 PCR primer 2.
 XX
 KW Human; CCR4; cancer; HIV; Human immunodeficiency virus; infection;
 KW PCR primer; ss.

```

XX OS Homo sapiens.
XX PN CNI296960-A.
XX PD 30-MAY-2001.
XX PF 22-NOV-1999; 99CN-0124049.
XX PR 22-NOV-1999; 99CN-0124049.
XX PA (SHAN-) SHANGHAI BORONG GENE DEV CO LTD.
XX PI Mao Y, Xie Y;
XX WPI; 2001-489558/54.
XX DR Polypeptide-human CCR4 related protein 31 and polynucleotide for coding
XX PT polypeptide, useful for treating e.g. cancer and HIV infection, is
XX FT prepared by DNA recombination -
XX PS Example 3; Page 17 (Disclosure); 34pp; Chinese.
XX CC The invention relates to human CCR4 related protein 31, the
XX CC polynucleotide encoding it and the use of the protein in treating
XX CC e.g. cancer and HIV infection. The present sequence is that of a human
XX CC CCR4 PCR primer of the invention.
XX SQ Sequence 24 BP; 3 A; 1 C; 2 G; 18 T; 0 other;
Query Match 1.6%; Score 17.8; DB 1; Length 24;
Best Local Similarity 90.5%; Pred. No. 1.9e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1080 TATTAATAAAAAAAAAAAAAA 1100
DB 22 TAATAATAAGAGAAAAA 2
RESULT 157
ABS54833
ID ABS54833 standard; DNA; 24 BP.
AC ABS54833;
XX 07-JAN-2003 (first entry)
XX Human fkbp 12.87 specific RT-PCR primer #1.
XX Human; ss; fkbp; 12.87; malignant tumour; haemopathy;
XX human immunodeficiency virus; HIV; infection; immunological disease;
XX inflammation; RT-PCR; primer; reverse transcription.
XX OS Homo sapiens.
XX CN1352169-A.
XX 05-JUN-2002.
XX 10-NOV-2000; 2000CN-0127372.
XX 10-NOV-2000; 2000CN-0127372.
XX (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX PI Mao Y, Xie Y;
XX WPI; 2002-714435/78.
XX New human fkbp protein 12.87 and encoding polynucleotide for treating
XX malignant tumors, hemopathy, human immunodeficiency virus infection,
XX immunological diseases and various inflammations -
XX
XX Example 2; Page 17 (disclosure); 33pp; Chinese.
XX This invention relates to the DNA and protein sequences of a novel human
XX fkbp protein 12.87. The invention also comprises a method for producing
XX the polypeptide by recombinant DNA technology. The polypeptide is
XX useful in treating malignant tumours, haemopathy, human immunodeficiency
XX virus infection, immunological diseases and various inflammations. Also
XX disclosed in the invention is an antagonist to the fkbp protein and
XX a method for its use. The present sequence represents a reverse
XX transcriptase (RT) PCR primer used to isolate the human fkbp 12.87
XX cDNA of the invention.
XX SQ Sequence 24 BP; 5 A; 0 C; 6 G; 13 T; 0 other;
Query Match 1.6%; Score 17.8; DB 1; Length 24;
Best Local Similarity 90.5%; Pred. No. 1.9e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 930 TTCAGGTTTGTATTATGAGT 950
DB 4 TTAAGGTTTATTATTATGAGT 24
RESULT 158
AAC96082/c
ID AAC96082 standard; DNA; 25 BP.
XX AAC96082;
XX 26-FEB-2001 (first entry)
XX 16s rRNA gene PCR primer #49.
XX DNA sequence analysis; sequencing; protein sequence; protein structure;
XX gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
XX human leukocyte antigen; PCR primer; ss.
XX OS Homo sapiens.
XX WO200065088-A2.
XX 02-NOV-2000.
XX 20-APR-2000; 2000WO-EP03636.
XX 26-APR-1999; 99EP-0303215.
XX (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX Ulfendahl P, Wong K;
XX WPI; 2000-679677/66.
XX Identifying extendible primers for use in identification, or
XX classification of a nucleic acid of an organism, allele or gene such as
XX class 1/2 HLA comprises identifying all possible nucleotide sequences
XX of specific length -
XX Claim 14; Page 45; 66pp; English.
XX The present invention provides a method for identifying a set of
XX extendible primers which can be used in the identification, typing and
XX classification of genes. This can then be used to predict protein
XX sequence and structure, in organ donation to match the organ with the
XX receiver, and to identify bacteria in a sample. The method can be used to
XX type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
XX particular.
XX SQ Sequence 25 BP; 5 A; 1 C; 3 G; 16 T; 0 other;
Query Match 1.6%; Score 17.8; DB 1; Length 25;
Best Local Similarity 90.5%; Pred. No. 2e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 1077 AACTATTAAAAA 1097
DB 21 ATCTCTTAAAAA 1

RESULT 159
AAT9286
ID AAT9286 standard; DNA; 24 BP.
XX
AC AAT9286;
XX
XX 15-APR-1998 (first entry)
XX
DE POLYA, a competitor oligonucleotide for binding human PUR-alpha.
XX
KW PUR element; human; c-myc; inhibitor; hyperproliferative disease; ss;
KW cancer; probe; hybridisation.
XX
OS Synthetic.
OS Homo sapiens.
PN US5672479-A.
XX
PD 30-SEP-1997.
XX
XX 07-JUN-1995; 95US-0486421.
XX
PR 06-JUN-1995; 95US-0470911.
PR 28-AUG-1992; 92US-0938189.
PR 02-FEB-1993; 93US-0014943.
PR 07-JUN-1995; 95US-0486421.
XX
XX (MOUN ) MOUNT SINAI SCHOOL MEDICINE.
XX
XX Bergemann AD, Johnson EM;
XX
XX WPI; 1997-488859/45.
XX
XX Assays for PUR protein ligands or modulators - using immobilised PUR
XX protein or fragments, to treat hyper-proliferative diseases, e.g.
XX cancer
XX
XX Examples; Column 33; 64pp; English.
XX
XX The oligonucleotides AAT9279-T99286 were used as competitor
XX oligonucleotides for the binding of PUR protein to DNA. The PUR sequence
XX can be used to identify chemical or biological compounds that bind to
XX PUR or binding fragments of PUR. Inhibitors of PUR activity may be
XX used to treat hyperproliferative diseases such as cancer.
XX
XX Sequence 24 BP; 24 A; 0 C; 0 G; 0 U; 0 other;
XX
XX Query Match 1.6%; Score 17.6; DB 1; Length 24;
XX Best Local Similarity 83.3%; Pred. No. 2e+02;
XX Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX QY 1077 AACTATTAAAAA 1100
XX DB 1 AAAAAA 24

RESULT 160
AAV31743
ID AAV31743 standard; DNA; 24 BP.
XX
AC AAV31743;
XX
XX 24-SEP-1998 (first entry)
XX
DE Nucleotide sequence of the oligonucleotide POLYA.
XX
KW PUR-alpha gene; inhibition; viral infection; cancer; PUR element;

```

```

KW hyperproliferative disease; ss.
XX
XX Synthetic.
XX
XX US5756684-A.
XX
XX 26-MAY-1998.
XX
XX 06-JUN-1995; 95US-0470911.
XX
XX 06-JUN-1995; 95US-0470911.
XX 28-AUG-1992; 92US-0938189.
XX 02-FEB-1993; 93US-0014943.
XX
XX (MOUN ) MOUNT SINAI SCHOOL MEDICINE.
XX
XX Bergemann AD, Johnson EM;
XX
XX WPI; 1998-321632/28.
XX
XX PUR protein and its fragments - that inhibit PUR protein binding to
XX PUR element or other proteins
XX
XX Example 7.1.1; Column 33; 63pp; English.
XX
XX This is the nucleotide sequence of an oligonucleotide used as a
XX competitor with the PUR element in the method of the invention,
XX involving the use of the PUR protein and its fragments, which inhibit
XX PUR protein binding to PUR element or other proteins. Inhibitors of
XX PUR activity may be useful for treating viral infections and
XX hyperproliferative diseases such as cancer.
XX
XX Sequence 24 BP; 24 A; 0 C; 0 G; 0 U; 0 other;
XX
XX Query Match 1.6%; Score 17.6; DB 1; Length 24;
XX Best Local Similarity 83.3%; Pred. No. 2e+02;
XX Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX QY 1077 AACTATTAAAAA 1100
XX DB 1 AAAAAA 24

RESULT 161
AAX04086
ID AAX04086 standard; DNA; 24 BP.
XX
XX AAX04086;
XX
XX 12-APR-1999 (first entry)
XX
XX Oligonucleotide POLYA used in PUR cloning and sequencing.
XX
XX PUR element; PUR-alpha; hyperproliferative disease; cancer; human;
XX monoclonal antibody; identification; characterisation; ss.
XX
XX Synthetic.
XX Homo sapiens.
XX
XX US5869622-A.
XX
XX 09-FEB-1999.
XX
XX 07-JUN-1995; 95US-0486809.
XX
XX 06-JUN-1995; 95US-0470911.
XX 28-AUG-1992; 92US-0938189.
XX 02-FEB-1993; 93US-0014943.
XX 07-JUN-1995; 95US-0486809.
XX
XX (MOUN ) MOUNT SINAI SCHOOL MEDICINE.
XX
XX Bergemann AD, Johnson EM;

```

```
XX WPI; 1999-152881/13.
XX Monoclonal antibody specific for PUR protein - useful for treating
XX cancer
XX
XX Example; Column 33; 64pp; English.
XX
XX The present invention describes a monoclonal antibody that specifically
XX binds to an epitope of the PUR protein. Antibodies that bind to the PUR
XX protein and neutralise PUR activity may be used to treat
XX hyperproliferative diseases such as cancer. PUR antibodies may be used
XX diagnostically to detect aberrant expression of the PUR protein and/or
XX mutations in the PUR gene. The present sequence represents an
XX oligonucleotide used in the cloning and sequencing of the PUR protein
XX and its sequence element PUR repeat, in an example from the present
XX invention.
XX
XX Sequence 24 BP; 24 A; 0 C; 0 G; 0 U; 0 other;
XX
XX Query Match 1.6%; Score 17.6; DB 1; Length 24;
XX Best Local Similarity 83.3%; Pred. No. 2e+02;
XX Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX QY 1077 AACTATTATAAAAAAAAAAAAAAAAA 1100
XX ||| ||||| ||||| ||||| |||||
XX Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 24
XX
XX RESULT 162
XX AAA40353/c
XX ID AAA40353 standard; DNA; 24 BP.
XX
XX AC AAA40353;
XX
XX DT 10-NOV-2000 (first entry)
XX DE pBluescriptSK+ phagemid primer SEQ ID NO: 3.
XX
XX KW Primer; cloning; ligation; ss.
XX
XX OS Synthetic.
XX
XX PN WO200036088-A1.
XX
XX PD 22-JUN-2000.
XX
XX PF 17-DEC-1999; 99WO-US30277.
XX
XX PR 17-DEC-1998; 98US-0213834.
XX
XX PA (ROMA/) ROMANTCHIKOV Y.
XX
XX PI Romantchikov Y;
XX
XX OS WPI; 2000-442381/38.
XX
XX PN Inserting a nucleic acid into a circular vector comprising joining
XX their ends, melting, and reannealing ends at two different
XX concentrations, useful for cloning small amounts of nucleic acids and
XX forming genomic libraries -
XX
XX PS Example 1; Page 66; 71pp; English.
XX
XX CC This invention describes a novel method (M1) for inserting a nucleic
XX acid (N1) into a circular vector (V1) comprising joining ends of N1 and
XX V1 under a first nucleic acid concentration, melting hybridized cohesive
XX circularization ends, and reannealing the ends at a second
XX concentration. The methods are useful for the cloning small amounts of
XX nucleic acids and forming genomic libraries of complex populations of
XX or cDNA. The methods allow the cloning of minute amounts of nucleic acids
XX efficiently and avoids the size selection problems of prior art systems.
XX Larger nucleic acid fragments are just as easily cloned, allowing highly
XX representative libraries to be made. Vector to vector ligation is
XX avoided using the methods. AAA40351-A40366 represents primers used to
XX illustrate the method of the invention.
XX
XX SQ Sequence 24 BP; 0 A; 0 C; 0 G; 0 U; 0 other;
```

```
CC representative libraries to be made. Vector to vector ligation is
CC avoided using the methods. AAA40351-A40366 represents primers used to
CC illustrate the method of the invention.
XX
XX SQ Sequence 24 BP; 0 A; 0 C; 0 G; 0 U; 0 other;
XX
XX Query Match 1.6%; Score 17.6; DB 1; Length 24;
XX Best Local Similarity 83.3%; Pred. No. 2e+02;
XX Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX QY 1077 AACTATTATAAAAAAAAAAAAAAAAA 1100
XX ||| ||||| ||||| ||||| |||||
XX Db 24 AAAAAAAAAAAAAAAAAAAAAAAAAA 1
XX
XX RESULT 163
XX AAA40359/c
XX ID AAA40359 standard; RNA; 24 BP.
XX
XX AC AAA40359;
XX
XX DT 10-NOV-2000 (first entry)
XX DE pBluescriptSK+ phagemid primer SEQ ID NO: 9.
XX
XX KW Primer; cloning; ligation; ss.
XX
XX OS Synthetic.
XX
XX PN WO200036088-A1.
XX
XX PD 22-JUN-2000.
XX
XX PF 17-DEC-1999; 99WO-US30277.
XX
XX PR 17-DEC-1998; 98US-0213834.
XX
XX PA (ROMA/) ROMANTCHIKOV Y.
XX
XX PI Romantchikov Y;
XX
XX OS WPI; 2000-442381/38.
XX
XX PN Inserting a nucleic acid into a circular vector comprising joining
XX their ends, melting, and reannealing ends at two different
XX concentrations, useful for cloning small amounts of nucleic acids and
XX forming genomic libraries -
XX
XX PS Example 3; Page 67; 71pp; English.
XX
XX CC This invention describes a novel method (M1) for inserting a nucleic
XX acid (N1) into a circular vector (V1) comprising joining ends of N1 and
XX V1 under a first nucleic acid concentration, melting hybridized cohesive
XX circularization ends, and reannealing the ends at a second
XX concentration. The methods are useful for the cloning small amounts of
XX nucleic acids and forming genomic libraries of complex populations of
XX or cDNA. The methods allow the cloning of minute amounts of nucleic acids
XX efficiently and avoids the size selection problems of prior art systems.
XX Larger nucleic acid fragments are just as easily cloned, allowing highly
XX representative libraries to be made. Vector to vector ligation is
XX avoided using the methods. AAA40351-A40366 represents primers used to
XX illustrate the method of the invention.
XX
XX SQ Sequence 24 BP; 0 A; 0 C; 0 G; 0 U; 0 other;
```

```
XX Query Match 1.6%; Score 17.6; DB 1; Length 24;
XX Best Local Similarity 83.3%; Pred. No. 2e+02;
XX Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX QY 1077 AACTATTATAAAAAAAAAAAAAAAAA 1100
XX ||| ||||| ||||| ||||| |||||
XX Db 24 AAAAAAAAAAAAAAAAAAAAAAAAAA 1
```

```

RESULT 164
ID AAF99304/c
XX AAF99304 standard; DNA; 24 BP.
AC AAF99304;
XX
DT 12-JUN-2001 (first entry)
XX
XX Immunostimulatory nucleic acid #420.
DE
XX Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
KW immunostimulatory; tumour; viral infection; bacterial infection;
KW fungal infection; parasitic infection; cancer; asthma;
KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.
XX
OS Synthetic.
XX
XX WO200122972-A2.
PN
XX
XX 05-APR-2001.
PD
XX
XX 25-SEP-2000; 2000WO-US26383.
PF
XX
XX 25-SEP-1999; 99US-0156113.
PR
XX 27-SEP-1999; 99US-0156135.
PR
XX 23-AUG-2000; 2000US-0227436.
PR
XX
XX (IOWA ) UNIV IOWA RES FOUND.
PA (COLE-) COLEY PHARM GMBH.
PA
XX Krieg AM, Schetter C, Vollmer J;
PI WPI; 2001-273485/28.
XX
XX Vaccinating against tumors, infectious diseases, allergies and asthma
PT using immunostimulatory Py-rich and TG nucleic acids -
PT
XX Claim 101; Page 46; 338pp; English.
PS
XX The present invention relates to a method for stimulating an immune
CC response. The method comprises administering an immunostimulatory nucleic
CC acid to a non-rodent subject in sufficient quantity to stimulate an
CC immune response. The present sequence is one such immunostimulatory
CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
CC haemophilus, campylobacter, clostridium, Escherichia coli and/or
CC staphylococcus), fungal antigens and/or parasitic antigens. The method is
CC also useful for preventing cancer, asthma, infectious disease, allergy or
CC immune deficiency. The present sequence can also be used to redirect a
CC Th2 to a Th1 immune response and to activate immune cells.
CC Note: the present sequence may have a phosphorothioate backbone.
XX
XX Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 other;
SQ
Query Match 1.6%; Score 17.6; DB 1; Length 24;
Best Local Similarity 83.3%; Pred. No. 2e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1077 AACTATTATTAATAAAAAAAAAAAAAA 1100
DB 24 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 165
ID AAF99756/c
XX AAF99756 standard; DNA; 24 BP.
AC AAF99756;
XX
XX 12-JUN-2001 (first entry)
DT
XX
XX Immunostimulatory nucleic acid #873.
DE
XX Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
KW immunostimulatory; tumour; viral infection; bacterial infection;
KW fungal infection; parasitic infection; cancer; asthma;
KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.
XX
OS Synthetic.
XX
XX WO200122972-A2.
PN
XX
XX 05-APR-2001.
PD
XX
XX 25-SEP-2000; 2000WO-US26383.
PF
XX
XX 25-SEP-1999; 99US-0156113.
PR
XX 27-SEP-1999; 99US-0156135.
PR
XX 23-AUG-2000; 2000US-0227436.
PR
XX
XX (IOWA ) UNIV IOWA RES FOUND.
PA (COLE-) COLEY PHARM GMBH.
PA
XX Krieg AM, Schetter C, Vollmer J;
PI WPI; 2001-273485/28.
XX
XX Vaccinating against tumors, infectious diseases, allergies and asthma
PT using immunostimulatory Py-rich and TG nucleic acids -
PT
XX Claim 101; Page 46; 338pp; English.
PS
XX The present invention relates to a method for stimulating an immune
CC response. The method comprises administering an immunostimulatory nucleic
CC acid to a non-rodent subject in sufficient quantity to stimulate an
CC immune response. The present sequence is one such immunostimulatory
CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
CC haemophilus, campylobacter, clostridium, Escherichia coli and/or
CC staphylococcus), fungal antigens and/or parasitic antigens. The method is
CC also useful for preventing cancer, asthma, infectious disease, allergy or
CC immune deficiency. The present sequence can also be used to redirect a
CC Th2 to a Th1 immune response and to activate immune cells.
CC Note: the present sequence may have a phosphorothioate backbone.
XX
XX Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 other;
SQ
Query Match 1.6%; Score 17.6; DB 1; Length 24;
Best Local Similarity 83.3%; Pred. No. 2e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1077 AACTATTATTAATAAAAAAAAAAAAAA 1100
DB 24 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 166
ID AAF99757
XX AAF99757 standard; DNA; 24 BP.
AC AAF99757;
XX
XX 12-JUN-2001 (first entry)
DT
XX
XX Immunostimulatory nucleic acid #873.
DE
XX Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
KW immunostimulatory; tumour; viral infection; bacterial infection;
KW fungal infection; parasitic infection; cancer; asthma;
KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.
XX

```

```
OS Synthetic.
XX
PN WO200122972-A2.
XX
XX 05-APR-2001.
XX
XX 25-SEP-2000; 2000WO-US26383.
XX
XX 25-SEP-1999; 99US-0156113.
PR 27-SEP-1999; 99US-0156135.
PR 23-AUG-2000; 2000US-0227436.
XX
XX (IOWA ) UNIV IOWA RES FOUND.
PA (COLE-) COLEY PHARM GMBH.
XX
XX Krieg AM, Schetter C, Vollmer J;
XX
XX WPI; 2001-273485/28.
XX
XX Vaccinating against tumors, infectious diseases, allergies and asthma
PT using immunostimulatory Py-rich and TG nucleic acids -
XX
XX Claim 101; Page 57; 338pp; English.
XX
XX The present invention relates to a method for stimulating an immune
CC response. The method comprises administering an immunostimulatory nucleic
CC acid to a non-rodent subject in sufficient quantity to stimulate an
CC immune response. The present sequence is one such immunostimulatory
CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
CC against tumor antigens, viral antigens (e.g. herpesviridae, retroviridae
CC and/or thymoxoviridae), bacterial antigens (e.g. toxoplasma,
CC haemophilus, campylobacter, clostridium, Escherichia coli and/or
CC staphylococcus), fungal antigens and/or parasitic antigens. The method is
CC also useful for preventing cancer, asthma, infectious disease, allergy or
CC immune deficiency. The present sequence can also be used to redirect a
CC Th2 to a Th1 immune response and to activate immune cells.
CC Note: the present sequence may have a phosphorothioate backbone.
XX
XX Sequence 24 BP; 24 A; 0 C; 0 G; 0 U; 0 other;
SQ
Query Match 1.6%; Score 17.6; DB 1; Length 24;
Best Local Similarity 83.3%; Pred. No. 2e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1077 AACTATTAAAAA 1100
Db 1 AAAAAAAAAAAAAAAAAAAAAA 24
RESULT 167
ABV14842/c
ID ABV14842 standard; cDNA; 24 BP.
XX
XX ABV14842;
XX
XX 13-SEP-2002 (first entry)
DE Human prostate expression marker cDNA 14833.
XX
XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
XX pharmacogenomic marker; gene; ss.
XX Homo sapiens.
XX
XX WO200160860-A2.
PN
XX 23-AUG-2001.
XX
XX 20-FEB-2001; 2001WO-US05171.
XX
XX 17-FEB-2000; 2000US-183319P.
PR 16-MAR-2000; 2000US-189862P.
XX
```

```
PR 25-MAY-2000; 2000US-207454P.
PR 09-JUN-2000; 2000US-211314P.
PR 18-JUL-2000; 2000US-219007P.
PR 13-DEC-2000; 2000US-255281P.
XX
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
PA
XX Schlegel R, Endege WO, Monahan JB;
PI
XX WPI; 2001-662795/76.
XX
XX Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer -
XX
XX Claim 1; Page 2483; 11750pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;
CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX
XX Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 other;
SQ
Query Match 1.6%; Score 17.6; DB 1; Length 24;
Best Local Similarity 83.3%; Pred. No. 2e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1077 AACTATTAAAAA 1100
Db 24 AAAAAAAAAAAAAAAAAAAAAA 1
RESULT 168
ABS77949/c
ID ABS77949 standard; DNA; 24 BP.
XX
XX ABS77949;
XX
XX 13-DEC-2002 (first entry)
DT
XX
XX Angiogenesis inhibitory oligonucleotide #433.
DE
XX
XX Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
XX tumour metastasis; precancerous lesion; rheumatoid arthritis;
XX psoriasis; diabetic retinopathy; retinopathy of prematurity; glaucoma;
XX macular degeneration; corneal graft rejection; neovascular glaucoma;
XX retrolental fibroplasia; rubeosis; Osler-Webber Syndrome;
XX myocardial angiogenesis; plaque neovascularisation; telangiectasia;
XX haemophilic joint; angiofibroma; wound granulation;
XX intestinal adhesion; atherosclerosis; scleroderma; hypertrophic scar.
XX
XX Synthetic.
XX
XX WO200253141-A2.
PN
XX 11-JUL-2002.
XX
XX 14-DEC-2001; 2001WO-US48458.
XX
XX 14-DEC-2000; 2000US-255534P.
XX
```

one antiangiogenic nucleic acid molecule to the subject -

PT
XX
XX
PS Claim 2; Page 36; 276pp; English.
XX
CC The invention relates to inhibiting angiogenesis in a subject, comprising
CC administering at least one antiangiogenic nucleic acid molecule.
CC Also included is a kit comprising a first container housing the
CC antiangiogenic nucleic acids, and instructions for administering them to
CC a subject having a condition characterised by unwanted angiogenesis.
CC The method is useful for inhibiting angiogenesis associated with solid
CC tumour growth, tumour metastasis, precancerous lesion, rheumatoid
CC arthritis, psoriasis, diabetic retinopathy, retinopathy of prematurity,
CC macular degeneration, corneal graft rejection, neovascular glaucoma,
CC retrolental fibroplasia, rubeosis, Osler-Weber Syndrome, myocardi
CC angiogenesis, plaque neovascularisation, telangiectasia, haemophilic
CC joints, angiofibroma, wound granulation, intestinal adhesions,
CC atherosclerosis, scleroderma and hypertrophic scars. The present
CC sequence is an antiangiogenic nucleic acid of the invention.
XX
SQ Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 other;

Query Match 1.6%; Score 17.6; DB 1; Length 24;
Best Local Similarity 83.3%; Pred. No. 2e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0

QY 1077 AACTATTAAAAA
DB 24 AAAAAA
RESULT 170
ABS78478
ID ABS78478 standard; DNA; 24 BP.
XX
AC ABS78478;
XX
XX 13-DEC-2002 (first entry)
XX
DE Angiogenesis inhibitory oligonucleotide #962.
XX
XX Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
XX tumour metastasis; precancerous lesion; rheumatoid arthritis;
XX psoriasis; diabetic retinopathy; retinopathy of prematurity;
XX macular degeneration; corneal graft rejection; neovascular glaucoma;
XX retrolental fibroplasia; rubeosis; Osler-Weber Syndrome;
XX myocardial angiogenesis; plaque neovascularisation; telangiectasia;
XX haemophilic joint; angiofibroma; wound granulation;
XX intestinal adhesion; atherosclerosis; scleroderma; hypertrophic scar.
XX
OS Synthetic.
XX
XX WO200253141-A2.
XX
XX 11-JUL-2002.
XX
XX 14-DEC-2001; 2001WO-US48458.
XX
XX 14-DEC-2000; 2000US-255534P.
XX
XX (COLE-) COLEY PHARM GROUP INC.
XX
XX Bratzler RL;
XX
XX WPI; 2002-566690/60.
XX
XX Inhibiting angiogenesis in a subject, involves administering at least
XX one antiangiogenic nucleic acid molecule to the subject -
XX
XX Claim 2; Page 36; 276pp; English.
XX
XX The invention relates to inhibiting angiogenesis in a subject, comprising
XX administering at least one antiangiogenic nucleic acid molecule.
XX Also included is a kit comprising a first container housing the
XX antiangiogenic nucleic acids, and instructions for administering them to
XX a subject having a condition characterised by unwanted angiogenesis.
XX The method is useful for inhibiting angiogenesis associated with solid
XX tumour growth, tumour metastasis, precancerous lesion, rheumatoid
XX arthritis, psoriasis, diabetic retinopathy, retinopathy of prematurity,
XX macular degeneration, corneal graft rejection, neovascular glaucoma,
XX retrolental fibroplasia, rubeosis, Osler-Weber Syndrome, myocardi
XX angiogenesis, plaque neovascularisation, telangiectasia, haemophilic
XX joints, angiofibroma, wound granulation, intestinal adhesions,
XX atherosclerosis, scleroderma and hypertrophic scars. The present
XX sequence is an antiangiogenic nucleic acid of the invention.
XX
SQ Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 other;

Query Match 1.6%; Score 17.6; DB 1; Length 24;
Best Local Similarity 83.3%; Pred. No. 2e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1077 AACTATTAAAAA
DB 24 AAAAAA
RESULT 169
ABS78477/c
ID ABS78477 standard; DNA; 24 BP.
XX
AC ABS78477;
XX
XX 13-DEC-2002 (first entry)
XX
DE Angiogenesis inhibitory oligonucleotide #961.
XX
XX Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
XX tumour metastasis; precancerous lesion; rheumatoid arthritis;
XX psoriasis; diabetic retinopathy; retinopathy of prematurity;
XX macular degeneration; corneal graft rejection; neovascular glaucoma;
XX retrolental fibroplasia; rubeosis; Osler-Weber Syndrome;
XX myocardial angiogenesis; plaque neovascularisation; telangiectasia;
XX haemophilic joint; angiofibroma; wound granulation;
XX intestinal adhesion; atherosclerosis; scleroderma; hypertrophic scar.
XX
OS Synthetic.
XX
XX WO200253141-A2.
XX
XX 11-JUL-2002.
XX
XX 14-DEC-2001; 2001WO-US48458.
XX
XX 14-DEC-2000; 2000US-255534P.
XX
XX (COLE-) COLEY PHARM GROUP INC.
XX
XX Bratzler RL;
XX
XX WPI; 2002-566690/60.
XX
XX Inhibiting angiogenesis in a subject, involves administering at least
XX one antiangiogenic nucleic acid molecule to the subject -
XX
XX Claim 2; Page 36; 276pp; English.
XX
XX The invention relates to inhibiting angiogenesis in a subject, comprising
XX administering at least one antiangiogenic nucleic acid molecule.
XX Also included is a kit comprising a first container housing the
XX antiangiogenic nucleic acids, and instructions for administering them to
XX a subject having a condition characterised by unwanted angiogenesis.
XX The method is useful for inhibiting angiogenesis associated with solid
XX tumour growth, tumour metastasis, precancerous lesion, rheumatoid
XX arthritis, psoriasis, diabetic retinopathy, retinopathy of prematurity,
XX macular degeneration, corneal graft rejection, neovascular glaucoma,
XX retrolental fibroplasia, rubeosis, Osler-Weber Syndrome, myocardi
XX angiogenesis, plaque neovascularisation, telangiectasia, haemophilic
XX joints, angiofibroma, wound granulation, intestinal adhesions,
XX atherosclerosis, scleroderma and hypertrophic scars. The present
XX sequence is an antiangiogenic nucleic acid of the invention.
XX
SQ Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 other;

Query Match 1.6%; Score 17.6; DB 1; Length 24;
Best Local Similarity 83.3%; Pred. No. 2e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1077 AACTATTAAAAA
DB 24 AAAAAA
RESULT 169
ABS78477/c
ID ABS78477 standard; DNA; 24 BP.
XX
AC ABS78477;
XX
XX 13-DEC-2002 (first entry)
XX
DE Angiogenesis inhibitory oligonucleotide #961.
XX
XX Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
XX tumour metastasis; precancerous lesion; rheumatoid arthritis;
XX psoriasis; diabetic retinopathy; retinopathy of prematurity;
XX macular degeneration; corneal graft rejection; neovascular glaucoma;
XX retrolental fibroplasia; rubeosis; Osler-Weber Syndrome;
XX myocardial angiogenesis; plaque neovascularisation; telangiectasia;
XX haemophilic joint; angiofibroma; wound granulation;
XX intestinal adhesion; atherosclerosis; scleroderma; hypertrophic scar.
XX
OS Synthetic.
XX
XX WO200253141-A2.
XX
XX 11-JUL-2002.
XX
XX 14-DEC-2001; 2001WO-US48458.
XX
XX 14-DEC-2000; 2000US-255534P.
XX
XX (COLE-) COLEY PHARM GROUP INC.
XX
XX Bratzler RL;
XX
XX WPI; 2002-566690/60.
XX
XX Inhibiting angiogenesis in a subject, involves administering at least
XX one antiangiogenic nucleic acid molecule to the subject -
XX
XX Claim 2; Page 36; 276pp; English.
XX
XX The invention relates to inhibiting angiogenesis in a subject, comprising
XX administering at least one antiangiogenic nucleic acid molecule.
XX Also included is a kit comprising a first container housing the
XX antiangiogenic nucleic acids, and instructions for administering them to
XX a subject having a condition characterised by unwanted angiogenesis.
XX The method is useful for inhibiting angiogenesis associated with solid
XX tumour growth, tumour metastasis, precancerous lesion, rheumatoid
XX arthritis, psoriasis, diabetic retinopathy, retinopathy of prematurity,
XX macular degeneration, corneal graft rejection, neovascular glaucoma,
XX retrolental fibroplasia, rubeosis, Osler-Weber Syndrome, myocardi
XX angiogenesis, plaque neovascularisation, telangiectasia, haemophilic
XX joints, angiofibroma, wound granulation, intestinal adhesions,
XX atherosclerosis, scleroderma and hypertrophic scars. The present
XX sequence is an antiangiogenic nucleic acid of the invention.
XX
SQ Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 other;

Query Match 1.6%; Score 17.6; DB 1; Length 24;
Best Local Similarity 83.3%; Pred. No. 2e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1077 AACTATTAAAAA
DB 24 AAAAAA
RESULT 169
ABS78477/c
ID ABS78477 standard; DNA; 24 BP.
XX
AC ABS78477;
XX
XX 13-DEC-2002 (first entry)
XX
DE Angiogenesis inhibitory oligonucleotide #961.
XX
XX Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
XX tumour metastasis; precancerous lesion; rheumatoid arthritis;
XX psoriasis; diabetic retinopathy; retinopathy of prematurity;
XX macular degeneration; corneal graft rejection; neovascular glaucoma;
XX retrolental fibroplasia; rubeosis; Osler-Weber Syndrome;
XX myocardial angiogenesis; plaque neovascularisation; telangiectasia;
XX haemophilic joint; angiofibroma; wound granulation;
XX intestinal adhesion; atherosclerosis; scleroderma; hypertrophic scar.
XX
OS Synthetic.
XX
XX WO200253141-A2.
XX
XX 11-JUL-2002.
XX
XX 14-DEC-2001; 2001WO-US48458.
XX
XX 14-DEC-2000; 2000US-255534P.
XX
XX (COLE-) COLEY PHARM GROUP INC.
XX
XX Bratzler RL;
XX
XX WPI; 2002-566690/60.
XX
XX Inhibiting angiogenesis in a subject, involves administering at least
XX one antiangiogenic nucleic acid molecule to the subject -
XX
XX Claim 2; Page 36; 276pp; English.
XX
XX The invention relates to inhibiting angiogenesis in a subject, comprising
XX administering at least one antiangiogenic nucleic acid molecule.
XX Also included is a kit comprising a first container housing the
XX antiangiogenic nucleic acids, and instructions for administering them to
XX a subject having a condition characterised by unwanted angiogenesis.
XX The method is useful for inhibiting angiogenesis associated with solid
XX tumour growth, tumour metastasis, precancerous lesion, rheumatoid
XX arthritis, psoriasis, diabetic retinopathy, retinopathy of prematurity,
XX macular degeneration, corneal graft rejection, neovascular glaucoma,
XX retrolental fibroplasia, rubeosis, Osler-Weber Syndrome, myocardi
XX angiogenesis, plaque neovascularisation, telangiectasia, haemophilic
XX joints, angiofibroma, wound granulation, intestinal adhesions,
XX atherosclerosis, scleroderma and hypertrophic scars. The present
XX sequence is an antiangiogenic nucleic acid of the invention.
XX
SQ Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 other;

Query Match 1.6%; Score 17.6; DB 1; Length 24;
Best Local Similarity 83.3%; Pred. No. 2e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1077 AACTATTAAAAA
DB 24 AAAAAA
RESULT 169
ABS78477/c
ID ABS78477 standard; DNA; 24 BP.
XX
AC ABS78477;
XX
XX 13-DEC-2002 (first entry)
XX
DE Angiogenesis inhibitory oligonucleotide #961.
XX
XX Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
XX tumour metastasis; precancerous lesion; rheumatoid arthritis;
XX psoriasis; diabetic retinopathy; retinopathy of prematurity;
XX macular degeneration; corneal graft rejection; neovascular glaucoma;
XX retrolental fibroplasia; rubeosis; Osler-Weber Syndrome;
XX myocardial angiogenesis; plaque neovascularisation; telangiectasia;
XX haemophilic joint; angiofibroma; wound granulation;
XX intestinal adhesion; atherosclerosis; scleroderma; hypertrophic scar.
XX
OS Synthetic.
XX
XX WO20025314

CC antiangiogenic nucleic acids, and instructions for administering them to
 CC a subject having a condition characterised by unwanted angiogenesis.
 CC The method is useful for inhibiting angiogenesis associated with solid
 CC tumour growth, tumour metastasis, precancerous lesion, rheumatoid
 CC arthritis, psoriasis, diabetic retinopathy, retinopathy of prematurity,
 CC macular degeneration, corneal graft rejection, neovascular glaucoma,
 CC retrolental fibroplasia, rubeosis, Osler-Webber Syndrome, myocardial
 CC angiogenesis, plaque neovascularisation, telangiectasia, haemophilic
 CC joints, angiofibroma, wound granulation, intestinal adhesions,
 CC atherosclerosis, scleroderma and hypertrophic scars. The present
 CC sequence is an antiangiogenic nucleic acid of the invention.

XX
 SQ Sequence 24 BP; 24 A; 0 C; 0 G; 0 U; 0 other;

Query Match 1.6%; Score 17.6; DB 1; Length 24;
 Best Local Similarity 83.3%; Pred. No. 2e+02;
 Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1077 AACTATTAAAAA 1100
 ||| |||||
 Db 1 AAAAAAAAAA 24

RESULT 171
 ABA98840
 ID ABA98840 standard; DNA; 24 BP.
 AC ABA98840;
 DT 01-JUL-2002 (first entry)
 DE A24 oligonucleotide for the creation of Pc-A24.
 DE Component detection; clinical diagnosis; cell detection; drug detection;
 KW metabolite detection; pesticide detection; ligand detection; ss.
 XX Synthetic.

Key Location/Qualifiers
 modified_base 24
 /*tag= a
 /label= OTHER
 /note= "modified by PO2OCH2CH2CH2SSCH2CH2CH2OH"
 WO200184157-A2.
 08-NOV-2001.
 03-MAY-2001; 2001WO-US14528.
 04-MAY-2000; 2000US-0564230.
 (DADE-) DADE BEHRING INC.

Pease JS, Cromer R, Patel R, Kurn N, De Keczzer S;
 WPI; 2002-164078/21.
 Detection of multiple analytes, e.g. ligands, receptors,
 polynucleotides and pollutants, involves adding a combination of
 sensitizer reagents and reactive reagent actuatable by a product of the
 sensitizer reagents -
 Examples; Page 58; 87pp; English.

The invention relates to the detection of multiple components in a
 medium, comprising combining the medium with at least two sensitizer
 reagents, and at least one reactive reagent activated by a product
 generated by the sensitizer reagents when activated; and differentially
 activating the sensitizer reagents. The combination of sensitizer
 reagents and reactive reagent(s) allows differential detection of the
 components. Methods of the invention may be used for the detection of
 ligands, receptors and polynucleotides, and also for the detection of

CC e.g. cells, various drugs, metabolites, pesticides (e.g.
 CC polyhalogenated biphenyls, phosphate esters, thiophosphates, carbamates
 CC and polyhalogenated sulfenamides) and pollutants. Methods of the
 CC invention allow the detection of multiple analytes in a single test
 CC medium. An application of the methods of the present invention would be
 CC in the field of clinical diagnostics. The current sequence represents
 CC A24 oligonucleotide for the creation of oligonucleotide coated
 CC phthalocyanine sensitizer particles (Pc-A24).

XX
 SQ Sequence 24 BP; 24 A; 0 C; 0 G; 0 U; 0 other;

Query Match 1.6%; Score 17.6; DB 1; Length 24;
 Best Local Similarity 83.3%; Pred. No. 2e+02;
 Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1077 AACTATTAAAAA 1100
 ||| |||||
 Db 1 AAAAAAAAAA 24

RESULT 172
 AAS17869
 ID AAS17869 standard; DNA; 24 BP.
 AC AAS17869;
 DT 08-MAY-2002 (first entry)
 DE A24 oligonucleotide used to create doPTAR chemiluminescer particles.
 DE Polymorphism detection; sequence detection; mutation detection; A24;
 KW probe; non-dissociative termolecular complex; doPTAR sensitizer particle;
 KW single nucleotide polymorphism; SNP; ss.
 XX Synthetic.

Key Location/Qualifiers
 modified_base 24
 /*tag= a
 /note= "A is covalently linked to a
 PO2OCH2CH2CH2SSCH2CH2CH2OH moiety"
 WO200190399-A2.
 29-NOV-2001.
 17-MAY-2001; 2001WO-US16089.
 19-MAY-2000; 2000US-0574596.
 (DADE-) DADE BEHRING INC.

Patel RD;
 WPI; 2002-097664/13.
 Detecting presence of polynucleotide, differences between
 polynucleotide sequences, useful for detecting single nucleotide
 polymorphism and alleles of polynucleotide sequence involves use of
 three competitive probes -
 Examples; Page 47; 75pp; English.

This invention represents a method for detecting the presence of a
 polynucleotide sequence, differences in polynucleotide sequences or
 mutations in genomic DNA. The method involves contacting
 oligonucleotide probes with a sample containing a polynucleotide.
 The first probe hybridises to a region of the polynucleotide sequence
 and the second and third probes can bind a second region of the
 polynucleotide sequence. The second and third probes are identical
 except for the presence or difference of one or more nucleotides. The
 reaction medium is then subjected to conditions for forming substantially
 non-dissociative termolecular complexes, which can be at least one of,

the polynucleotide sequence with the first and second probes or the polynucleotide sequence with the first and third probes. The oligonucleotide probes have labels non-covalently bound to allow for their detection upon binding. The method of the invention is useful for detecting the presence of a single nucleotide polymorphism (SNP) in a fragment of genomic DNA. The method can be used for the direct detection of nucleic acid in very small quantities without amplification. In addition, the method may be carried out with amplification. In and reference sequences. This sequence represents an oligonucleotide probe A24 used to create dotPCR chimiluminescer sensitizer particles the method of the invention. Binding the nucleic acid to a suspendable particle acts as a support and provides a means of segregating the bound polynucleotide target from the bulk solution

Sequence 24 BP; 24 A; 0 C; 0 G; 0 U; 0 other;

Query Match 1.6%; Score 17.6; DB 1; Length 24;
Best Local Similarity 83.3%; Pred. No. 2e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1077 AACTATTAAAAA 1100
Db 1 AAAAAA 24

RESULT 173
ABK15639/C
ID ABK15639 standard; DNA; 24 BP.

AC ABK15639;

DT 08-MAY-2002 (first entry)

DE RNA-PCR procedure primer poly(dT)24.

RNA-PCR; primer; ss; poly(dT)24; cytostatic; antibacterial; gene therapy;
RNA-cDNA hybrid; gene function inhibition; cancer; PTGS; antisense;
high throughput screening; D-RNAi; DNA-RNA interference; RDRP;
RNA dependent RNA polymerase; posttranscriptional gene silencing.
Synthetic.

WO200210374-A2.

07-FEB-2002.

02-AUG-2001; 2001WO-US24412.

02-AUG-2000; 2000US-222479P.

(UYSC-) UNIV SOUTHERN CALIFORNIA.

Lin S, Chuong C, Widelitz RB;

WPI; 2002-188740/24.

Generating mRNA-cDNA hybrids for suppressing cancer-related genes, or treating or preventing microbe related genes, comprises thermocycling steps of promoter-linked double-stranded cDNA or RNA synthesis

Example 5; Page 26; 53pp; English.

The invention relates to generating mRNA-cDNA hybrids, comprising (a) providing a solution containing a nucleic acid template, one or more primers complementary to the sense conformation of the nucleic acid template, and one or more promoter-linked primers complementary to the antisense conformation of the nucleic acid template, and with an RNA promoter, (b) treating the nucleic acid template with the one of more primers to synthesise a first cDNA strand, (c) treating the first cDNA strand with one or more promoter-linked primers to synthesise a promoter-linked double-stranded nucleic acid, (d) treating the promoter-linked double-stranded nucleic acid to synthesise amplified mRNA fragments and (e) treating the mRNA fragments with one or more primers to synthesise

mRNA-cDNA hybrids by reverse transcription of the amplified mRNA fragments. The method is useful for preparing high amounts of pure and specific mRNA-cDNA hybrids for transducing biological effects of interest in vitro as well as in vivo, for inhibiting gene function in prokaryotes and eukaryotes in vivo and in vitro, for suppressing cancer-related genes, in treating or preventing microbe related genes, in studying candidate molecular pathways with systematic knock out of involved molecules, in high throughput screening of gene functions based on microarray analysis, and as a tool in studying gene function in physiological conditions. The mRNA-cDNA hybrids may be used to screen for special gene functions, for manipulating gene expression in vitro, and for designing therapy for genetic diseases in vivo. The cDNA part of a D-RNAi (DNA-RNA interference) can be modified by nucleotide analogue incorporation to increase the stability and effectiveness of transcribed probe activities. The RDRP (RNA dependent RNA polymerase) enzyme may provide higher affinity of the mRNA template of a D-RNAi compared to ds-RNA due to lower binding interaction between DNA-RNA duplexes than RNA-RNA duplexes. The cDNA part of a D-RNAi provides further antisense gene knockout activity in addition to the posttranscriptional gene silencing (PTGS) mechanisms of the sense-RNA template, resulting in multiple specific gene interference effects with one probe. The present sequence is a poly(dT) PCR primer used in conjunction with oligo(dC)10N primers to reverse transcribe mRNA into first strand cDNA in the method of the invention.

Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 other;

Query Match 1.6%; Score 17.6; DB 1; Length 24;
Best Local Similarity 83.3%; Pred. No. 2e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1077 AACTATTAAAAA 1100
Db 24 AAAAAA 1

RESULT 174
ABL39405/C

ID ABL39405 standard; DNA; 24 BP.

AC ABL39405;

16-APR-2002 (first entry)

Immunostimulatory nucleic acid SEQ ID NO: 841.

Antibody-induced cell lysis; cancer; immunostimulatory; CD20;
angiogenesis; metastasis; cytostatic; phosphorothioate backbone; ss.
Synthetic.

Key Location/Qualifiers
modified_base 1..24
/*tag= a
/mod_base= OTHER
/note= "phosphorothioate backbone"

WO200197843-A2.

27-DEC-2001.

22-JUN-2001; 2001WO-US20154.

22-JUN-2000; 2000US-213346P.

(IOWA) UNIV IOWA RES FOUND.

Weiner G, Hartmann G;

WPI; 2002-154611/20.

Treating or preventing cancer, such as basal cell carcinoma, comprises administering immunostimulatory nucleic acids that induce expression of

PT cell surface antigens and antibodies to a subject having or at risk of
PT developing cancer -

PS Disclosure; Page 309; 312pp; English.

XX The present invention relates to methods for treating or preventing
CC cancer, involving administering to a subject having or at risk of
CC developing cancer immunostimulatory nucleic acids that induce expression
CC of cell surface antigens and antibodies. The methods are useful for
CC treating or preventing cancer such as basal cell carcinoma, bladder
CC cancer, bone cancer, brain and central nervous system (CNS) cancer,
CC breast cancer, cervical cancer, colon and rectum cancer, connective
CC tissue cancer, oesophageal cancer, eye cancer, kidney cancer, larynx
CC cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma,
CC non-Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian
CC cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin
CC cancer, stomach cancer, testicular cancer, and uterine cancer. The
CC present sequence is an immunostimulatory oligonucleotide described in
CC the exemplification of the invention.

XX Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 other;

Query Match 1.6%; Score 17.6; DB 1; Length 24;
Best Local Similarity 83.3%; Pred. No. 2e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1077 AACTATTATTAATAAAAAAAAAAAAA 1100
Db 24 AAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 175

ACAS8802/C
ID ACAS8802 standard; DNA; 24 BP.

XX ACAS8802;

XX 10-JUN-2003 (first entry)

DE Gastric ulcer treatment immunostimulatory nucleic acid #148.

XX Gastric ulcer; ss; immunostimulant; equine gastric ulcer syndrome; EGUS;
KW Helicobacter pylori.

XX Synthetic.

XX US2002198165-A1.

XX 26-DEC-2002.

XX 01-AUG-2001; 2001US-0920313.

XX 01-AUG-2000; 2000US-222248P.

XX (BRAT/) BRATZLER R L.
PA (PETE/) PETERSEN D M.

XX Bratzler RL, Petersen DM;

XX WPI; 2003-370798/35.

XX Prevention or treatment of gastric ulcer involves administering nucleic
PT acid -

PS Disclosure; Page 14; 45pp; English.

XX The invention relates to a method of prevention or treatment of gastric
CC ulcer comprising administering a nucleic acid to a subject in need for
CC treatment of gastric ulcer. A nucleic acid sample comprising
CC oligonucleotide 2006 was administered to a mouse model by an oral route
CC or a vehicle control. Colonisation of mice by Helicobacter pylori was
CC assessed at time points from 1 day to 1 month after treatment. The
CC ability of the nucleic acid to reduce H. pylori colonisation was

CC assessed. The method is useful for preventing or treating a gastric ulcer
CC on a subject e.g. human or non-human vertebrate animal including dog,
CC cat, horse (equine gastric ulcer syndrome, EGUS), cow, goat, sheep, pig,
CC rabbit, turkey, chicken, primate, rat and mouse. The method effectively
CC treats or prevents gastric ulcers. The present sequence represents an
CC immunostimulatory nucleic acid for the treatment of gastric ulcers.

XX Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 other;

Query Match 1.6%; Score 17.6; DB 1; Length 24;
Best Local Similarity 83.3%; Pred. No. 2e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1077 AACTATTATTAATAAAAAAAAAAAAA 1100
Db 24 AAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 176

ABZ80181/C
ID ABZ80181 standard; DNA; 24 BP.

XX ABZ80181;

XX 23-MAY-2003 (first entry)

DE Immunostimulatory oligonucleotide SEQ ID NO:53.

XX Immunostimulation; immune response; natural killer cell; interferon;
KW type 1 interferon; IFN; cancer; infectious disease; allergic disorder;
KW immune related disorder; ss.

XX Synthetic.

XX Key Location/Qualifiers
FH modified_base 1..24

FT /*tag= a

FT /mod_base= OTHER

FT /note= "optionally phosphorothioate backbone"

XX WO2003015711-A2.

XX 27-FEB-2003.

XX 19-AUG-2002; 2002WO-US26468.

XX 17-AUG-2001; 2001US-313273P.

XX 03-JUL-2002; 2002US-393952P.

XX (COLE-) COLEY PHARM GROUP INC.

XX (COLE-) COLEY PHARM GMBH.

XX (IOWA) UNIV IOWA RES FOUND.

XX Krieg AM, Vollmer J, Uihman E;

XX WPI; 2003-268241/26.

XX New immunostimulatory nucleic acid, useful for preparing a composition
PT for treating an allergic condition -

XX Example 1; Page 44; 115pp; English.

XX The present invention describes immunostimulatory nucleic acids of 14-100
CC nucleotides in length comprising the formula 5' X1DCGHX2 3' (1), where X1
CC or X2 = independently any sequence 0-10 nucleotides; D = nucleotide other
CC than C; C = cytosine; G = guanine; H = nucleotide other than G. The
CC immunostimulatory nucleic acid further comprises a sequence consisting of
CC P and N positioned immediately 5' to X1 or 3' to X2 and N is a B cell
CC neutralising sequence, where N begins with a CGG trinucleotide and is at
CC least 10 nucleotides long and P is GC-rich palindromic containing sequence
CC at least 10 nucleotides long. Also described: (1) a pharmaceutical
CC composition comprising the immunostimulatory nucleic acid and a carrier;
CC and (2) treating an allergic condition. (1) has anti-allergic activity and

CC can be used in gene therapy. (I) can be used for preparing a composition
 CC for treating a variety of immune related disorders such as cancer,
 CC infectious diseases and allergic disorders. (I) also stimulates the
 CC activation of natural killer cells and the production of type 1
 CC interferon (IFN). The present sequence represents an immunostimulatory
 CC oligonucleotide, which is used in an example from the present invention.
 XX
 SQ Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 other;

Query Match 1.6%; Score 17.6; DB 1; Length 24;
 Best Local Similarity 83.3%; Pred. No. 2e+02;
 Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1077 AACTATTAAAAA 1100
 DB 24 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 177
 AAQ95960/c
 ID AAQ95960 standard; DNA; 25 BP.
 XX
 AC AAQ95960;
 XX
 DT 06-FEB-1996 (first entry)
 XX
 DE Oligonucleotide biotin-T25 for novel nucleic acid immobilisation method.
 XX
 KW Immobilisation; solid support; salt; cationic detergent; capture probe;
 KW hybridisation; primer; template-dependent extension; target organism;
 KW sequencing; genetic polymorphism; ss.
 XX
 OS Synthetic.

Key Location/Qualifiers
 misc_feature 1
 /*tag= a
 /*note= "biotinylated"

W09515970-A1.
 15-JUN-1995.
 06-DEC-1994; 94WO-US14096.
 16-NOV-1994; 94US-0341148.
 06-DEC-1993; 93US-0162397.
 (MOLE-) MOLECULAR TOOL INC.
 Knapp MR, Nikiforov T;
 WPI; 1995-224282/29.
 Immobilising synthetic nucleic acid on solid support - by incubation
 in presence of salt or cationic detergent, for use in hybridisation
 assays, sequencing and analysis of polymorphism
 Example 1; Page 18; 61pp; English.

Oligonucleotides AAQ95959-82 are examples of oligonucleotides used in a
 novel method of immobilising oligonucleotides to a solid support by
 incubating in the presence of a salt or cationic detergent e.g. NaCl
 (50-250 mM, pH 6.0-8.0) or 1-ethyl-3-(3'-dimethyl amino propyl)-1,3
 carbodiimide hydrochloride (EDC). The oligonucleotides can be capture
 probes for detection of specific nucleic acids by hybridisation or can
 be primers for template-dependent extension from the immobilised primers
 on nucleic acid from a target organism. The method can be used in
 hybridisation assays, sequencing and analysis of genetic polymorphism.
 Sequence 25 BP; 0 A; 0 C; 0 G; 25 T; 0 other;

Query Match 1.6%; Score 17.6; DB 1; Length 25;

Best Local Similarity 83.3%; Pred. No. 2.1e+02;
 Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1077 AACTATTAAAAA 1100
 DB 25 AAAAAAAAAAAAAAAAAAAAAA 2

RESULT 178
 AAX84260/c
 ID AAX84260 standard; DNA; 25 BP.
 XX
 AC AAX84260;
 XX
 DT 08-SEP-1999 (first entry)
 XX
 DE PCR primer for human Nck associated protein 1 coding sequence.
 XX
 KW Nck associated protein 1; Napi; human; apoptosis; Alzheimer's disease;
 KW therapy; PCR primer; ss.

OS Synthetic.
 OS Homo sapiens.
 XX
 PN W09931239-A1.
 XX
 PD 24-JUN-1999.
 XX
 PF 14-DEC-1998; 98WO-JP05646.
 XX
 PR 15-DEC-1997; 97JP-0363183.
 XX
 PA (KYOW) KYOWA HAKKO KOGYO KK.
 PA (SAKA/) SAKAKI Y.
 PI Sakaki Y;
 XX
 DR WPI; 1999-395181/33.

Protein inhibiting apoptosis, useful in the diagnosis and treatment
 of Alzheimer's disease
 Disclosure; Page 77; 90pp; Japanese.

This sequence represents a PCR primer used to isolate DNA encoding the
 human Nck associated protein 1 (Napi) of the invention. Napi inhibits
 apoptosis. The protein can be used in the investigation, diagnosis and
 treatment (e.g. by gene therapy) of Alzheimer's disease.

Sequence 25 BP; 0 A; 1 C; 0 G; 24 T; 0 other;

Query Match 1.6%; Score 17.6; DB 1; Length 25;
 Best Local Similarity 83.3%; Pred. No. 2.1e+02;
 Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1077 AACTATTAAAAA 1100
 DB 24 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 179
 AAC96201/c
 ID AAC96201 standard; DNA; 25 BP.
 XX
 AC AAC96201;
 XX
 DT 26-FEB-2001 (first entry)
 XX
 DE 16s rRNA gene PCR primer #168.

DNA sequence analysis; sequencing; protein sequence; protein structure;
 gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
 human leukocyte antigen; PCR primer; ss.

```

XX OS Homo sapiens.
XX PN WO200065088-A2.
XX PD 02-NOV-2000.
XX PF 20-APR-2000; 2000WO-EP03636.
XX PR 26-APR-1999; 99EP-0303215.
XX PA (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX PI Ulfendahl P, Wong K;
XX PF 2000-679677/66.
XX PT Identifying extendible primers for use in identification, or
PT PT classification of a nucleic acid of an organism, allele or gene such as
PT PT class 1/2 HLA comprises identifying all possible nucleotide sequences
PT PT of specific length -
XX PS Claim 14; Page 47; 66pp; English.
XX CC The present invention provides a method for identifying a set of
XX CC extendible primers which can be used in the identification, typing and
XX CC classification of genes. This can then be used to predict protein
XX CC sequence and structure, in organ donation to match the organ with the
XX CC receiver, and to identify bacteria in a sample. The method can be used to
XX CC type the human leukocyte antigen genes (HLA) and 16S rRNA genes in
XX CC particular.
XX SQ Sequence 25 BP; 1 A; 3 C; 3 G; 18 T; 0 other;

Query Match 1.6%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 2.1e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1075 GCAACTATTATTAATAAAAAAAAAAAAA 1098
DB 24 GCAAGACTGAAAAAAAAAAAAAAAAAAAA 1

RESULT 180
AAC96858/c
ID AAC96858 standard; DNA; 25 BP.
XX AC AAC96858;
XX DT 26-FEB-2001 (first entry)
XX DE HLA HLA-C gene PCR primer #63.
XX KW DNA sequence analysis; sequencing; protein sequence; protein structure;
XX KW gene typing; organ donation; bacteria identification; 16S rRNA; HLA;
XX KW human leukocyte antigen; PCR primer; ss.
XX OS Homo sapiens.
XX PN WO200065088-A2.
XX PD 02-NOV-2000.
XX PF 20-APR-2000; 2000WO-EP03636.
XX PR 26-APR-1999; 99EP-0303215.
XX PA (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX PI Ulfendahl P, Wong K;
XX PF 2000-679677/66.
XX PT Identifying extendible primers for use in identification, or
PT PT classification of a nucleic acid of an organism, allele or gene such as
PT PT class 1/2 HLA comprises identifying all possible nucleotide sequences
PT PT of specific length -
XX PS Claim 14; Page 58; 66pp; English.
XX CC The present invention provides a method for identifying a set of
XX CC extendible primers which can be used in the identification, typing and
XX CC classification of genes. This can then be used to predict protein
XX CC sequence and structure, in organ donation to match the organ with the
XX CC receiver, and to identify bacteria in a sample. The method can be used to
XX CC type the human leukocyte antigen genes (HLA) and 16S rRNA genes in
XX CC particular.
XX SQ Sequence 25 BP; 3 A; 3 C; 4 G; 15 T; 0 other;

Query Match 1.6%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 2.1e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1073 AAGCAACTATTATTAATAAAAAAAAAAAAA 1096
DB 24 ACGGCGCTACTAAAAAAAAAAAAAAAAAAAA 1

RESULT 181
AAA39306/c
ID AAA39306 standard; RNA; 25 BP.
XX AC AAA39306;
XX DT 11-SEP-2000 (first entry)
XX DE Rapid capture probe designated Neu-probe SEQ ID NO:1.
XX KW Rapid detection; probe; target nucleic acid; enzymatic amplification;
XX KW isolation; detection; ss.
XX OS Synthetic.
XX PN US6060246-A.
XX PD 09-MAY-2000.
XX PF 13-NOV-1997; 97US-0969813.
XX PR 15-NOV-1996; 96US-0030963.
XX PA (AVIB-) AVI BIOPHARMA INC.
XX PI Wages JM, Summerton JE, Weller DD;
XX PF 2000-364413/31.
XX PT Reagent for rapidly detecting or isolating target nucleic acid
XX PT sequences in polynucleotide-containing sample, comprises capture
XX PT component and target-specific probe linked to solid substrate -
XX PF Example 3; Column 17; 24pp; English.
XX CC The present invention describes a rapid pairing reagent (I) for the
XX CC isolation or detection of a polynucleotide (PN) analyte molecule having
XX CC a selected target base sequence, in a sample containing the analyte
XX CC molecule and non-target polynucleotide, comprising a capture component
XX CC (A) and a target-specific probe (B) linked to a solid substrate. The
XX CC isolated sequences are useful for enzymatic amplification. (I) is
XX CC capable of rapidly binding nucleic acids in the sample and placing them
XX CC in close proximity to target probes on the reagent, thus enabling
XX CC binding under low stringency. Combination of rapid capture and
XX CC concentration of polynucleotides with selective targeting of analyte
XX CC molecules, greatly enhances the isolation process. Non-ionic morpholino
XX CC oligomers used as probes are not extended by polymerases and therefore

```

| | | | | |
|-----------------------|------------------|--------------------|-----------|------------|
| Query Match | 1.6%; | Score 17.6; | DB 1; | Length 25; |
| Best Local Similarity | 83.3%; | Pred. No. 2.1e+02; | | |
| Matches | 20; Conservative | 0; Mismatches | 4; Indels | |

XX
AC
AA075556:

DT 04-AUG-1995 (first entry)
 XX Reverse transcription primer used in cDNA analysis technique.
 DE Analysis; gene expression; reverse transcription; primer; cDNA;
 KW aggregate; restriction enzyme; ss.
 KW Synthetic.
 OS
 XX JP06303997-A.
 PN
 XX 01-NOV-1994.
 PD
 XX 16-APR-1993; 93JP-0112515.
 PF
 XX 16-APR-1993; 93JP-0112515.
 PR
 XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 PA
 XX WPI; 1995-018287/03.
 DR
 XX Analysis of cDNA and gene expression - by amplification of mRNA
 PT followed by digestion with restriction enzymes
 PT Disclosure; Page 5; 11pp; Japanese.
 XX
 PS A method for the analysis of cDNA comprises (a) preparing an
 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
 CC and a plural type of labelled reverse transcription primers
 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
 CC template for each reverse transcription primer; (b) digesting each of
 CC the prepared aggregates of the double-stranded cDNAs with restriction
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
 CC separate lanes. The method can be used to analyse gene expression
 CC rapidly and easily.
 CC
 XX Sequence 19 BP; 1 A; 1 C; 0 G; 17 T; 0 other;
 SQ
 Query Match 1.6%; Score 17.4; DB 1; Length 19;
 Best Local Similarity 94.7%; Pred. No. 1.7e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 DT 04-AUG-1995 (first entry)
 XX Reverse transcription primer used in cDNA analysis technique.
 DE Analysis; gene expression; reverse transcription; primer; cDNA;
 KW aggregate; restriction enzyme; ss.
 KW Synthetic.
 OS
 XX JP06303997-A.
 PN
 XX 01-NOV-1994.
 PD
 XX 16-APR-1993; 93JP-0112515.
 PF
 XX 16-APR-1993; 93JP-0112515.
 PR
 XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 PA
 XX WPI; 1995-018287/03.
 DR
 XX Analysis of cDNA and gene expression - by amplification of mRNA
 PT followed by digestion with restriction enzymes
 PT Disclosure; Page 5; 11pp; Japanese.
 XX
 PS A method for the analysis of cDNA comprises (a) preparing an
 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
 CC and a plural type of labelled reverse transcription primers
 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
 CC template for each reverse transcription primer; (b) digesting each of
 CC the prepared aggregates of the double-stranded cDNAs with restriction
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
 CC separate lanes. The method can be used to analyse gene expression
 CC rapidly and easily.
 CC
 XX Sequence 19 BP; 1 A; 1 C; 0 G; 17 T; 0 other;
 SQ
 Query Match 1.6%; Score 17.4; DB 1; Length 19;
 Best Local Similarity 94.7%; Pred. No. 1.7e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

XX
 PT Analysis of cDNA and gene expression - by amplification of mRNA
 PT followed by digestion with restriction enzymes
 XX Disclosure; Page 5; 11pp; Japanese.
 XX
 XX A method for the analysis of cDNA comprises (a) preparing an
 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
 CC and a plural type of labelled reverse transcription primers
 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
 CC template for each reverse transcription primer; (b) digesting each of
 CC the prepared aggregates of the double-stranded cDNAs with restriction
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
 CC separate lanes. The method can be used to analyse gene expression
 CC rapidly and easily.
 XX
 SQ Sequence 19 BP; 1 A; 0 C; 1 G; 17 T; 0 other;
 Query Match 1.6%; Score 17.4; DB 1; Length 19;
 Best Local Similarity 94.7%; Pred. No. 1.7e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1082 TTAAAAA1100
 Db 19 TCAAAAA1100
 RESULT 186
 AAQ75596/c
 ID AAQ75596 standard; DNA; 20 BP.
 XX
 AC AAQ75596;
 XX
 DT 04-AUG-1995 (first entry)
 XX Reverse transcription primer used in cDNA analysis technique.
 DE Analysis; gene expression; reverse transcription; primer; cDNA;
 KW aggregate; restriction enzyme; ss.
 XX Synthetic.
 OS
 PN JP06303997-A.
 XX
 PD 01-NOV-1994.
 XX
 PF 16-APR-1993; 93JP-0112515.
 XX
 PR 16-APR-1993; 93JP-0112515.
 XX
 PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX
 DR WPI; 1995-018287/03.
 XX
 DE Analysis of cDNA and gene expression - by amplification of mRNA
 PT followed by digestion with restriction enzymes
 PT Disclosure; Page 5; 11pp; Japanese.
 XX
 PS A method for the analysis of cDNA comprises (a) preparing an
 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
 CC and a plural type of labelled reverse transcription primers
 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
 CC template for each reverse transcription primer; (b) digesting each of
 CC the prepared aggregates of the double-stranded cDNAs with restriction
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
 CC separate lanes. The method can be used to analyse gene expression
 CC rapidly and easily.
 XX
 SQ Sequence 20 BP; 2 A; 1 C; 0 G; 17 T; 0 other;
 Query Match 1.6%; Score 17.4; DB 1; Length 20;
 Best Local Similarity 94.7%; Pred. No. 1.8e+02;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1082 TTAAAAA 1100
 ID AAQ75598 standard; DNA; 20 BP.
 DB 20 TTGAAAAA 2

RESULT 187
 AAQ75598/c
 ID AAQ75598 standard; DNA; 20 BP.
 AC AAQ75598;
 XX
 XX
 DT 04-AUG-1995 (first entry)
 XX
 XX Reverse transcription primer used in cDNA analysis technique.
 XX
 XX Analysis; gene expression; reverse transcription; primer; cDNA;
 KW aggregate; restriction enzyme; ss.
 XX
 OS Synthetic.
 XX
 XX JP06303997-A.
 XX
 XX 01-NOV-1994.
 XX
 XX 16-APR-1993; 93JP-0112515.
 XX
 XX 16-APR-1993; 93JP-0112515.
 XX
 XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX
 XX WPI; 1995-018287/03.
 XX
 XX Analysis of cDNA and gene expression - by amplification of mRNA
 PT followed by digestion with restriction enzymes
 XX
 XX Disclosure; Page 5; 11pp; Japanese.
 XX
 XX A method for the analysis of cDNA comprises (a) preparing an
 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
 CC and a plural type of labelled reverse transcription primers
 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
 CC template for each reverse transcription primer; (b) digesting each of
 CC the prepared aggregates of the double-stranded cDNAs with restriction
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
 CC separate lanes. The method can be used to analyse gene expression
 CC rapidly and easily.
 XX
 XX Sequence 20 BP; 1 A; 2 C; 0 G; 17 T; 0 other;
 SQ

Query Match 1.6%; Score 17.4; DB 1; Length 20;
 Best Local Similarity 94.7%; Pred. No. 1.8e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1082 TTAAAAA 1100
 ID AAQ75598 standard; DNA; 20 BP.
 DB 20 TTGAAAAA 1

RESULT 188
 AAQ75598/c
 ID AAQ75598 standard; DNA; 20 BP.
 AC AAQ75598;
 XX
 XX
 DT 04-AUG-1995 (first entry)
 XX
 XX Reverse transcription primer used in cDNA analysis technique.
 XX
 XX Analysis; gene expression; reverse transcription; primer; cDNA;
 KW aggregate; restriction enzyme; ss.
 XX
 XX
 XX A method for the analysis of cDNA comprises (a) preparing an

OS Synthetic.
 XX
 XX JP06303997-A.
 XX
 XX 01-NOV-1994.
 XX
 XX 16-APR-1993; 93JP-0112515.
 XX
 XX 16-APR-1993; 93JP-0112515.
 XX
 XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX
 XX WPI; 1995-018287/03.
 XX
 XX Analysis of cDNA and gene expression - by amplification of mRNA
 PT followed by digestion with restriction enzymes
 XX
 XX Disclosure; Page 5; 11pp; Japanese.
 XX
 XX A method for the analysis of cDNA comprises (a) preparing an
 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
 CC and a plural type of labelled reverse transcription primers
 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
 CC template for each reverse transcription primer; (b) digesting each of
 CC the prepared aggregates of the double-stranded cDNAs with restriction
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
 CC separate lanes. The method can be used to analyse gene expression
 CC rapidly and easily.
 XX
 XX Sequence 20 BP; 1 A; 1 C; 1 G; 17 T; 0 other;
 SQ

Query Match 1.6%; Score 17.4; DB 1; Length 20;
 Best Local Similarity 94.7%; Pred. No. 1.8e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1082 TTAAAAA 1100
 ID AAQ75566 standard; DNA; 20 BP.
 DB 19 TGAAAAA 1

RESULT 189
 AAQ75566/c
 ID AAQ75566 standard; DNA; 20 BP.
 AC AAQ75566;
 XX
 XX 04-AUG-1995 (first entry)
 XX
 XX Reverse transcription primer used in cDNA analysis technique.
 XX
 XX Analysis; gene expression; reverse transcription; primer; cDNA;
 KW aggregate; restriction enzyme; ss.
 XX
 OS Synthetic.
 XX
 XX JP06303997-A.
 XX
 XX 01-NOV-1994.
 XX
 XX 16-APR-1993; 93JP-0112515.
 XX
 XX 16-APR-1993; 93JP-0112515.
 XX
 XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX
 XX WPI; 1995-018287/03.
 XX
 XX Analysis of cDNA and gene expression - by amplification of mRNA
 PT followed by digestion with restriction enzymes
 XX
 XX Disclosure; Page 5; 11pp; Japanese.
 XX
 XX A method for the analysis of cDNA comprises (a) preparing an

CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
 CC and a plural type of labelled reverse transcription primers
 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
 CC template for each reverse transcription primer; (b) digesting each of
 CC the prepared aggregates of the double-stranded cDNAs with restriction
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
 CC separate lanes. The method can be used to analyse gene expression
 CC rapidly and easily.
 XX
 SQ Sequence 20 BP; 1 A; 1 C; 1 G; 17 T; 0 other;
 Query Match 1.6%; Score 17.4; DB 1; Length 20;
 Best Local Similarity 94.7%; Pred. No. 1.8e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1082 TTAATAAAAAAAAAAAAAA 1100
 DB 19 TCAAAAAAAAAAAAAAAAAA 1
 RESULT 190
 AAQ75563/c
 ID AAQ75563 standard; DNA; 20 BP.
 XX
 AC AAQ75563;
 XX
 DT 04-AUG-1995 (first entry)
 XX
 DE Reverse transcription primer used in cDNA analysis technique.
 DE
 KW Analysis; gene expression; reverse transcription; primer; cDNA;
 KW aggregate; restriction enzyme; ss.
 XX
 OS Synthetic.
 XX
 PN JP06303997-A.
 XX
 PD 01-NOV-1994.
 XX
 PF 16-APR-1993; 93JP-0112515.
 XX
 PR 16-APR-1993; 93JP-0112515.
 XX
 PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX
 DR WPI; 1995-018287/03.
 XX
 PT Analysis of cDNA and gene expression - by amplification of mRNA
 PT followed by digestion with restriction enzymes
 XX
 PS Disclosure; Page 5; 1lpp; Japanese.
 XX
 CC A method for the analysis of cDNA comprises (a) preparing an
 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
 CC and a plural type of labelled reverse transcription primers
 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
 CC template for each reverse transcription primer; (b) digesting each of
 CC the prepared aggregates of the double-stranded cDNAs with restriction
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
 CC separate lanes. The method can be used to analyse gene expression
 CC rapidly and easily.
 XX
 SQ Sequence 20 BP; 1 A; 0 C; 2 G; 17 T; 0 other;
 Query Match 1.6%; Score 17.4; DB 1; Length 20;
 Best Local Similarity 94.7%; Pred. No. 1.8e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1082 TTAATAAAAAAAAAAAAAA 1100
 DB 19 TCAAAAAAAAAAAAAAAAAA 1
 RESULT 190
 AAQ75563/c
 ID AAQ75563 standard; DNA; 20 BP.
 XX
 AC AAQ75563;
 XX
 DT 04-AUG-1995 (first entry)
 XX
 DE Reverse transcription primer used in cDNA analysis technique.
 DE
 KW Analysis; gene expression; reverse transcription; primer; cDNA;
 KW aggregate; restriction enzyme; ss.
 XX
 OS Synthetic.
 XX
 PN JP06303997-A.
 XX
 PD 01-NOV-1994.
 XX
 PF 16-APR-1993; 93JP-0112515.
 XX
 PR 16-APR-1993; 93JP-0112515.
 XX
 PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX
 DR WPI; 1995-018287/03.
 XX
 PT Analysis of cDNA and gene expression - by amplification of mRNA
 PT followed by digestion with restriction enzymes
 XX
 PS Disclosure; Page 5; 1lpp; Japanese.
 XX
 CC A method for the analysis of cDNA comprises (a) preparing an
 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
 CC and a plural type of labelled reverse transcription primers
 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
 CC template for each reverse transcription primer; (b) digesting each of
 CC the prepared aggregates of the double-stranded cDNAs with restriction
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
 CC separate lanes. The method can be used to analyse gene expression
 CC rapidly and easily.
 XX
 SQ Sequence 20 BP; 1 A; 0 C; 2 G; 17 T; 0 other;
 Query Match 1.6%; Score 17.4; DB 1; Length 20;
 Best Local Similarity 94.7%; Pred. No. 1.8e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1082 TTAATAAAAAAAAAAAAAA 1100
 DB 19 TCAAAAAAAAAAAAAAAAAA 1

RESULT 191
 AAQ75564/c
 ID AAQ75564 standard; DNA; 20 BP.
 XX
 AC AAQ75564;
 XX
 DT 04-AUG-1995 (first entry)
 XX
 DE Reverse transcription primer used in cDNA analysis technique.
 DE
 KW Analysis; gene expression; reverse transcription; primer; cDNA;
 KW aggregate; restriction enzyme; ss.
 XX
 OS Synthetic.
 XX
 PN JP06303997-A.
 XX
 PD 01-NOV-1994.
 XX
 PF 16-APR-1993; 93JP-0112515.
 XX
 PR 16-APR-1993; 93JP-0112515.
 XX
 PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX
 DR WPI; 1995-018287/03.
 XX
 PT Analysis of cDNA and gene expression - by amplification of mRNA
 PT followed by digestion with restriction enzymes
 XX
 PS Disclosure; Page 5; 1lpp; Japanese.
 XX
 CC A method for the analysis of cDNA comprises (a) preparing an
 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
 CC and a plural type of labelled reverse transcription primers
 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
 CC template for each reverse transcription primer; (b) digesting each of
 CC the prepared aggregates of the double-stranded cDNAs with restriction
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
 CC separate lanes. The method can be used to analyse gene expression
 CC rapidly and easily.
 XX
 SQ Sequence 20 BP; 2 A; 0 C; 1 G; 17 T; 0 other;
 Query Match 1.6%; Score 17.4; DB 1; Length 20;
 Best Local Similarity 94.7%; Pred. No. 1.8e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1082 TTAATAAAAAAAAAAAAAA 1100
 DB 20 TTCAAAAAAAAAAAAAAAAA 2
 RESULT 192
 AAQ91207/c
 ID AAQ91207 standard; DNA; 20 BP.
 XX
 AC AAQ91207;
 XX
 DT 08-MAY-2001 (first entry)
 XX
 DE Antisense IGFBP-5 inhibitor #13.
 XX
 KW Insulin-like growth factor binding protein-5; IGFBP-5; human;
 KW antisense oligonucleotide; hormone-regulated cancer; prostatic cancer;
 KW breast cancer; therapy; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200105435-A2.
 XX
 PD 25-JAN-2001.
 XX

Query Match 1.6%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1082 TTAAAAAATAAAAAAAAAA 1100
DB 19 TGAATAAAAAAAAAAAAAA 1

RESULT 195
AAQ75754/C
ID AAQ75754 standard; DNA; 21 BP.
XX AC AAQ75754;
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX KW aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-0112515.
XX PR 16-APR-1993; 93JP-0112515.
XX PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX PT Analysis of cDNA and gene expression - by amplification of mRNA
XX PT followed by digestion with restriction enzymes
XX PS Disclosure; Page 9; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an
XX CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
XX CC and a plural type of labelled reverse transcription primers
XX CC (GENESQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
XX CC template for each reverse transcription primer; (b) digesting each of
XX CC the prepared aggregates of the double-stranded cDNAs with restriction
XX CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
XX CC separate lanes. The method can be used to analyse gene expression
XX CC rapidly and easily.
XX SQ Sequence 21 BP; 1 A; 2 C; 1 G; 17 T; 0 other;

Query Match 1.6%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1082 TTAAAAAATAAAAAAAAAA 1100
DB 19 TGAATAAAAAAAAAAAAAA 1

RESULT 196
AAQ75772/C
ID AAQ75772 standard; DNA; 21 BP.
XX AC AAQ75772;
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.

KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-0112515.
XX PR 16-APR-1993; 93JP-0112515.
XX PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX PT Analysis of cDNA and gene expression - by amplification of mRNA
XX PT followed by digestion with restriction enzymes
XX PS Disclosure; Page 9; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an
XX CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
XX CC and a plural type of labelled reverse transcription primers
XX CC (GENESQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
XX CC template for each reverse transcription primer; (b) digesting each of
XX CC the prepared aggregates of the double-stranded cDNAs with restriction
XX CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
XX CC separate lanes. The method can be used to analyse gene expression
XX CC rapidly and easily.
XX SQ Sequence 21 BP; 2 A; 1 C; 0 G; 18 T; 0 other;

Query Match 1.6%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1082 TTAAAAAATAAAAAAAAAA 1100
DB 21 TTAAAAAATAAAAAAAAAA 3

RESULT 197
AAQ75755/C
ID AAQ75755 standard; DNA; 21 BP.
XX AC AAQ75755;
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX KW aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-0112515.
XX PR 16-APR-1993; 93JP-0112515.
XX PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX PT Analysis of cDNA and gene expression - by amplification of mRNA
XX PT followed by digestion with restriction enzymes

```
PS Disclosure; Page 8; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an
XX aggregate of double-stranded cDNAs by using an aggregate of mRNAs
XX and a plural type of labelled reverse transcription primers
XX (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
XX template for each reverse transcription primer; (b) digesting each of
XX the prepared aggregates of the double-stranded cDNAs with restriction
XX enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
XX separate lanes. The method can be used to analyse gene expression
XX rapidly and easily.
XX
XX Sequence 21 BP; 2 A; 1 C; 1 G; 17 T; 0 other;
XX
XX Query Match 1.6%; Score 17.4; DB 1; Length 21;
XX Best Local Similarity 94.7%; Pred. No. 1.9e+02;
XX Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 1082 TTAAAAA...AAAAAAAAA 1100
DB 20 TTGAAAAA...AAAAAAAAA 2

RESULT 198
AAQ75758/c
ID AAQ75758 standard; DNA; 21 BP.
AC AAQ75758;
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-0112515.
XX
XX 16-APR-1993; 93JP-0112515.
XX
XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA
XX followed by digestion with restriction enzymes
XX
XX Disclosure; Page 8; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an
XX aggregate of double-stranded cDNAs by using an aggregate of mRNAs
XX and a plural type of labelled reverse transcription primers
XX (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
XX template for each reverse transcription primer; (b) digesting each of
XX the prepared aggregates of the double-stranded cDNAs with restriction
XX enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
XX separate lanes. The method can be used to analyse gene expression
XX rapidly and easily.
XX
XX Sequence 21 BP; 2 A; 2 C; 0 G; 17 T; 0 other;
XX
XX Query Match 1.6%; Score 17.4; DB 1; Length 21;
XX Best Local Similarity 94.7%; Pred. No. 1.9e+02;
XX Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 1082 TTAAAAA...AAAAAAAAA 1100
DB 20 TTGAAAAA...AAAAAAAAA 2

RESULT 199
AAQ75763/c
ID AAQ75763 standard; DNA; 21 BP.
XX
XX AAQ75763;
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-0112515.
XX
XX 16-APR-1993; 93JP-0112515.
XX
XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA
XX followed by digestion with restriction enzymes
XX
XX Disclosure; Page 8; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an
XX aggregate of double-stranded cDNAs by using an aggregate of mRNAs
XX and a plural type of labelled reverse transcription primers
XX (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
XX template for each reverse transcription primer; (b) digesting each of
XX the prepared aggregates of the double-stranded cDNAs with restriction
XX enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
XX separate lanes. The method can be used to analyse gene expression
XX rapidly and easily.
XX
XX Sequence 21 BP; 1 A; 2 C; 1 G; 17 T; 0 other;
XX
XX Query Match 1.6%; Score 17.4; DB 1; Length 21;
XX Best Local Similarity 94.7%; Pred. No. 1.9e+02;
XX Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 1082 TTAAAAA...AAAAAAAAA 1100
DB 19 TGA...AAAAAAAAA 1

RESULT 200
AAQ75765/c
ID AAQ75765 standard; DNA; 21 BP.
XX
XX AAQ75765;
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX
XX JP06303997-A.
XX
```

PD 01-NOV-1994.
 XX
 PF 16-APR-1993; 93JP-0112515.
 XX
 PR 16-APR-1993; 93JP-0112515.
 XX
 PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX
 DR WPI; 1995-018287/03.
 XX
 XX
 PT Analysis of cDNA and gene expression - by amplification of mRNA
 followed by digestion with restriction enzymes
 XX
 PS Disclosure; Page 9; 11pp; Japanese.
 XX
 CC A method for the analysis of cDNA comprises (a) preparing an
 aggregate of double-stranded cDNAs by using an aggregate of mRNAs
 and a plural type of labelled reverse transcription primers
 (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
 template for each reverse transcription primer; (b) digesting each of
 the prepared aggregates of the double-stranded cDNAs with restriction
 enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
 separate lanes. The method can be used to analyse gene expression
 rapidly and easily.
 XX
 SQ Sequence 21 BP; 1 A; 2 C; 0 G; 18 T; 0 other;
 Query Match 1.6%; Score 17.4; DB 1; Length 21;
 Best Local Similarity 94.7%; Pred. NO. 1.9e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 XX
 Qy 1082 TTAATAAAAAAAAAAAAAA 1100
 Db 19 TGAATAAAAAAAAAAAAAA 1
 RESULT 201
 AAQ75766/c
 ID AAQ75766 standard; DNA; 21 BP.
 AC AAQ75766;
 XX
 DT 04-AUG-1995 (first entry)
 XX
 DE Reverse transcription primer used in cDNA analysis technique.
 XX
 XX Analysis; gene expression; reverse transcription; primer; cDNA;
 aggregate; restriction enzyme; ss.
 XX
 OS Synthetic.
 XX
 PN JP06303997-A.
 XX
 PD 01-NOV-1994.
 XX
 PF 16-APR-1993; 93JP-0112515.
 XX
 PR 16-APR-1993; 93JP-0112515.
 XX
 PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX
 DR WPI; 1995-018287/03.
 XX
 XX
 PT Analysis of cDNA and gene expression - by amplification of mRNA
 followed by digestion with restriction enzymes
 XX
 PS Disclosure; Page 9; 11pp; Japanese.
 XX
 CC A method for the analysis of cDNA comprises (a) preparing an
 aggregate of double-stranded cDNAs by using an aggregate of mRNAs
 and a plural type of labelled reverse transcription primers
 (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
 template for each reverse transcription primer; (b) digesting each of
 the prepared aggregates of the double-stranded cDNAs with restriction
 enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
 separate lanes. The method can be used to analyse gene expression
 rapidly and easily.

CC the prepared aggregates of the double-stranded cDNAs with restriction
 enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
 separate lanes. The method can be used to analyse gene expression
 rapidly and easily.
 XX
 SQ Sequence 21 BP; 1 A; 3 C; 0 G; 17 T; 0 other;
 Query Match 1.6%; Score 17.4; DB 1; Length 21;
 Best Local Similarity 94.7%; Pred. NO. 1.9e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 XX
 Qy 1082 TTAATAAAAAAAAAAAAAA 1100
 Db 19 TGAATAAAAAAAAAAAAAA 1
 RESULT 202
 AAQ75630/c
 ID AAQ75630 standard; DNA; 21 BP.
 AC AAQ75630;
 XX
 DT 04-AUG-1995 (first entry)
 XX
 DE Reverse transcription primer used in cDNA analysis technique.
 XX
 XX Analysis; gene expression; reverse transcription; primer; cDNA;
 aggregate; restriction enzyme; ss.
 XX
 OS Synthetic.
 XX
 PN JP06303997-A.
 XX
 PD 01-NOV-1994.
 XX
 PF 16-APR-1993; 93JP-0112515.
 XX
 PR 16-APR-1993; 93JP-0112515.
 XX
 PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX
 DR WPI; 1995-018287/03.
 XX
 DE Analysis of cDNA and gene expression - by amplification of mRNA
 followed by digestion with restriction enzymes
 XX
 PS Disclosure; Page 6; 11pp; Japanese.
 XX
 CC A method for the analysis of cDNA comprises (a) preparing an
 aggregate of double-stranded cDNAs by using an aggregate of mRNAs
 and a plural type of labelled reverse transcription primers
 (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
 template for each reverse transcription primer; (b) digesting each of
 the prepared aggregates of the double-stranded cDNAs with restriction
 enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
 separate lanes. The method can be used to analyse gene expression
 rapidly and easily.
 XX
 SQ Sequence 21 BP; 2 A; 1 C; 1 G; 17 T; 0 other;
 Query Match 1.6%; Score 17.4; DB 1; Length 21;
 Best Local Similarity 94.7%; Pred. NO. 1.9e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 XX
 Qy 1082 TTAATAAAAAAAAAAAAAA 1100
 Db 20 TTCAATAAAAAAAAAAAAAA 2
 RESULT 203
 AAQ75635/c
 ID AAQ75635 standard; DNA; 21 BP.
 XX

AC AAQ75635;
 XX 04-AUG-1995 (first entry)
 XX Reverse transcription primer used in cDNA analysis technique.
 DE Analysis; gene expression; reverse transcription; primer; cDNA;
 XX aggregate; restriction enzyme; ss.
 XX Synthetic.
 OS
 PN JP06303997-A.
 XX 01-NOV-1994.
 XX 16-APR-1993; 93JP-0112515.
 XX 16-APR-1993; 93JP-0112515.
 XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX WPI; 1995-018287/03.
 XX Analysis of cDNA and gene expression - by amplification of mRNA
 PT followed by digestion with restriction enzymes
 XX Disclosure; Page 6; 11pp; Japanese.
 XX A method for the analysis of cDNA comprises (a) preparing an
 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
 CC and a plural type of labelled reverse transcription primers
 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
 CC template for each reverse transcription primer; (b) digesting each of
 CC the prepared aggregates of the double-stranded cDNAs with restriction
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
 CC separate lanes. The method can be used to analyse gene expression
 CC rapidly and easily.
 XX Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 other;
 XX
 XX Query Match 1.6%; Score 17.4; DB 1; Length 21;
 XX Best Local Similarity 94.7%; Pred. No. 1.9e+02;
 XX Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 XX
 QY 1082 TTAAAAA AAAAAAAAAA 1100
 DB 19 TCAAAAA AAAAAAAAAA 1
 XX
 XX RESULT 204
 XX AAQ75637/c
 ID AAQ75637 standard; DNA; 21 BP.
 XX AAQ75637;
 XX 04-AUG-1995 (first entry)
 XX Reverse transcription primer used in cDNA analysis technique.
 DE Analysis; gene expression; reverse transcription; primer; cDNA;
 XX aggregate; restriction enzyme; ss.
 XX Synthetic.
 OS
 PN JP06303997-A.
 XX 01-NOV-1994.
 XX 16-APR-1993; 93JP-0112515.
 XX 16-APR-1993; 93JP-0112515.
 XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX WPI; 1995-018287/03.
 XX Analysis of cDNA and gene expression - by amplification of mRNA
 PT followed by digestion with restriction enzymes
 XX Disclosure; Page 6; 11pp; Japanese.
 XX A method for the analysis of cDNA comprises (a) preparing an
 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
 CC and a plural type of labelled reverse transcription primers
 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
 CC template for each reverse transcription primer; (b) digesting each of
 CC the prepared aggregates of the double-stranded cDNAs with restriction
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
 CC separate lanes. The method can be used to analyse gene expression
 CC rapidly and easily.
 XX Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 other;
 XX
 XX Query Match 1.6%; Score 17.4; DB 1; Length 21;
 XX Best Local Similarity 94.7%; Pred. No. 1.9e+02;
 XX Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 XX
 QY 1082 TTAAAAA AAAAAAAAAA 1100
 DB 19 TCAAAAA AAAAAAAAAA 1
 XX
 XX RESULT 204
 XX AAQ75637/c
 ID AAQ75637 standard; DNA; 21 BP.
 XX AAQ75637;
 XX 04-AUG-1995 (first entry)
 XX Reverse transcription primer used in cDNA analysis technique.
 DE Analysis; gene expression; reverse transcription; primer; cDNA;
 XX aggregate; restriction enzyme; ss.
 XX Synthetic.
 OS
 PN JP06303997-A.
 XX 01-NOV-1994.
 XX 16-APR-1993; 93JP-0112515.
 XX 16-APR-1993; 93JP-0112515.
 XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX WPI; 1995-018287/03.
 XX Analysis of cDNA and gene expression - by amplification of mRNA
 PT followed by digestion with restriction enzymes
 XX Disclosure; Page 6; 11pp; Japanese.
 XX A method for the analysis of cDNA comprises (a) preparing an
 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
 CC and a plural type of labelled reverse transcription primers
 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
 CC template for each reverse transcription primer; (b) digesting each of
 CC the prepared aggregates of the double-stranded cDNAs with restriction
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
 CC separate lanes. The method can be used to analyse gene expression
 CC rapidly and easily.
 XX Sequence 21 BP; 1 A; 2 C; 1 G; 17 T; 0 other;
 XX

XX WPI; 1995-018287/03.
 XX Analysis of cDNA and gene expression - by amplification of mRNA
 PT followed by digestion with restriction enzymes
 XX Disclosure; Page 6; 11pp; Japanese.
 XX A method for the analysis of cDNA comprises (a) preparing an
 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
 CC and a plural type of labelled reverse transcription primers
 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
 CC template for each reverse transcription primer; (b) digesting each of
 CC the prepared aggregates of the double-stranded cDNAs with restriction
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
 CC separate lanes. The method can be used to analyse gene expression
 CC rapidly and easily.
 XX Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 other;
 XX
 XX Query Match 1.6%; Score 17.4; DB 1; Length 21;
 XX Best Local Similarity 94.7%; Pred. No. 1.9e+02;
 XX Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 XX
 QY 1082 TTAAAAA AAAAAAAAAA 1100
 DB 19 TCAAAAA AAAAAAAAAA 1
 XX
 XX RESULT 205
 XX AAQ75638/c
 ID AAQ75638 standard; DNA; 21 BP.
 XX AAQ75638;
 XX 04-AUG-1995 (first entry)
 XX Reverse transcription primer used in cDNA analysis technique.
 DE Analysis; gene expression; reverse transcription; primer; cDNA;
 XX aggregate; restriction enzyme; ss.
 XX Synthetic.
 OS
 PN JP06303997-A.
 XX 01-NOV-1994.
 XX 16-APR-1993; 93JP-0112515.
 XX 16-APR-1993; 93JP-0112515.
 XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX WPI; 1995-018287/03.
 XX Analysis of cDNA and gene expression - by amplification of mRNA
 PT followed by digestion with restriction enzymes
 XX Disclosure; Page 6; 11pp; Japanese.
 XX A method for the analysis of cDNA comprises (a) preparing an
 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
 CC and a plural type of labelled reverse transcription primers
 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
 CC template for each reverse transcription primer; (b) digesting each of
 CC the prepared aggregates of the double-stranded cDNAs with restriction
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
 CC separate lanes. The method can be used to analyse gene expression
 CC rapidly and easily.
 XX Sequence 21 BP; 1 A; 2 C; 1 G; 17 T; 0 other;
 XX

XX aggregate; restriction enzyme; ss.
XX Synthetic.
XX JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-0112515.
XX PR 16-APR-1993; 93JP-0112515.
XX PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX WPI; 1995-018287/03.
XX Analysis of cDNA and gene expression - by amplification of mRNA
XX followed by digestion with restriction enzymes
XX Disclosure; Page 6; 11pp; Japanese.

CC A method for the analysis of cDNA comprises (a) preparing an
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC and a plural type of labelled reverse transcription primers
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
CC template for each reverse transcription primer; (b) digesting each of
CC the prepared aggregates of the double-stranded cDNAs with restriction
CC enzyme and; and (c) electrophoresing the digested aggregate of cDNAs in
CC separate lanes. The method can be used to analyse gene expression
XX rapidly and easily.

XX SQ Sequence 21 BP; 1 A; 0 C; 2 G; 18 T; 0 other;

Query Match 1.6%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps

Qy 1082 TTAAAAAATAAAAAAAAAAA 1100
| | | | | | | | | | | | |
Db 19 TCACAAAATAAAAAAAAAAA 1

RESULT 208
AAQ75626/c
ID AAQ75626 standard; DNA; 21 Bp.
XX AC AAQ75626;
XX DT 04-AUG-1995 (first entry)
XX Reverse transcription primer used in cDNA analysis technique.
XX Analysis; Gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX Synthetic.
XX JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-0112515.
XX PR 16-APR-1993; 93JP-0112515.
XX PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX WPI; 1995-018287/03.
XX Analysis of cDNA and gene expression - by amplification of mRNA
XX followed by digestion with restriction enzymes
XX Disclosure; Page 6; 11pp; Japanese.

```

XX A method for the analysis of cDNA comprises (a) preparing an
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC and a plural type of labelled reverse transcription primers
CC (GENESEQ files AAQ7547-Q75798) and using the aggregate of mRNAs as the
CC template for each reverse transcription primer; (b) digesting each of
CC the prepared aggregates of the double-stranded cDNAs with restriction
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC separate lanes. The method can be used to analyse gene expression
CC rapidly and easily.
XX
XX Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 other;
XX
Query Match 1.6%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1082 TTAACAAAAAATAAAAAA 1100
Db 19 TCAAAAAAATAAAAAA 1
RESULT 209
AAQ75627/c
ID AAQ75627 standard; DNA; 21 BP.
AC AAQ75627;
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX Synthetic.
XX
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-0112515.
XX
XX 16-APR-1993; 93JP-0112515.
XX
XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA
XX followed by digestion with restriction enzymes
XX Disclosure; Page 6; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an
XX aggregate of double-stranded cDNAs by using an aggregate of mRNAs
XX and a plural type of labelled reverse transcription primers
XX (GENESEQ files AAQ7547-Q75798) and using the aggregate of mRNAs as the
XX template for each reverse transcription primer; (b) digesting each of
XX the prepared aggregates of the double-stranded cDNAs with restriction
XX enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
XX separate lanes. The method can be used to analyse gene expression
XX rapidly and easily.
XX
XX Sequence 21 BP; 2 A; 0 C; 2 G; 17 T; 0 other;
XX
Query Match 1.6%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1082 TTAACAAAAAATAAAAAA 1100
Db 20 TCAAAAAAATAAAAAA 2
RESULT 209
AAQ75627/c
ID AAQ75627 standard; DNA; 21 BP.
AC AAQ75627;
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX Synthetic.
XX
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-0112515.
XX
XX 16-APR-1993; 93JP-0112515.
XX
XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA
XX followed by digestion with restriction enzymes
XX Disclosure; Page 6; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an
XX aggregate of double-stranded cDNAs by using an aggregate of mRNAs
XX and a plural type of labelled reverse transcription primers
XX (GENESEQ files AAQ7547-Q75798) and using the aggregate of mRNAs as the
XX template for each reverse transcription primer; (b) digesting each of
XX the prepared aggregates of the double-stranded cDNAs with restriction
XX enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
XX separate lanes. The method can be used to analyse gene expression
XX rapidly and easily.
XX
XX Sequence 21 BP; 2 A; 0 C; 2 G; 17 T; 0 other;
XX
Query Match 1.6%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1082 TTAACAAAAAATAAAAAA 1100
Db 20 TCAAAAAAATAAAAAA 2

```

```

RESULT 210
AAQ75644/c
ID AAQ75644 standard; DNA; 21 BP.
XX
XX AAQ75644;
AC AAQ75644;
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX Synthetic.
XX
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-0112515.
XX
XX 16-APR-1993; 93JP-0112515.
XX
XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA
XX followed by digestion with restriction enzymes
XX Disclosure; Page 6; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an
XX aggregate of double-stranded cDNAs by using an aggregate of mRNAs
XX and a plural type of labelled reverse transcription primers
XX (GENESEQ files AAQ7547-Q75798) and using the aggregate of mRNAs as the
XX template for each reverse transcription primer; (b) digesting each of
XX the prepared aggregates of the double-stranded cDNAs with restriction
XX enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
XX separate lanes. The method can be used to analyse gene expression
XX rapidly and easily.
XX
XX Sequence 21 BP; 2 A; 0 C; 1 G; 18 T; 0 other;
XX
Query Match 1.6%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1082 TTAACAAAAAATAAAAAA 1100
Db 21 TTACAAAAAATAAAAAA 3
RESULT 211
AAQ26584
ID AAQ26584 standard; DNA; 21 BP.
XX
XX AAQ26584;
XX
XX 30-NOV-1999 (first entry)
XX
XX Human polymorphic region 773.
XX
XX Polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH;
XX cell viability; loss of heterozygosity; precancerous condition; ASI;
XX allele specific inhibitor; somatic cell; diagnosis; prevention;
XX atherosclerotic plaque; premalignant metaplastic lesion; endometriosis;
XX dysplastic lesion; benign tumour; polycystic kidney disease; transplant;
XX graft versus host disease; malignant cell removal; bone marrow; ss.
XX
XX Homo sapiens.

```


XX WO9841648-A2.
 XX 24-SEP-1998.
 XX 19-MAR-1998; 98WO-US05419.
 XX 20-MAR-1997; 97US-0041057.
 XX (VARI-) VARIAGENICS INC.
 XX Housman D, Ledley FD, Stanton VP;
 XX WPI; 1998-521232/44.
 XX Identifying target genes for allele-specific drugs - used for
 XX diagnosis, prevention and treatment of, e.g. cancers, atherosclerotic
 XX plaque, dysplastic lesions, endometriosis or graft versus host disease
 XX Disclosure; Figure 7; 605pp; English.
 XX This invention describes a novel method for identifying an inhibitor
 XX potentially useful for treatment of cancer, where the inhibitor is
 XX active on a gene vital for cell growth or viability, and where the gene
 XX is subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is
 XX used for preventing the development of cancer in a patient having a
 XX precancerous condition, by administering to the patient a first allele
 XX specific inhibitor (ASI) targeted to an allele of a first essential gene
 XX present in cells of the precancerous condition, where the normal somatic
 XX cells of the patient are heterozygous for the first gene, the inhibitor
 XX is active on at least one but less than all allelic forms of the gene
 XX present in a population and targets only one allelic form present in the
 XX normal somatic cells, and the first gene. The products and methods can
 XX be used in the diagnosis, prevention and treatment of LOH disorders,
 XX e.g. cancers, atherosclerotic plaques, premalignant metaplastic or
 XX dysplastic lesions, benign tumours, endometriosis, polycystic kidney
 XX disease, and graft versus host disease. The method can also be used to
 XX remove malignant cells from bone marrow transplants. AA225812-226825
 XX represent human polymorphic sites described in the method of the
 XX invention.
 XX Sequence 21 BP; 15 A; 0 C; 1 G; 5 T; 0 other;
 Query Match 1.6%; Score 17.4; DB 1; Length 21;
 Best Local Similarity 94.7%; Pred. No. 1.9e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1080 TATTAAAAA 1098
 Db 3 TTTAAAAA 21
 RESULT 212
 AAI64873/c
 ID AAI64873 standard; DNA; 24 BP.
 XX AAI64873;
 XX 04-DEC-2001 (first entry)
 XX Human serine/threonine protein kinase 48 cDNA PCR primer #2.
 XX Human; serine/threonine protein kinase 48; cancer; HIV infection;
 XX gene therapy; PCR primer; ss.
 XX Homo sapiens.
 XX CN1300831-A.
 XX 27-JUN-2001.
 XX 22-DEC-1999; 99CN-0125686.

PR 22-DEC-1999; 99CN-0125686.
 XX (BODE-) BODE GENE DEV CO LTD SHANGHAI.
 XX Mao Y, Xie Y;
 XX WPI; 2001-530471/59.
 XX New human serine/threonine protein kinase 48 and its encoding
 XX polynucleotide, useful for treating cancer and human immunodeficiency
 XX virus infection -
 XX Example 3; Page 17(Disclosure); 33pp; Chinese.
 XX The present invention provides the protein and coding sequences of human
 XX serine/threonine protein kinase 48. The sequences can be used in the
 XX treatment of cancer and HIV infection. The present sequence is a PCR
 XX primer for the coding sequence of the invention.
 XX Sequence 24 BP; 3 A; 1 C; 3 G; 17 T; 0 other;
 Query Match 1.6%; Score 17.4; DB 1; Length 24;
 Best Local Similarity 94.7%; Pred. No. 2.2e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1082 TTTAAAAA 1100
 Db 19 TTACAAAAA 1
 RESULT 213
 ABZ23536
 ID ABZ23536 standard; DNA; 24 BP.
 XX ABZ23536;
 XX 07-APR-2003 (first entry)
 XX fragment of a plasmid used to detect somatic instability.
 XX Replication error; drug development; somatic instability; ss.
 XX Synthetic.
 XX Key Location/Qualifiers
 XX misc_feature 4
 XX /*tag= a
 XX /note= "this base represents an unspecified number of
 XX bases"
 XX misc_feature 21
 XX /*tag= b
 XX /note= "this base represents an unspecified number of
 XX bases"
 XX WO200295071-A2.
 XX 28-NOV-2002.
 XX 22-MAY-2002; 2002WO-NL00322.
 XX 22-MAY-2001; 2001EP-0201936.
 XX (NEVW-) KONINK NEDERLANDSE AKAD VAN WETENSCHAPPE.
 XX (TIJS/) TIJSTERMAN M.
 XX Plasterk RHA;
 XX WPI; 2003-129440/12.
 XX Determining whether a product of a gene is involved in preventing a
 XX replication error in a cell comprises providing a specific inhibitor
 XX for the product and determining the level of expression of a marker
 XX gene -

XX Example 1; Fig 3; 47pp; English.

CC The specification describes a method for determining whether a product
 CC of a gene is involved in preventing a replication error in a cell. The
 CC method comprises providing the cell with a specific inhibitor for the
 CC product and determining the level of functional expression of a marker
 CC gene in the cell, where the level of expression of the marker gene is
 CC dependent on the occurrence of the replication error. The method is
 CC used for determining whether a product of a gene is involved in
 CC preventing a replication error in a cell. The identified genes are
 CC useful for developing diagnostic tools, or as targets for drug
 CC development to manipulate cells on the basis of the presence or absence
 CC of function of the gene. AB223535-36 represents fragments of plasmids
 CC used to detect somatic instability, in the course of the invention.

XX SQ Sequence 24 BP; 20 A; 0 C; 1 G; 1 T; 2 other;

Query Match 1.6%; Score 17.4; DB 1; Length 24;
 Best Local Similarity 90.0%; Pred. No. 2.2e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1081 ATTAAAAAATAAAAAAAAAA 1100
 :|||||
 Db 1 ATGNAAAAAAAAAA 20

RESULT 214
 AAT94431
 ID AAT94431 standard; mRNA; 19 BP.
 AC AAT94431;
 XX
 DT 02-MAR-1998 (first entry)
 XX
 DE Template mRNA poly-A tail SEQ ID NO:1 from WO9729211.
 XX
 KW Primer: detection; characterisation; mRNA; restriction display PCR;
 KW synthesis; cDNA; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO9729211-A1.
 XX
 PD 14-AUG-1997.
 XX
 PF 07-FEB-1997; 97WO-US02009.
 XX
 PR 09-FEB-1996; 96US-0011379.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Boulaawini J, Weinstein JN;
 XX
 WI; 1997-415362/38.
 XX
 PT Detection and characterisation of mRNA by restriction display PCR -
 PT comprising synthesis of cDNA, digestion with a restriction
 PT endonuclease, ligation to an adaptor DNA and PCR amplification
 XX
 PS Disclosure; Page 24; 40pp; English.

CC A method has been improved for detecting and characterising mRNA
 CC molecules which includes synthesising a double stranded (ds) cDNA from
 CC isolated mRNA, digesting the ds cDNA with a restriction endonuclease to
 CC produce cDNA fragments in which at least one end of the cDNA fragments
 CC has a sequence capable of hybridising to an adaptor DNA sequence. The
 CC improvement comprises: (a) hybridising adaptor DNA sequences to at least
 CC one end of the cDNA fragments; (b) ligating the adaptor DNA sequences
 CC to the cDNA fragments; (c) amplifying the cDNA fragments having ligated
 CC adaptor DNA sequences by a PCR using primers that hybridise to the ends
 CC of the cDNA fragments, where the primers have at least one nucleotide

CC at the 3' end that specifically hybridises to a subset of cDNA
 CC molecules; and (d) detecting the presence of the resulting amplified
 CC cDNA fragments. The present sequence represents a template poly-A tail
 CC used in the present specification. The method designates restriction
 CC display PCR can be used for characterising cells based on their mRNA
 CC content, for representing expressed genes, and for discovery of
 CC therapeutics that alter cellular gene expression. The method is also
 CC useful for characterising cells of a variety of types and under a
 CC variety of physiological conditions. The method is also useful for
 CC identifying cells or tissue from particular individuals or species
 CC based on the fingerprint obtained from the mRNA content of isolated
 CC cells or tissue and comparing it to cells or tissue from a known source.

XX SQ Sequence 19 BP; 17 A; 0 C; 0 G; 0 U; 2 other;

Query Match 1.6%; Score 17.2; DB 1; Length 19;
 Best Local Similarity 94.4%; Pred. No. 1.9e+02;
 Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAATAAAAAAAAAA 1100
 :|||||
 Db 2 BAAAAAATAAAAAAAAAA 19

RESULT 215
 AAX18390/c
 ID AAX18390 standard; DNA; 19 BP.
 XX
 AC AAX18390;
 XX
 DT 11-MAY-1999 (first entry)
 XX
 DE RT-PCR primer of the invention SEQ ID 31.
 XX
 KW RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
 OS Synthetic.
 XX
 PN JPI1032765-A.
 XX
 PD 09-FEB-1999.
 XX
 PF 18-JUL-1997; 97JP-0208312.
 XX
 PR 18-JUL-1997; 97JP-0208312.
 XX
 PA (TAKI) TAKARA SHUZO CO LTD.
 XX
 WI; 1999-183822/16.
 XX
 PT Peptides having at least two new nucleotides - useful as primers in
 PT RT-PCR
 XX
 PS Example 1; Page 12; 19pp; Japanese.

CC This sequence represents a primer of the invention. The invention relates
 CC to sequences of at least two nucleotides of formula:
 CC (X)m5'-(alpha)n-beta-N3'; or (X)m5'-(gamma)k-delta-N3'; where
 CC X = a labelled compound and/or a nucleotide with voluntary sequence;
 CC m = 0 or 1; alpha = thymine; n = natural number indicating the repetition
 CC of alpha; beta, delta = V or N; V = adenine, guanine or cytosine;
 CC N = adenine, guanine, cytosine or thymine; gamma = thymine;
 CC k = natural number of 3 or over indicating the repetition of gamma, in
 CC which thymine expressed by gamma is composed of 1/3 or less of adenine,
 CC guanine and/or cytosine. The new nucleotides are useful as primers for
 CC RT-PCR and determination of base sequences. The new sequences allow for
 CC reproductive and highly efficient analysis of gene sequences.

XX SQ Sequence 19 BP; 0 A; 0 C; 0 G; 17 T; 2 other;

Query Match 1.6%; Score 17.2; DB 1; Length 19;
 Best Local Similarity 94.4%; Pred. No. 1.9e+02;
 Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAAAAAAAAAAAAA 1100
 :|||||
 Db 18 BAAAAAAAAAAAAAAAAA 1

RESULT 216
 AAX06572/c
 ID AAX06572 standard; DNA; 19 BP.
 XX AC AAX06572;
 XX DT 06-APR-1999 (first entry)
 XX DE (-)-limonene-6-hydroxylase primer 3.B.
 XX KW (-)-limonene-6-hydroxylase; (-)-limonene-3-hydroxylase; L3H; L6H;
 KW spear mint; peppermint; enzyme; limonene hydroxylase; trans-carveol;
 KW trans-isopiperitenol; pathogen defense mechanism; attractant;
 KW environmental signal; monoterpene hydroxylase; PCR primer; ss.
 XX OS Synthetic.
 XX OS Mentha spicata.
 XX FN WO9859042-A1.
 XX PD 30-DEC-1998.
 XX PF 15-JUN-1998; 98WO-US12581.
 XX PR 24-JUN-1997; 97US-0881784.
 XX PA (UNIW) UNIV WASHINGTON STATE RES FOUND.
 XX PI Croteau RB, Karp F, Lupien SL;
 XX WPI; 1999-105618/09.
 XX DR New isolated limonene hydroxylase nucleic acids - which encode
 PT limonene-6-hydroxylase and limonene-3-hydroxylase, which can be used
 PT to produce trans-carveol and trans-isopiperitenol
 XX Example 4; Page 27; 80pp; English.
 XX The invention relates to nucleotide sequences encoding spearmint
 CC (-)-limonene-6-hydroxylase (L6H) and peppermint (-)-limonene-3-
 CC hydroxylase (L3H). Host cells containing a vector comprising the
 CC nucleotide sequences can be used for the recombinant production of
 CC limonene hydroxylases or of primary enzyme products. The primary enzyme
 CC products are trans-carveol in the case of (-)-L6H or
 CC trans-isopiperitenol in the case of (-)-L3H, which are of subsequent use,
 CC to obtain enhanced expression of limonene hydroxylase in plants to attain
 CC enhanced trans- carveol or trans-isopiperitenol production as a predator
 CC or pathogen defense mechanism, attractant or environmental signal. The
 CC limonene hydroxylase cDNAs also provide a useful tool for isolating
 CC other monoterpene hydroxylase genes and for examining the developmental
 CC regulation of monoterpene biosynthesis. Sequences AAX06564-73 represent
 CC primers for the PCR amplification of (-)-limonene-6-hydroxylase cDNA.
 XX SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 1 other;
 Query Match 1.6%; Score 17.2; DB 1; Length 19;
 Best Local Similarity 94.4%; Pred. No. 1.9e+02;
 Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAAAAAAAAAAAAA 1100
 :|||||
 Db 19 DAAAAAAAAAAAAAAAAA 2

RESULT 217
 AAZ99489/c
 ID AAZ99489 standard; DNA; 19 BP.
 XX AC AAZ99489;
 XX DT 03-JUL-2000 (first entry)
 XX DE Primer HOOK for cDNA encoding a C-20 oxidase polypeptide.
 XX KW Gibberellic acid; copalyl diphosphate synthase; 3beta-hydroxylase;
 KW 2-oxidase; phytoene synthase; C-20 oxidase; 2beta,3beta-hydroxylase;
 KW seed germination; seedling growth; gibberellin biosynthetic pathway;
 KW transgenic plant; hypocotyl; epicotyl; PCR primer; ss.
 XX OS Cucurbita maxima.
 XX FN WO200009722-A2.
 XX PD 24-FEB-2000.
 XX PF 10-AUG-1999; 99WO-US18066.
 XX PR 10-AUG-1998; 98US-0096111.
 XX PR 07-JUN-1999; 99US-0137977.
 XX PA (MONS) MONSANTO CO.
 XX PI Brown SM, Eich TD, Heck GR, Kishore GM, Logusch EW, Logusch SJ;
 PI Pillar KJ, Rao S, Ream JE;
 XX WPI; 2000-224351/19.
 XX DR Obtaining transgenic plant useful for controlling seed germination and
 PT seedling growth comprises transgene comprising a sequence expressing
 PT altered levels of an essential hormone -
 XX Example 17; Page 262; 267pp; English.
 XX The present primer was used to reverse transcribe cDNA encoding a C-20
 CC oxidase. The amplification fragment is used in the method of the invention.
 CC The specification describes methods for the inhibition and control of
 CC gibberellic acid levels. Gibberellic acid levels may be inhibited or
 CC controlled by use of a chimeric expression construct expressing a RNA or
 CC protein which suppresses the gibberellin biosynthetic pathway sequence,
 CC diverts substrate from the pathway, or degrades pathway substrates or
 CC products. The methods uses copalyl diphosphate synthase,
 CC 3beta-hydroxylase, 2-oxidase, phytoene synthase, C-20 oxidase, and a
 CC 2beta,3beta-hydroxylase polynucleotides to achieve this. The method is
 CC used to control seed germination and seedling growth especially to
 CC regulate gene products of gibberellin biosynthetic pathway and
 CC restoration of normal seed germination, in transgenic plants. The
 CC plants produced are gibberellin deficient, and have shortened hypocotyl
 CC and/or epicotyl phenotypes compared to normal plants.
 XX SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 1 other;
 Query Match 1.6%; Score 17.2; DB 1; Length 19;
 Best Local Similarity 94.4%; Pred. No. 1.9e+02;
 Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAAAAAAAAAAAAA 1100
 :|||||
 Db 19 BAAAAAAAAAAAAAAAAA 2

RESULT 218
 AAD15201/c
 ID AAD15201 standard; DNA; 19 BP.
 XX AC AAD15201;
 XX DT 01-NOV-2001 (first entry)
 XX DE 3' sequencing primer #1 to identify and characterise polynucleotides.

KW Fatty lesion development; atherosclerosis; Alzheimer's disease;
 KW nervous system disorder; Parkinson's disease; immune system disorder;
 KW ischaemia; lymphopenia; leukocyte adhesion deficiency syndrome;
 KW haemoglobinuria; anaemia; hyperproliferative disorder; Gaucher's disease;
 KW coagulation disorder; blood platelet disorder; autoimmune disorder;
 KW dermatitis; herpes simplex; Addison's disease; rheumatoid arthritis;
 KW Grave's disease; gene therapy; antiarteriosclerotic; immunostimulant;
 KW cardiovascular; antiviral; primer; ss.
 XX Unidentified.
 OS
 XX
 XX WO200154651-A2.
 PN
 XX
 XX 02-AUG-2001.
 XX
 XX 25-JAN-2001; 2001WO-US02439.
 XX
 XX 25-JAN-2000; 2000US-0177963.
 XX
 XX (DIGI-) DIGITAL GENE TECHNOLOGIES INC.
 PA
 XX Leonardi A, Sartani A, Glass JR, Sutcliffe JG, Hasel KW;
 XX WPI; 2001-514526/56.
 DR
 XX New polynucleotides regulated by fatty lesion development and their
 PT encoded polypeptides, useful for preventing, treating or ameliorating
 PT atherosclerosis, as well as for immune or hyperproliferative disorders
 PT -
 PS
 XX Example 1; Page 79; 189pp; English.
 XX
 CC The present invention relates to an isolated nucleic acid regulated by
 CC fatty lesion development, which comprises any of 55 polynucleotide
 CC sequences from Oryctolagus cuniculus. The polynucleotide, polypeptide or
 CC antibody is useful for preventing, treating, modulating or ameliorating
 CC a medical condition, particularly atherosclerosis. The invention is used
 CC as a marker or detector of nervous system disorder or disease (e.g.
 CC Parkinson's disease, Alzheimer's disease, ischaemia, dementia). The
 CC invention may also be useful for treating deficiencies or disorders of
 CC the immune system (e.g. lymphopenia, leukocyte adhesion deficiency
 CC syndrome or haemoglobinuria, anaemia), hyperproliferative disorders
 CC (e.g. Gaucher's disease), infectious disease (e.g. herpes simplex),
 CC coagulation disorders, blood platelet disorders and autoimmune disorders
 CC (Addison's disease, rheumatoid arthritis, dermatitis, Grave's disease).
 CC The polynucleotide sequence is also used in gene therapy. The present
 CC sequence is a 3' sequencing primer used in the identification and
 CC characterisation of polynucleotides up-regulated by fatty lesion
 CC development.
 XX
 SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 1 other;
 Query Match 1.6%; Score 17.2; DB 1; Length 19;
 Best Local Similarity 94.4%; Pred. No. 1.9e+02;
 Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1083 TAAAAAATAAAAAAAAAA 1100
 :|||||
 Db 19 BAAAAAATAAAAAAAAAA 2
 RESULT 219
 AAS06525/c
 ID AAS06525 standard; DNA; 19 BP.
 XX
 XX AAS06525;
 XX
 XX 07-SEP-2001 (first entry)
 XX
 DE Mouse microglia and macrophage regulatory gene primer #60.
 XX
 KW Mouse; microglia; macrophage; regulatory gene; digital sequence tag;
 KW DST; PCR-based total gene expression analysis; TOGA; infectious disorder;

KW neuroinflammatory pathology; neurodegenerative disease; gene therapy;
 KW hyperproliferative disorder; autoimmune; inflammatory disorder;
 KW primer; ss.
 XX
 OS Mus musculus.
 XX WO200134770-A2.
 PN
 XX 17-MAY-2001.
 PD
 XX
 XX 06-NOV-2000; 2000WO-US30585.
 XX
 XX 12-NOV-1999; 99WO-US26824.
 PR
 XX 03-MAR-2000; 2000US-0186770.
 PR
 XX 19-JUN-2000; 2000US-0212465.
 XX
 XX (DIGI-) DIGITAL GENE TECHNOLOGIES INC.
 PA
 XX Carson MJ, Sutcliffe JG, Almazan MT, Tobal GW;
 PI WPI; 2001-308782/32.
 DR
 XX New regulated genes of microglia and macrophages, useful for
 PT diagnosing, preventing or treating neuroinflammatory pathology and
 PT neurodegenerative disease -
 PT
 XX Example 1; Page 88; 244pp; English.
 PS
 XX The present sequence represents a primer used to isolate novel
 CC mouse microglia and macrophage regulatory gene DST (digital sequence
 CC tag) sequences. AAS06401-AAS06590 represent these novel sequences and
 CC the primer sequences used to isolate them. The PCR-based total gene
 CC expression analysis (TOGA) system is used to examine the expression
 CC pattern of molecules corresponding to genes that are regulated in
 CC unstimulated microglia, activated microglia, unstimulated macrophage and
 CC activated macrophage. The polynucleotides of the invention, the
 CC polypeptides encoded by them and antibodies that bind to these
 CC polypeptides are useful for the diagnosis, prevention,
 CC treatment or amelioration of a medical condition, preferably a
 CC neuroinflammatory pathology or a neurodegenerative disease such as
 CC Alzheimer's disease, senile dementia, Parkinson's disease, obsessive
 CC compulsive disorders, epilepsy, schizophrenia, multiple sclerosis,
 CC depression and bipolar manic-depressive disorder. The sequences and
 CC methods of the invention can also be used for detecting or treating
 CC infectious disorders (e.g. AIDS), hyperproliferative disorders
 CC (e.g. cancer), immune disorders (e.g. severe combined immunodeficiency,
 CC SCID) autoimmune diseases (e.g. insulin dependent diabetes mellitus),
 CC inflammatory disorders (e.g. arthritis). The polynucleotides can be used
 CC for gene therapy.
 XX
 SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 1 other;
 Query Match 1.6%; Score 17.2; DB 1; Length 19;
 Best Local Similarity 94.4%; Pred. No. 1.9e+02;
 Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1083 TAAAAAATAAAAAAAAAA 1100
 :|||||
 Db 19 BAAAAAATAAAAAAAAAA 2
 RESULT 220
 AAH21968/c
 ID AAH21968 standard; DNA; 19 BP.
 XX
 XX AAH21968;
 XX
 XX 16-AUG-2001 (first entry)
 XX
 DE Mouse total gene expression analysis (TOGA) 3' sequencing primer SEQ:92.
 XX
 KW Mouse; human; total gene expression analysis; TOGA; DST; EST;
 KW digital sequence tag; expressed sequence tag; neuroleptic; antimanic;

central nervous system; antidepressant; gene therapy; diagnosis; neuropsychiatric disorder; schizophrenia; bipolar disorder; addition-related behaviour; chromosome identification; immune response; PCR primer; probe; ss.

Mus musculus.

WO200130972-A2.

03-MAY-2001.

26-OCT-2000; 2000WO-US29690.

26-OCT-1999; 99US-0161379.

(DIGI-) DIGITAL GENE TECHNOLOGIES INC.

Thomas EA, Sutcliffe JG, Pribyl TM, Hilbush B, Hasel KW; WPI; 2001-300499/31.

New neuroleptic-regulated polynucleotides expressed in the central nervous system for diagnosing and treating neuropsychiatric disorders such as schizophrenia, bipolar disorder and addiction-related behavior

Example 1; Page 87; 210pp; English.

The present invention describes isolated neuroleptic-regulated nucleic acid molecules. (I) have neuroleptic, antimanic and antidepressant activities, and can be used in gene therapy. (I), polypeptides (II) encoded by (I), or a host cell (III) comprising (I), are useful for preventing, treating, modulating or ameliorating a medical condition such as a neuropsychiatric disorder. (I) are useful as diagnostic agents for diagnosing a pathological condition or susceptibility to a pathological condition such as neuropsychiatric disorder e.g. schizophrenia, a bipolar disorder or addiction-related behavior. (I) are useful for detecting the presence of a nucleic acid encoding a protein in a mammalian tissue sample. (I) can be used as probes and primers, for chromosome identification, to control gene expression through triple helix formation or antisense DNA or RNA, in gene therapy to treat the above mentioned disorders, identifying individuals from minute biological samples, as an alternative to restriction fragment length polymorphism (RFLP) and as polymorphic markers for forensic purposes. (I) is also useful as molecular weight markers on Southern gels, diagnostic probes for the presence of specific mRNA in a particular cell type, as a probe to subtract-out known sequences in the process of discovering novel polynucleotides, for selecting and making oligomers for attachment to a gene chip or other support, to raise anti-DNA antibodies using DNA immunisation technique, and as an antigen to elicit an immune response. AAH21877 to AAH21984, AAB98083 and AAB98084 represent sequences used in the exemplification of the present invention.

Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 1 other;

Query Match 1.6%; Score 17.2; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 1.9e+02;
Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1083 TAAAAAATAAAAAAAAAA 1100
:|||||
Db 19 BAAAAAATAAAAAAAAAA 2

RESULT 221
AAF76617/c
ID AAF76617 standard; DNA; 19 BP.
AC AAF76617;
XX
XX
DT 15-MAY-2001 (first entry)
XX
DE Spearmint (-)-limonene-6-hydroxylase PCR primer SEQ ID NO: 18.

central nervous system; antidepressant; gene therapy; diagnosis; neuropsychiatric disorder; schizophrenia; bipolar disorder; addition-related behaviour; chromosome identification; immune response; PCR primer; probe; ss.

Mus musculus.

WO200130972-A2.

03-MAY-2001.

26-OCT-2000; 2000WO-US29690.

26-OCT-1999; 99US-0161379.

(DIGI-) DIGITAL GENE TECHNOLOGIES INC.

Thomas EA, Sutcliffe JG, Pribyl TM, Hilbush B, Hasel KW; WPI; 2001-300499/31.

New neuroleptic-regulated polynucleotides expressed in the central nervous system for diagnosing and treating neuropsychiatric disorders such as schizophrenia, bipolar disorder and addiction-related behavior

Example 1; Page 87; 210pp; English.

The present invention describes isolated neuroleptic-regulated nucleic acid molecules. (I) have neuroleptic, antimanic and antidepressant activities, and can be used in gene therapy. (I), polypeptides (II) encoded by (I), or a host cell (III) comprising (I), are useful for preventing, treating, modulating or ameliorating a medical condition such as a neuropsychiatric disorder. (I) are useful as diagnostic agents for diagnosing a pathological condition or susceptibility to a pathological condition such as neuropsychiatric disorder e.g. schizophrenia, a bipolar disorder or addiction-related behavior. (I) are useful for detecting the presence of a nucleic acid encoding a protein in a mammalian tissue sample. (I) can be used as probes and primers, for chromosome identification, to control gene expression through triple helix formation or antisense DNA or RNA, in gene therapy to treat the above mentioned disorders, identifying individuals from minute biological samples, as an alternative to restriction fragment length polymorphism (RFLP) and as polymorphic markers for forensic purposes. (I) is also useful as molecular weight markers on Southern gels, diagnostic probes for the presence of specific mRNA in a particular cell type, as a probe to subtract-out known sequences in the process of discovering novel polynucleotides, for selecting and making oligomers for attachment to a gene chip or other support, to raise anti-DNA antibodies using DNA immunisation technique, and as an antigen to elicit an immune response. AAH21877 to AAH21984, AAB98083 and AAB98084 represent sequences used in the exemplification of the present invention.

Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 1 other;

Query Match 1.6%; Score 17.2; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 1.9e+02;
Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1083 TAAAAAATAAAAAAAAAA 1100
:|||||
Db 19 BAAAAAATAAAAAAAAAA 2

RESULT 221
AAF76617/c
ID AAF76617 standard; DNA; 19 BP.
AC AAF76617;
XX
XX
DT 15-MAY-2001 (first entry)
XX
DE Spearmint (-)-limonene-6-hydroxylase PCR primer SEQ ID NO: 18.

XX
KW Spearmint; peppermint; (-)-limonene-6-hydroxylase;
KW (-)-limonene-3-hydroxylase; flavour; aroma; probe; PCR primer; ss.
XX
OS Mentha spicata.
XX
PN US6194185-B1.
XX
PD 27-FEB-2001.
XX
PF 14-APR-1999; 99US-0292768.
XX
PR 24-JUN-1997; 97US-0881784.
XX
PA (UNIW) UNIV WASHINGTON STATE RES FOUND.
XX
PI Croteau RB, Lupien SL, Karp F;
XX
DR WPI; 2001-243405/25.
XX
PT Novel isolated limonene hydroxylase encoding nucleic acid molecule,
PT useful for altering production of limonene-6-hydroxylase or
PT limonene-3-hydroxylase in suitable host cell -
XX
PS Example 4; Column 55; 57pp; English.
XX
CC The present invention provides the protein and coding sequences of the
CC peppermint and spearmint (-)-limonene-3-hydroxylase and the spearmint
CC (-)-limonene-6-hydroxylase. Also provided are a number of probes and PCR
CC primers which were used to isolate the sequences. These are useful in the
CC production of transgenic plants with altered flavour and aroma.
XX
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 1 other;
Query Match 1.6%; Score 17.2; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 1.9e+02;
Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1083 TAAAAAATAAAAAAAAAA 1100
:|||||
Db 19 BAAAAAATAAAAAAAAAA 2

RESULT 222
AAD40279/c
ID AAD40279 standard; DNA; 19 BP.
XX
AC AAD40279;
XX
DT 22-OCT-2002 (first entry)
XX
DE HOOK PCR primer used to isolate pumpkin 2beta-3beta hydroxylase cDNA.
XX
KW Gibberellin; transgenic plant; seed germination; seedling growth; GA;
KW transgenic; 2beta-3beta hydroxylase; enzyme; pumpkin; PCR; primer; ss.
OS Cucurbita pepo.
XX
PN US2002053095-A1.
XX
PD 02-MAY-2002.
XX
PF 10-AUG-1999; 99US-0371307.
XX
PR 10-AUG-1999; 99US-0371307.
XX
PA (BROW/) BROWN S M.
XX
PI Brown SM, Elich TD, Heck GR, Kishore GM, Logusch EW, Logusch SJ;
PI Piller KU, Rao S, Ream JE;
XX
DR WPI; 2002-489107/52.

PT Control of gibberellin levels in plants useful to avoid unfavorable
 PT conditions in crops to increase yields, using transgenic plants having
 PT reduced seed germination and early seedling growth then treatment to
 PT restore these properties -
 XX Example 19; Page 104; 155pp; English.

XX The invention relates to control of gibberellin (GA) levels in plants.
 CC The method involves producing transgenic plants having a phenotype
 CC of reduced seed germination and reduced early seedling growth, then
 CC restoring seed germination and early seedling growth by treating
 CC plants with an appropriate compound when conditions are favourable.
 CC The method is useful to control seed germination and/or early seedling
 CC growth in agricultural production so that unfavorable environmental
 CC conditions normally reducing agronomic output can be avoided and
 CC yields increased. Plants also demonstrate increased uniformity of
 CC germination, emergence and seedling vigor, so increasing yields at
 CC harvest. The method is especially useful in crop plants such as e.g.
 CC canola, soybean, cotton, etc., and is also useful in storage and
 CC transport of seeds to reduce premature germination which may affect
 CC agronomic or food quality of the seeds. The present sequence is a
 CC PCR primer used to isolate pumpkin 2beta-3beta hydroxylase cDNA.
 CC This primer is used in the exemplification of the invention

XX Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 1 other;

Query Match 1.6%; Score 17.2; DB 1; Length 19;
 Best Local Similarity 94.4%; Pred. No. 1.9e+02;
 Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAATAAAAAAAAAA 1100
 :|||||
 Db 19 BAAAAAATAAAAAAAAAA 2

RESULT 223

ABQ73231/c

ID ABQ73231 standard; DNA; 19 BP.

AC ABQ73231;

XX 27-SEP-2002 (first entry)

DE Rabbit atherosclerosis related TOGA primer SEQ ID NO:26.

XX Rabbit; Oryctolagus cuniculus; atherosclerosis; intimal hyperplasia;
 KW TOGA primer; ss.
 KW Oryctolagus cuniculus.
 OS Synthetic.

OS WO200242420-A2.

FN 30-MAY-2002.

PD 21-NOV-2001; 2001WO-US44072.

XX 21-NOV-2000; 2000US-252216P.

PR (DIGI-) DIGITAL GENE TECHNOLOGIES INC.

PA Leonard A, Sartani A, Glass JR, Hasel KW;

PI WPI; 2002-575233/61.

DR New polynucleotides related to regulated genes characteristic of

XX atherosclerosis, useful for diagnosing, preventing, treating,
 PT modulating or ameliorating atherosclerosis in a mammalian subject
 XX Disclosure: Page 28; 130pp; English.

PS The present invention describes an isolated polynucleotide (I) and its
 CC complements, and degenerate variants, comprising a sequence selected
 CC

CC from those given in ABQ73206 to ABQ73222 (NS), which is a digital
 CC sequence tag (NST) corresponding to mRNAs whose expression is regulated
 CC by proliferative lesion development caused by mechanically induced
 CC intimal hyperplasia, or by lercanidipine treatment, or by proliferative
 CC lesions and reversed by lercanidipine treatment. (I) has
 CC antiatherosclerotic activity and can be used in gene therapy. (I) can be
 CC used for diagnosing a medical condition (e.g. atherosclerosis) in a
 CC subject which involves determining the presence or absence of a mutation
 CC in (I) and diagnosing the medical condition based on the presence or
 CC absence of the mutation. (I) is also useful for diagnosing
 CC atherosclerosis, or the susceptibility to atherosclerosis in a subject
 CC which involves detecting an alteration (an increase or decrease) in
 CC amount of expression of (I). (I) is also useful for diagnosing or
 CC monitoring the effects of treating a subject with dihydropyridine
 CC calcium antagonist e.g., lercanidipine. (I) can also be used for
 CC preventing, treating, modulating, or ameliorating a medical condition
 CC such as atherosclerosis in a mammalian subject. The present sequence
 CC represents a TOGA primer which is used in the exemplification of the
 CC present invention.

XX Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 1 other;

Query Match 1.6%; Score 17.2; DB 1; Length 19;
 Best Local Similarity 94.4%; Pred. No. 1.9e+02;
 Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAATAAAAAAAAAA 1100
 :|||||
 Db 19 BAAAAAATAAAAAAAAAA 2

RESULT 224

ABK71509/c

ID ABK71509 standard; DNA; 19 BP.

AC ABK71509;

XX 30-JUL-2002 (first entry)

DE CNS related 3' sequencing primer.

XX Central nervous system; CNS; neuroleptic; mouse; human; psychoses;
 KW neuropsychiatric disorder; psychiatric disorder; Alzheimer's disease;
 KW Pick's disease; Binswanger's disease; senile dementia; encephalopathy;
 KW Parkinson's disease; obsessive compulsive disorder; epilepsy;
 KW ischaemia; addiction; multiple sclerosis; depression;
 KW manic-depressive disorder; primer; ss.

OS Synthetic.

OS WO200226936-A2.

FN 04-APR-2002.

PD 01-OCT-2001; 2001WO-US30695.

XX 29-SEP-2000; 2000US-236790P.

PR 18-JAN-2001; 2001US-263084P.

XX (DIGI-) DIGITAL GENE TECHNOLOGIES INC.

PA Thomas EA, Sutcliffe JG, Pribyl TM, Hilbush BS, Hasel KW;

PI WPI; 2002-383271/41.

DR New polynucleotide useful in gene therapy for preventing, treating
 XX modulating or ameliorating a medical condition such as psychoses or a
 PT neuro psychiatric disorder e.g. schizophrenia, or a bipolar disorder in
 XX a mammal -
 PS Example 1; Page 40; 254pp; English.

XX This invention relates to the cDNA sequences of novel isolated

CC polynucleotides associated with psychoses or other neuropsychiatric disorders. The sequences of the invention may act as blockers of D₂ receptors in the meso-limbic dopamine system. The nucleotide sequences of the invention and the polypeptides encoded by them are useful in the manufacture of a medicament useful for preventing, treating, modulating or ameliorating a medical condition e.g. a neuropsychiatric disorder. An antibody that binds the proteins of the invention is useful for preventing, treating, modulating or ameliorating neurological disorders such as psychoses or other neuropsychiatric disorders in a subject. The sequences are also useful for diagnosing neurological disorders or a susceptibility to a neurological disorder such as psychoses and other neuropsychiatric disorders in a subject by determining the presence or absence of mutation in the nucleotide sequence of apolipoprotein D or by determining the alteration (increase or decrease) in the expression of apolipoprotein D. The sequences of the invention are useful in treating deficiencies or disorders of the central nervous system or peripheral nervous system by activating or inhibiting the proliferation, differentiation or mobilisation (chemotaxis) of neuroblasts, stem cells or glial cells. The sequences are useful as a marker or detector of a particular nervous system disease or disorder such as Alzheimer's disease, Pick's disease, Binswanger's disease, other senile dementia, Parkinson's disease, obsessive compulsive disorders, epilepsy, encephalopathy, ischaemia, addiction, multiple sclerosis, depression and manic-depressive disorder. The present sequence represents an oligonucleotide primer used in the identification of the cDNA sequences of the invention.

SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 1 other;

Query Match 1.6%; Score 17.2; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 1.9e+02;
Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1083 TAAAAA...AAAAA 1100
Db 19 BAAAAA...AAAAA 2

RESULT 225
AAD34663/C

ID AAD34663 standard; DNA; 19 BP.

AC AAD34663;

DT 16-JUL-2002 (first entry)

DE PCR primer #4 used for direct sequencing of TOGA generated PCR products.
KW Hepatitis B virus; HBV infection; chronic hepatitis; toxicity; virucide;
KW acute hepatitis; therapeutic; gene therapy; vaccine; infectious disease;
KW TOGA; Total Gene Expression Analysis; PCR; primer; ss.

OS Unidentified.

PN W0200222783-A2.

PD 21-MAR-2002.

PF 17-SEP-2001; 2001WO-US29123.

PR 15-SEP-2000; 2000US-233176P.

PA (DIGI-) DIGITAL GENE TECHNOLOGIES INC.

PI Chisari FV, Wieland SF, Guidotti LGDVM, Mueller R, Hilbush BS;

DR WPI; 2002-339865/37.

PT Preventing and treating hepatitis viral infection in a mammal,
PT comprises administering nucleic acid molecules that up- or
PT down-regulate in hepatitis B virus infection or polypeptides encoded by
PT the nucleic acid molecules -

PS Disclosure; Page 28; 125pp; English.

XX The present invention relates to a method for preventing, treating, modulating or ameliorating a medical condition. The method involves administering one or more nucleic acid molecules up- or down-regulated in hepatitis B virus (HBV) infection or polypeptides encoded by the nucleic acid molecules or antibodies that bind to the polypeptide. The method is useful for preventing, treating, modulating or ameliorating a medical condition. It is also useful for determining the presence or absence of a mutation in the nucleic acid molecules or detecting an alteration in expression of the polypeptide which is useful for the diagnosis of hepatitis viral infection. The method is useful for assessing the stage of hepatitis viral infection (e.g., acute hepatitis versus chronic hepatitis) or assessing the efficacy or toxicity of therapeutic treatment for hepatitis viral infection and a gene expression profile is useful for identifying polypeptides and polynucleotides which are associated with hepatitis viral infection. Sequences of the invention are used in gene therapy and as vaccines. Nucleic acid sequences are useful as a diagnostic marker for HBV infection and for treating infectious diseases. The present DNA sequence is a PCR primer which is used for direct sequencing of TOGA (Total Gene Expression Analysis) generated PCR products.

SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 1 other;

Query Match 1.6%; Score 17.2; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 1.9e+02;
Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1083 TAAAAA...AAAAA 1100
Db 19 BAAAAA...AAAAA 2

RESULT 226

ABZ68389/C

ID ABZ68389 standard; DNA; 19 BP.

AC ABZ68389;

DT 22-APR-2003 (first entry)

DE Reverse transcription primer used to produce yeast cDNA.

KW Histone acetyltransferase; histone deacetylase; gene expression profile;
KW chromatin-associated protein; gene expression; primer; ss.

OS Synthetic.

PN W02003000715-A1.

PD 03-JAN-2003.

PF 21-JUN-2002; 2002WO-US19750.

PR 22-JUN-2001; 2001US-300135P.

PA (CERE-) CERES INC.

PI Dang V, Okamura J;

DR WPI; 2003-175280/17.

XX New chimeric polypeptide comprising a histone acetyltransferase
XX polypeptide segment and a segment comprising a histone deacetylase
XX chromatin-associated protein complex subunit, useful for modulating
XX gene expression in cells -

PS Example 10; Page 54; 85pp; English.

CC The specification describes chimeric histone acetyltransferase
CC polypeptides. The chimeric polypeptides comprise a polypeptide segment
CC that exhibits histone acetyltransferase activity, and a polypeptide

CC segment having 40% or greater sequence identity to a subunit of a
 CC histone deacetylase chromatin-associated protein complex. The chimeric
 CC polypeptides are useful for determining gene expression profiles in
 CC specific cells, for modulating gene expression in specific cells, and
 CC for making genetically modified eukaryotes. The present sequence
 CC represents a reverse transcription primer used in the method of the
 CC invention.

XX SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 1 other;

Query Match 1.6%; Score 17.2; DB 1; Length 19;
 Best Local Similarity 94.4%; Pred. No. 1.9e+02;
 Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1083 TAAAAA...AAAAA 1100
 :|||||
 Db 19 BAAAAA...AAAAA 2

RESULT 227
 AAD50267/c

ID AAD50267 standard; DNA; 19 BP.
 XX AC AAD50267;
 AC

DT 24-MAR-2003 (first entry)

XX 3' sequencing primer #1 used to illustrate the method of the invention.
 DE Gene expression; drug interaction mechanism; drug screening; primer;
 XX genomic mapping; ss.

XX Unidentified.

XX WO200261045-A2.

XX 08-AUG-2002.

XX 01-FEB-2002; 2002WO-US02666.

XX 01-FEB-2001; 2001US-0775217.

XX (DIGI-) DIGITAL GENE TECHNOLOGIES INC.
 PA (QUAN/) QUAN J.

PI Quan J, Hilbush BS, Hasel KW, Sutcliffe GJ, Chang HW;
 PI Callahan MA;

XX WPI; 2003-092784/08.

XX Simplified TOGA method for simultaneous sequence-specific
 PT identification of multiple mRNA molecules in RNA population, useful
 PT for determining tissue-specific patterns of gene expression or
 PT mechanisms of drug interaction -

PS Disclosure; Page 39; 93pp; English.

XX The present invention relates to a novel simplified TOGA (RTM) method for
 CC simultaneous sequence-specific identification of multiple mRNA molecules
 CC in a RNA population. The method involves characterising each of the
 CC sequence-specific polymerase chain reaction (PCR) products by partial
 CC sequence and length. The method is useful for determining tissue-specific
 CC patterns of gene expression or mechanisms of drug interaction. It is
 CC also useful for drug screening, studying physiological processes, genomic
 CC mapping or manufacture of diagnostic, prognostic or therapeutic reagents.
 CC The present sequence is a primer used to illustrate the method of the
 CC invention.

XX SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 1 other;

Query Match 1.6%; Score 17.2; DB 1; Length 19;
 Best Local Similarity 94.4%; Pred. No. 1.9e+02;
 Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1083 TAAAAA...AAAAA 1100
 :|||||
 Db 19 BAAAAA...AAAAA 2

RESULT 228
 AAD49149/c

ID AAD49149 standard; DNA; 19 BP.

XX AC AAD49149;

XX DT 07-MAR-2003 (first entry)

XX 3' sequencing primer #1 used in the invention.

XX Atherosclerosis; vaccine; nervous system disorder; Alzheimer's disease;
 KW Parkinson's disease; multiple sclerosis; immune disorder; gene therapy;
 KW autoimmune disorder; rheumatoid arthritis; hyperproliferative disorder;
 KW haemolytic anaemia; graft-versus-host disease; inflammation; infection;
 KW epilepsy; Addison's disease; neoplasm; tissue regeneration; chemotaxis;
 KW food additive; food preservative; primer; ss.

XX Unidentified.

XX WO200281726-A2.

XX 17-OCT-2002.

XX 15-NOV-2001; 2001WO-US43741.

XX 15-NOV-2000; 2000US-248992P.

XX 28-NOV-2000; 2000US-253623P.

XX (DIGI-) DIGITAL GENE TECHNOLOGIES INC.

XX Leonardi A, Sartani A, Glass J, Sutcliffe JG, Hasel KW;

XX WPI; 2003-058561/05.

XX New polypeptide associated with atherosclerosis, useful for treating
 PT atherosclerosis, nervous system disorders, immune disorders,
 PT hyperproliferative disorders and infectious diseases -

PS Disclosure; Page 139; 146pp; English.

XX The invention relates to polynucleotides and polypeptides associated
 CC with atherosclerosis. Polynucleotides of the invention are useful
 CC for delivery of genes, DNA vaccines, diagnostic reagents, peptides,
 CC proteins or macromolecules. Sequences of the invention are useful
 CC for treating nervous system disorders (e.g., Alzheimer's disease,
 CC Parkinson's disease, multiple sclerosis, epilepsy), immune disorders
 CC (e.g., autoimmune disorders such as rheumatoid arthritis, Addison's
 CC disease, haemolytic anaemia, graft-versus-host disease, inflammation),
 CC hyperproliferative disorders (e.g., neoplasms) and infectious diseases
 CC (e.g., viral, bacterial, fungal or parasite infection). They are used
 CC for regeneration of tissues, to repair, replace or protect damage
 CC tissues, for increasing chemotaxis activity of cells, for increasing
 CC or decreasing the differentiation or proliferation of embryonic stem
 CC cells from a lineage, for modulating mammalian characteristics, (such
 CC as body weight or height), for modulating mammalian metabolism
 CC affecting catabolism, anabolism, processing utilisation and storage
 CC of energy, to change a mammal's mental or physical state, or as a food
 CC additive or preservative. The invention is useful in gene therapy. The
 CC present sequence is a sequencing primer used in the invention.

XX SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 1 other;

Query Match 1.6%; Score 17.2; DB 1; Length 19;
 Best Local Similarity 94.4%; Pred. No. 1.9e+02;
 Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1083 TAAAAA...AAAAA 1100

Db 19 BAAAAAAAAAAAAAAAAA 2

RESULT 229
AAZ09197/c
ID AAZ09197 standard; DNA; 20 BP.

XX AC AAZ09197;
XX DT 19-OCT-1999 (first entry)
XX DE Oligonucleotide 9 for DNA analysis.

XX KW Primer; DNA analysis; amplification; hybridisation; ss.
XX OS Synthetic.

XX PN JP11196874-A.

XX PD 27-JUL-1999.

XX PF 14-JAN-1998; 98JP-0005399.

XX PR 14-JAN-1998; 98JP-0005399.

XX PA (HITA) HITACHI LTD.

XX DR WPI; 1999-496652/42.

XX PT Analysis of DNA fragment - comprises addition of known common oligonucleotide, amplification of resultant DNA fragment and analysis and labelling of amplified DNA

XX PS Example 5; Page 12; 17pp; Japanese.

CC This invention describes a novel method for the analysis of a DNA fragment which comprises: (i) addition of a known common oligonucleotide sequence to at least one terminal of each DNA fragment, (ii) amplification of the resultant DNA fragment as a primer using a first common primer containing a complementary nucleotide sequence to the above mentioned known common oligonucleotide sequence, a second common primer containing a complementary nucleotide sequence to the prepared known common oligonucleotide sequence optionally having been introduced with complementary nucleotide sequence at a terminal, and a specific primer capable of hybridisation with a DNA fragment containing whole or part of the gene having known sequence, to give amplified DNA, (iii) analysis of the amplified DNA to find the information of the DNA fragment, in which the specific primer is designed to prepare fragments of the common first and second primers and to give short fragment of amplified DNA and (iv) labelling them to make their differentiation. Differentiation of information of known and unknown genes readily provides information of unknown gene and simultaneous monitoring of signals derived from minor genes. Furthermore, labelling of DNAs according to functions of known genes can be performed. AAZ09189-Z09201 represent oligonucleotide primers used to illustrate the method of the invention.

XX SQ Sequence 20 BP; 0 A; 0 C; 0 G; 18 T; 2 other;

Query Match 1.6%; Score 17.2; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 2e+02;
Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAAAAAAAAAAAAA 1100

Db 19 BAAAAAAAAAAAAAAAAA 2

RESULT 230
AAC69376
ID AAC69376 standard; DNA; 22 BP.

AC AAC69376;
XX 29-JAN-2001 (first entry)
XX Human ABC1 BAC contig polymorphic site, SEQ ID NO:275.
XX Human ABC1 cholesterol transporter; chromosome 9q31;
XX KW ATP-binding cassette; HDL deficiency disorder; high density lipoprotein;
XX KW Tangier disease; TD; familial HDL deficiency; FHA; polymorphism;
XX KW cerebrovascular disease; coronary artery disease; coronary restenosis;
XX KW Alzheimer's disease; Niemann-Pick disease; Huntington's disease;
XX KW X-linked adrenoleukodystrophy; cancer; gene therapy; genetic diagnosis;
XX KW prognosis; prophylaxis; drug screening; transgenic animal; ds.
XX OS Homo sapiens.
XX PN WO200055318-A2.
XX PD 21-SEP-2000.
XX PF 15-MAR-2000; 2000WO-IB00532.
XX PR 15-MAR-1999; 99US-0124702.
XX PR 08-JUN-1999; 99US-0138048.
XX PR 17-JUN-1999; 99US-0139600.
XX PR 01-SEP-1999; 99US-0151977.
XX PA (UYBR-) UNIV BRITISH COLUMBIA.
XX PA (XENO-) XENON BIORESEARCH INC.
XX PI Hayden MR, Wilson AR, Pimstone SN;
XX DR WPI; 2000-587528/55.
XX PT New ABC1 polypeptide is useful for treating diseases associated with
XX PT ABC1 biological activity, e.g. Alzheimer's disease, Huntington's
XX PS disease and cancer -
XX PS Examples; Fig 11; 229pp; English.
XX CC The invention relates to the human ABC1 cholesterol transporter protein
XX CC (B38082) and to nucleic acid sequences (C69120) which encode it. ABC1 is
XX CC a member of the ABC-binding cassette (ABC transporter) superfamily of
XX CC proteins, and plays a crucial role in cholesterol transport, particularly
XX CC intracellular cholesterol trafficking in monocytes and fibroblasts, being
XX CC involved in cholesterol efflux from the cell. The gene encoding ABC1 is
XX CC located on chromosome 9q31, and mutations in this gene are associated
XX CC with two genetic HDL (high density lipoprotein) deficiency disorders,
XX CC Tangier disease (TD) and familial HDL deficiency (FHA). These diseases
XX CC are distinguishable in that TD is an autosomal recessive disorder, while
XX CC FHA is inherited as an autosomal dominant trait. Low levels of HDL ("good
XX CC cholesterol") in the blood correlate with a high risk of cardiovascular
XX CC disease, particularly coronary artery disease, but also cerebrovascular
XX CC disease, coronary restenosis, and peripheral vascular disease.
XX CC Conversely, a high level of HDL has protective effects against
XX CC cardiovascular disease. The invention provides genetic constructs and
XX CC transgenic cells and non-human animals comprising human ABC1 nucleic
XX CC acids, and methods of gene therapy for the treatment or prevention of
XX CC cardiovascular disease comprising the administration of an expression
XX CC vector encoding ABC1 or an active fragment thereof. The invention also
XX CC encompasses compounds which mimic ABC1 activity, compounds which
XX CC stimulate ABC1 expression and methods of screening for such compounds.
XX CC It further relates to methods for determining whether a patient has an
XX CC increased risk for cardiovascular disease due to polymorphisms in the
XX CC ABC1 gene. Human ABC1 proteins and nucleotides can be used to treat
XX CC or prevent cardiovascular disease, especially coronary artery disease,
XX CC cerebrovascular disease, coronary restenosis or peripheral vascular
XX CC disease. They may also be used in the treatment of diseases associated
XX CC with ABC1 biological activity, such as Alzheimer's disease, Niemann-Pick
XX CC disease, Huntington's disease, X-linked adrenoleukodystrophy and cancer.
XX CC The invention specifically excludes proteins with the exact amino acid
XX CC sequences of GenBank Accession No: CAA10005.1 and X75926, and the nucleic

CC acid with the exact sequence as GenBank Accession No: AJ012376.1.
 CC The present sequence represents a polymorphic site of the human ABCI
 CC gene.

XX SQ Sequence 22 BP; 6 A; 2 C; 11 G; 3 T; 0 other;
 Query Match 1.6%; Score 17.2; DB 1; Length 22;
 Best Local Similarity 86.4%; Pred. No. 2.2e+02;
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 991 TTGGAGTCTGAGCTGGAGAA 1012
 ||||| ||||| ||||| |||||
 Db 1 TTGGAGGCTGAGCGAGAGAA 22

RESULT 231
 AAL50570/C
 ID AAL50570 standard; DNA; 22 BP.

XX AC AAL50570;

XX DT 12-DEC-2002 (first entry)

XX DE Molecular array production method-related PCR primer.

XX KW Molecular array; ss; target molecule identification; genetic analysis;
 XX gene expression; SNP detection; haplotyping; sequencing; PCR; primer.

XX OS Unidentified.

XX FN WO200274988-A2.

XX PD 26-SEP-2002.

XX PF 18-MAR-2002; 2002WO-GB01245.

XX PR 16-MAR-2001; 2001GB-0006635.

XX PR 02-AUG-2001; 2001GB-0018879.

XX PA (UYCH-) UNIV CHANCELLOR MASTER & SCHOLARS OXF.

XX PI Mir K;

XX XX WPI; 2002-732872/79.

XX PT Producing a molecular array with a plurality of molecules immobilized
 to a solid substrate, useful in genetic analysis, gene expression
 studies or the detection or typing of single nucleotide polymorphisms
 in a sample of nucleic acids -

XX FS Example 15; Page 122; 166pp; English.

XX CC The invention comprises a method for producing a molecular array, the
 method involves immobilising molecules to a solid phase at a density
 which allows individual immobilised molecules to be individually
 resolved. The molecular array produced by the method of the invention is
 useful for identifying one or more target molecules in a sample. The
 molecular array is also useful in genetic analysis, gene expression
 studies, identifying molecules which interact with a target molecule,
 detection/typing of single nucleotide polymorphisms, haplotyping and
 sequencing. The present DNA sequence represents a PCR primer that was
 used in an example of the invention.

XX SQ Sequence 22 BP; 0 A; 0 C; 0 G; 20 T; 2 other;

Query Match 1.6%; Score 17.2; DB 1; Length 22;
 Best Local Similarity 94.4%; Pred. No. 2.2e+02;
 Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAATAAAAAAAAAA 1100
 :|||||
 Db 21 BAAAAAATAAAAAAAAAA 4

RESULT 233
 ABX74887/C
 ID ABX74887 standard; DNA; 22 BP.
 XX

RESULT 232
 AAD51324/C

XX ID AAD51324 standard; DNA; 22 BP.

XX AC AAD51324;

XX DT 16-APR-2003 (first entry)

XX DE Anchored oligo dT primer used to illustrate the method of the invention.
 XX KW Laminitis; viral disease; vaccine; bacterial disease; primer; epistaxis;
 XX KW gastritis; gastric ulcer; respiratory ailment; fracture; joint disease;
 XX KW musculoskeletal damage; ss.

XX OS Unidentified.

XX FN WO200290579-A1.

XX PD 14-NOV-2002.

XX PF 03-MAY-2002; 2002WO-AU00553.

XX PR 04-MAY-2001; 2001AU-0004809.

XX PR 29-JUN-2001; 2001US-0896941.

XX PA (GENO-) GENOMICS RES PARTNERS PTY LTD.

XX PI Brandon RB;

XX XX WPI; 2003-120558/11.

XX PT Assessing condition e.g. athletic ability, stage of disease, presence
 of drugs, response to exercise, response to vaccines, therapies,
 nutritional states, of performance animal involves analyzing nucleic
 acid expression -

XX PS Disclosure; Page 46; 87pp; English.

XX CC The invention relates to a method for assessing a condition of a
 performance animal. The method involves determining in sample abundance
 of expressed target nucleic acid; transmitting digital sample signal to
 remote diagnostic server; processing digital sample signal at remotely
 located database to correlate digital signal with digital information
 and returning report of particular condition of animal. The method is
 useful for assessing a condition of a performance animal preferably
 human, dog or camel. The condition can be an athletic ability and a
 condition that enhances, hinders, impedes or does not change an expected
 ability of the performance animal; and also normal, pre-clinical, overt
 progress and/or stage of disease, undiagnosed or unclassified conditions,
 presence of drugs, response to exercise, response to vaccines, therapies,
 nutritional states and response to environmental conditions. Diseases
 assessed by the invention include laminitis, lameness, viral or bacterial
 disease, gastritis, gastric ulcers, respiratory ailments, fractures.
 epistaxis, musculoskeletal damage or disorders and joint diseases. The
 present sequence is a primer used to illustrate the method of the
 invention.

XX SQ Sequence 22 BP; 0 A; 0 C; 0 G; 20 T; 2 other;

Query Match 1.6%; Score 17.2; DB 1; Length 22;
 Best Local Similarity 94.4%; Pred. No. 2.2e+02;
 Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAATAAAAAAAAAA 1100
 :|||||
 Db 21 BAAAAAATAAAAAAAAAA 4

```

AC ABX74887;
DT 21-MAR-2003 (first entry)
DE Oligo-dT primer used in human CC-RCC invention.
DE Microarray; solid surface; immobilised probe; CC-RCC;
KW differential expression profile; aggressive CC-RCC tumour type;
KW non-aggressive CC-RCC tumour type; clear cell renal carcinoma;
KW gene expression profiling; tumour tissue; oligo-dT; primer; ss.
OS Synthetic.
XX WO200279411-A2.
XX 10-OCT-2002.
XX 29-MAR-2002; 2002WO-US09576.
XX 29-MAR-2001; 2001US-279411P.
XX (VAND-) VAN ANDEL INST.
XX Haab B, Rhodes D, Teh BT, Takashi M;
XX WPI; 2003-040679/03.
XX New microarray, comprising a matrix of cDNA probe from a set of probes
PT immobilised to a solid surface in predetermined order, useful in the
PT prognosis of patients with clear cell renal carcinoma -
XX Example 2; Page 30; 179pp; English.
XX The present invention relates to a microarray comprising a matrix of
CC at least one cDNA probe from a set of probes immobilised to a solid
CC surface in a predetermined order, where a row of pixels corresponds
CC to replicates of one distinct probe from the set. The probes are
CC complementary to nucleic acid sequences that are expressed
CC differentially in aggressive as compared to non-aggressive types of
CC clear cell renal carcinoma (CC-RCC) and that hybridise to the probes
CC under high stringency conditions. The microarray is useful for the
CC prognosis of patients with CC-RCC, wherein aggressive and
CC non-aggressive CC-RCC tumour types are characterised by differential
CC expression profiles of genes that hybridise with one or more probes
CC immobilised on the microarray. The arrays are useful for gene
CC expression profiling of tumour and normal tissues. The present
CC sequence represents an oligo-dT primer used in the examples of the
CC present invention.
XX SQ Sequence 22 BP; 0 A; 0 C; 0 G; 20 T; 2 other;

Query Match 1.6%; Score 17.2; DB 1; Length 22;
Best Local Similarity 94.4%; Pred. No. 2.2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAATAAAAAAAAAA 1100
Db :|||||
21 BAAAAAATAAAAAAAAAA 4

RESULT 234
ABK13916/c
ID ABK13916 standard; DNA; 23 BP.
XX AC ABK13916;
XX 21-MAY-2002 (first entry)
XX 3'-PCR primer used in method of identifying transcribed genes.
XX Identification of transcribed gene; mRNA profile; gene expression;
KW cellular process; fingerprinting; susceptibility to external factor;
KW development; disease; PCR; primer; ss.

```

```

XX OS Synthetic.
XX WO200208461-A2.
XX 31-JAN-2002.
XX 23-JUL-2001; 2001WO-IB01539.
XX 21-JUL-2000; 2000GB-0018016.
XX 21-JUL-2000; 2000US-219925P.
XX (GLOB-) GLOBAL GENOMICS AB.
XX Linnarsson S, Ernfors P, Bauren G;
XX WPI; 2002-217065/27.
XX Providing mRNA profile, by generating two independent patterns
XX characteristic of sample mRNA population, analysing patterns, comparing
XX gene expression by cell types under varied conditions, and identifying
XX genes -
XX Example 2; Page 45; 67pp; English.
XX The present invention relates to a method for providing a profile of
XX mRNA molecules present in a sample. The method comprises generating
XX two independent patterns characteristic of the population of mRNA
XX molecules expressed in the sample and analysing the patterns using a
XX combinatorial algorithm, comparing gene expression by different or
XX same cell types under different conditions, and identifying genes
XX having a role in various cellular processes. The method is useful
XX for the analysis and identification of transcribed genes, and
XX fingerprinting. The method can be used to identify genes which play a
XX role in determining various cellular processes, including susceptibility
XX to external factors, development, and disease. The present sequence for
XX a PCR primer is used in the methods of the present invention.
XX SQ Sequence 23 BP; 0 A; 0 C; 0 G; 20 T; 3 other;

Query Match 1.6%; Score 17.2; DB 1; Length 23;
Best Local Similarity 94.4%; Pred. No. 2.3e+02;
Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAATAAAAAAAAAA 1100
Db :|||||
21 BAAAAAATAAAAAAAAAA 4

RESULT 235
ABS55943
ID ABS55943 standard; DNA; 24 BP.
XX AC ABS55943;
XX 22-JAN-2003 (first entry)
XX DNA topoisomerase II (TOP2) 21.34 cDNA RT-PCR primer #2.
XX DNA topoisomerase II 21.34; TOP2; primer; ss; DNA recombination; cancer;
KW malignant tumour; haemopathy; human immunodeficiency virus; HIV; RT-PCR;
KW immunological disease; inflammation; development disturbance;
KW reverse transcriptase.
XX OS Unidentified.
XX CN1345941-A.
XX 24-APR-2002.
XX 29-SEP-2000; 2000CN-0125577.
XX 29-SEP-2000; 2000CN-0125577.

```

XX PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
 XX PI Mao Y, Xie Y;
 XX XW WPI; 2002-539340/58.
 XX
 XX New polypeptide-DNA topoisomerase II (Top2) 21.34 for treating
 PT malignant tumour, haemopathy, development disturbance, human
 PT immunodeficiency virus infection, immunological disease and various
 PT inflammations -
 XX
 XX Example 2; Page 18 (Disclosure); 34pp; Chinese.
 XX
 XX The invention relates to the polypeptide DNA topoisomerase II (TOP2)
 CC 21.34, a polynucleotide encoding the polypeptide and a method for
 CC producing the polypeptide by DNA recombination technology. The
 CC polypeptide is used for curing several diseases, such as malignant
 CC tumours, haemopathy, development disturbance, human immunodeficiency
 CC virus (HIV) infection, immunological diseases and various inflammations.
 CC This sequence represents a reverse transcriptase PCR (RT-PCR) primer used
 CC in isolation of cDNA encoding DNA topoisomerase II (TOP2) 21.34.
 XX
 XX Sequence 24 BP; 6 A; 6 C; 8 G; 4 T; 0 other;
 XX
 XX Query Match 1.6%; Score 17.2; DB 1; Length 24;
 XX Best Local Similarity 86.4%; Pred. No. 2.4e+02;
 XX Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 XX
 XX 323 CAGAGAGCTGTCGAGCACTT 344
 XX ||||| ||||| ||||| ||||| |||||
 XX 2 CAGAGCAGCTCGGAGCGACTT 23

RESULT 236
 ABK91269/c
 ID ABK91269 standard; DNA; 24 BP.
 XX
 XX AC ABK91269;
 XX
 XX DT 05-NOV-2002 (first entry)
 XX
 XX DE Leukaemia related protein 24.09 specific RT-PCR primer #2.
 XX
 XX KW Leukaemia related protein; leukaemia; lymphoma; primer; ss;
 XX KW haemopathy; growth development disturbance disease;
 XX KW reverse transcription; RT-PCR.
 XX
 XX OS Unidentified.
 XX
 XX PN CN1341647-A.
 XX
 XX PD 27-MAR-2002.
 XX
 XX PF 07-SEP-2000; 2000CN-0125055.
 XX
 XX PR 07-SEP-2000; 2000CN-0125055.
 XX
 XX PA (SHAN-) SHANGHAI BIODOOR GENE DEV CO LTD.
 XX
 XX PI Mao Y, Xie Y;
 XX
 XX DR WPI; 2002-520722/56.
 XX
 XX PT Novel leukemia related protein 24.09 -
 XX
 XX PS Example 3; Page 17 (disclosure); 32pp; Chinese.
 XX
 XX This invention relates to the DNA and protein sequences of leukemia
 CC related protein 24.09. The invention also comprises methods for
 CC producing the protein using recombinant DNA technology and
 CC antagonists of the protein which may be used for inhibiting the
 CC action of the protein. The sequences of the invention may be used

CC for treating several diseases such as leukaemia, lymphoma, other
 CC haemopathy and growth development disturbance disease. The present
 CC sequence represents a reverse transcription (RT) PCR primer used to
 CC isolate the leukaemia related protein cDNA 24.09 of the invention.
 XX
 XX SQ Sequence 24 BP; 4 A; 1 C; 2 G; 17 T; 0 other;
 XX
 XX Query Match 1.6%; Score 17.2; DB 1; Length 24;
 XX Best Local Similarity 86.4%; Pred. No. 2.4e+02;
 XX Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 XX
 XX QY 1079 CTATTAAAAA 1100
 XX ||||| ||||| ||||| ||||| |||||
 XX 23 CAATTGAAAAA 2
 XX
 XX RESULT 237
 XX ABQ76045/c
 XX ID ABQ76045 standard; DNA; 24 BP.
 XX
 XX AC ABQ76045;
 XX
 XX DT 30-SEP-2002 (first entry)
 XX
 XX DE Human actin similar protein 56.43 RT-PCR primer #2.
 XX
 XX KW Human; actin similar protein 56.43; palsy; arrhythmia; bronchial asthma;
 XX KW peptic ulcer; diabetes; tumour; PCR; primer; ss.
 XX
 XX OS Homo sapiens.
 XX
 XX PN CN1339501-A.
 XX
 XX PD 13-MAR-2002.
 XX
 XX PF 23-AUG-2000; 2000CN-0119737.
 XX
 XX PR 23-AUG-2000; 2000CN-0119737.
 XX
 XX PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
 XX
 XX PI Mao Y, Xie Y;
 XX
 XX DR WPI; 2002-472210/51.
 XX
 XX PT New polypeptide-human actin similar protein 56.43 for treating periodic
 XX PT palsy, arrhythmia, bronchial asthma, peptic ulcer, diabetes, and tumors
 XX
 XX PS Example 3; Page 20 (Disclosure); 35pp; Chinese.
 XX
 XX This invention describes a novel human actin similar protein 56.43,
 CC polynucleotides encoding the polypeptide and a DNA recombination process
 CC to produce the polypeptide. The present invention also discloses the
 CC method of applying the polypeptide in treating various diseases, such as
 CC periodic palsy, arrhythmia, bronchial asthma, peptic ulcer, diabetes,
 CC tumours, etc. The present invention also discloses the antagonist
 CC resisting the polypeptide and its treatment effect. This sequence
 CC represents a RT-PCR primer used in the amplification of the human actin
 CC similar protein 56.43 described in the disclosure of the invention.
 XX
 XX SQ Sequence 24 BP; 5 A; 0 C; 4 G; 15 T; 0 other;
 XX
 XX Query Match 1.6%; Score 17.2; DB 1; Length 24;
 XX Best Local Similarity 86.4%; Pred. No. 2.4e+02;
 XX Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 XX
 XX QY 1079 CTATTAAAAA 1100
 XX ||||| ||||| ||||| ||||| |||||
 XX 23 CTCTTCAAAAAA 2

RESULT 238

```

ABK48140/c
ID  ABK48140 standard; DNA; 24 BP.
AC  ABK48140;
XX
XX
XX  18-JUN-2002 (first entry)
DT
XX
DE  Aspergillus niger aminopeptidase RT-PCR primer poly-T.
XX
XX  Aminopeptidase; primer; ss; food composition; dough; flavour enhancer;
KW  baked product; cheese; poly-T; reverse transcriptase PCR.
KW
XX  Synthetic.
XX
XX  WO200216618-A1.
XX
XX  28-FEB-2002.
XX
XX  22-AUG-2001; 2001WO-EP09925.
XX
XX  23-AUG-2000; 2000EP-0202995.
XX
XX  (STAM ) DSM NV.
XX
XX  Basten D, Dekker PJT, Schuurhuizen PW, Schaap PJ, Visser J;
PI  WPI; 2002-257917/30.
XX
XX  An isolated polypeptide with aminopeptidase activity, for preparing
PT  food compositions, such as bread and cheese, with enhanced flavouring -
XX  Example 5; Page 40; 94pp; English.
XX
XX  The invention relates to an isolated polypeptide with aminopeptidase
CC  activity and the gene encoding it (including sequences complementary to
CC  the gene and which hybridise to it at high stringency), from Aspergillus
CC  niger. Also included are a nucleic acid construct comprising the above
CC  polynucleotide operably linked to one or more control sequences that
CC  direct the production of the polypeptide in a suitable expression host,
CC  a recombinant expression vector comprising the above nucleic acid
CC  construct, a recombinant host cell comprising the above nucleic acid
CC  vector, and producing the protein comprising the above construct or
CC  recombinant host cell to produce a supernatant and/or cells comprising
CC  the polypeptide and recovering the polypeptide. The aminopeptidase is
CC  used to prepare a food composition such as dough to enhance the flavour
CC  of a baked product from the dough and for preparing a cheese to enhance
CC  the flavour. The invention provides a bacterial enzyme for protein
CC  hydrolysis i.e. with aminopeptidase activity, to produce flavouring
CC  agents, and the enzyme has been isolated and characterised, compared to
CC  a previously observed weak aminopeptidase activity which was detected
CC  in an Aspergillus niger culture filtrate but the source was never
CC  isolated or identified. The use of enzymes to produce flavouring agents
CC  from proteinaceous material is better than use of strong acids which
CC  can severely degrade the amino acids obtained. The present sequence
CC  is a reverse transcriptase (RT)-PCR primer used to investigate the
CC  intron-exon structure of the aminopeptidase gene.
XX
SQ  Sequence 24 BP; 0 A; 0 C; 0 G; 23 T; 1 other;
Query Match 1.6%; Score 17.2; DB 1; Length 24;
Best Local Similarity 94.4%; Pred. No. 2.4e+02;
Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1083 TAAAAAATAAAAAA 1100
Db 24 BAAAAAATAAAAAA 7
RESULT 239
ABA04737/c
ID ABA04737 standard; DNA; 24 BP.
XX
XX ABA04737;
AC

```

```

XX
XX 22-FEB-2002 (first entry)
XX
XX Human alkylation DNA protein cysteine methyltransferase 11 PCR primer #2.
DE
XX
XX Human; alkylation DNA protein cysteine methyltransferase 11; cytostatic;
KW haemostatic; virucide; immunomodulatory; antiinflammatory; gene therapy;
KW tumour; haemopathy; HIV infection; immunological disease; inflammation;
KW PCR primer; ss.
XX
XX Homo sapiens.
XX
XX WO200188146-A1.
XX
XX 22-NOV-2001.
XX
XX 26-MAR-2001; 2001WO-CN00464.
XX
XX 28-MAR-2000; 2000CN-0115226.
XX
XX (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
XX
XX Mao Y, Xie Y;
XX
XX WPI; 2002-055701/07.
XX
XX Human alkylation-DNA-protein cysteine methyltransferase and encoding
PT polynucleotide, used in diagnosis and treatment of malignant tumors,
PT hemopathy, human immunodeficiency virus infection, immunological
PT diseases and inflammation -
XX
XX Example 2; Page 19; 40pp; Chinese.
XX
XX The present invention relates to human alkylation-DNA-protein cysteine
CC methyltransferase (see AAM47739). The protein and its coding sequence
CC are useful in the diagnosis and treatment of malignant tumors,
CC haemopathy, HIV infection, immunological diseases and various
CC inflammations. The present sequence is a PCR primer, which was used in an
CC example from the present invention.
XX
SQ Sequence 24 BP; 4 A; 0 C; 4 G; 16 T; 0 other;
Query Match 1.6%; Score 17.2; DB 1; Length 24;
Best Local Similarity 86.4%; Pred. No. 2.4e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1078 ACTATTAAAAAATAAAAAA 1099
Db 22 ACTACTAAAAATACAAAAA 1
RESULT 240
AAK18370/c
ID AAK18370 standard; DNA; 17 BP.
XX
XX AAK18370;
AC
XX
XX 11-MAY-1999 (first entry)
XX
XX RT-PCR primer of the invention SEQ ID 11.
DE
XX
XX RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
KW
XX Synthetic.
XX
XX JPI1032765-A.
XX
XX 09-FEB-1999.
XX
XX 18-JUL-1997; 97JP-0208312.
XX
XX 18-JUL-1997; 97JP-0208312.
XX

```

PA (TAKI) TAKARA SHUZO CO LTD.
 XX WPI; 1999-183822/16.
 XX Peptides having at least two new nucleotides - useful as primers in
 XX RT-PCR
 XX
 XX Disclosure; Page 11; 19pp; Japanese.
 XX
 XX This sequence represents a primer of the invention. The invention relates
 XX to sequences of at least two nucleotides of formula:
 XX (X)ms'-(alpha)n-beta-N3'; or (X)ms'-(gamma)k-delta-N3'; where
 XX X = a labelled compound and/or a nucleotide with voluntary sequence;
 XX m = 0 or 1; alpha = thymine; n = natural number indicating the repetition
 XX of alpha; beta; delta = V or N; V = adenine, guanine or cytosine;
 XX N = adenine, guanine, cytosine or thymine; gamma = thymine;
 XX k = natural number of 3' or over indicating the repetition of gamma, in
 XX which thymine expressed by gamma is composed of 1/3 or less of adenine,
 XX guanine and/or cytosine. The new nucleotides are useful as primers for
 XX RT-PCR and determination of base sequences. The new sequences allow for
 XX reproductive and highly efficient analysis of gene sequences.
 XX
 XX Sequence 17 BP; 2 A; 0 C; 0 G; 15 T; 0 other;
 SQ
 Query Match 1.5%; Score 17; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1082 TTAAAAAATAAAAAA 1098
 |||||
 Db 17 TTAAAAAATAAAAAA 1
 RESULT 241
 AAA98232/C
 ID AAA98232 standard; DNA; 17 BP.
 AC AAA98232;
 XX
 XX 30-JAN-2001 (first entry)
 XX Human retrovirus HERV LTR PCR primer #31.
 XX
 XX Cell-specific expression; tissue-specific expression; gene therapy; LTR;
 XX U3-R segment; long terminal repeat; retroviral expression vector;
 XX PCR primer; ss.
 XX
 XX Human retrovirus.
 XX
 XX WO200053789-A2.
 XX
 XX 14-SEP-2000.
 XX
 XX 09-MAR-2000; 2000WO-EP02064.
 XX
 XX 10-MAR-1999; 99DE-1010650.
 XX
 XX (GSFU-) GSF FORSCHUNGSZENTRUM UMWELT & GESUNDHEI.
 XX
 XX Leib-Moesch C, Schoen U, Baust C;
 XX
 XX WPI; 2000-587442/55.
 XX
 XX Retroviral expression vector, useful in gene therapy, contains a
 XX promoter from a human endogenous retrovirus to provide cell-specific
 XX expression -
 XX
 XX Disclosure; Page 27; 67pp; German.
 XX
 XX This invention describes a novel retroviral expression vector (A)
 XX containing DNA sequences (I) for packaging vector RNA and for
 XX cell-specific expression of proteins or peptides encoding by heterologous
 XX DNA (II). The sequences controlling cell-specific expression contain a

cell-specifically regulatable promoter region (P) from a human endogenous
 retrovirus (HERV) DNA sequence. The invention also describes (a) mRNA and
 RNA of (A); (b) prokaryotic and eukaryotic cells containing (A); (c)
 eukaryotic cells containing (A) in integrated form; (d) virions
 containing a retroviral expression vector RNA derived from (A); (e) a
 method for producing the virions of (d); (f) a method for incorporating
 protein-encoding nucleic acid sequences into a eukaryotic cell by
 infection with the virions of (d); and (g) a retroviral vector system
 containing (A) and a packaging cell line, that contains at least one
 (recombinant) retrovirus construct that encodes for the packaging
 proteins of (A). (A) are used for cell- or tissue-specific expression of
 foreign genes for gene therapy and to produce virions for introducing
 (II) into the chromosomal DNA of eukaryotic cells, preferably mammalian
 and specifically human. (A) retain the advantages of usual retroviral
 promoters with all the signal structures required for transcription in a
 small region within the U3-R segment, but without their disadvantages
 (excessive strength and limited cell specificity). Since (A) are derived
 from endogenous (harmless) viral sequences, they do not introduce any new
 viral sequences into the genome and recombination will not create new
 types of retrovirus. The promoters provide cell or tissue specific
 expression, according to which HERV they are derived from.
 XX
 XX Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 other;
 SQ
 Query Match 1.5%; Score 17; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1084 AAAAAAAAAAAAAAAAAA 1100
 |||||
 Db 17 AAAAAAAAAAAAAAAAAA 1
 RESULT 242
 AAA50197/C
 ID AAA50197 standard; DNA; 17 BP.
 AC AAA50197;
 XX
 XX 07-NOV-2000 (first entry)
 XX 2'-Methoxyethoxy-modified phosphorothioate oligonucleotide.
 XX
 XX Phosphorothioate oligonucleotide; H-phosphonate chemistry; ss.
 XX Synthetic.
 XX
 XX Key Location/Qualifiers
 XX modified_base 1..19
 XX /tag= a
 XX /note= "2'-methoxyethoxy modified thymidine"
 XX modified_base 1..17
 XX /tag= b
 XX /note= "phosphorothioate internucleoside linkages"
 XX
 XX WO200047593-A1.
 XX
 XX 17-AUG-2000.
 XX
 XX 11-FEB-2000; 2000WO-US03543.
 XX
 XX 12-FEB-1999; 99US-0250075.
 XX
 XX (ISIS-) ISIS PHARM INC.
 XX
 XX Manoharan M, Maier MA;
 XX
 XX WPI; 2000-558188/51.
 XX
 XX Preparation of mixed backbone oligomeric compounds useful as e.g.
 XX primers for diagnostic tests, involves oxidation of H-phosphonate
 XX internucleoside linkages to phosphodiester internucleoside linkages -

PT Example 12; Page 34; 49pp; English.

XX The present sequence is that of a phosphorothioate oligonucleotide

CC containing 20 T nucleobases, each having a 2'-methoxyethoxy group

CC on its 5' ribosyl sugar moiety. It is an example of an oligomeric

CC compound produced according to the methods of the invention. The

CC invention provides compounds and methods for the preparation of

CC mixed backbone oligomeric, or chimeric, compounds having

CC phosphodiester internucleoside linkages in addition to

CC phosphorothioate and/or phosphoramidate internucleoside linkages.

CC The methods also include incorporation of boranophosphate

CC internucleoside linkages. The methods utilize H-phosphonate

CC intermediates that are coupled together forming contiguous regions

CC of 1 or more H-phosphonate internucleoside linkages. Each

CC contiguous region is subsequently oxidized to phosphodiester,

CC phosphorothioate, phosphoramidate or boranophosphate

CC internucleoside linkages prior to further elongation. Mixed

CC backbone oligomeric compounds are prepared in this manner by

CC oxidizing adjacent regions with different reagents. Oligomeric

CC compounds of the invention are prepared using novel oxidation steps

CC that oxidize a region of 1 or more H-phosphonate internucleoside

CC linkages without degrading existing linkages that have been

CC previously oxidized. The oligonucleotides obtained are useful as

CC primers in PCR, probes, linkers, gene fragments and for other

CC diagnostic tests on e.g. biological tissue, fluid, cells etc., as

CC research reagents, and as antiviral agents.

XX

SQ Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 1.8e+02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1084 AAAAAAAAAAAAAAAAAA 1100

DB 17 AAAAAAAAAAAAAAAAAA 1

RESULT 243

AAA25450/C

ID AAA25450 standard; DNA; 17 BP.

XX AAA25450;

AC

XX 19-JUL-2000 (first entry)

DT

XX

DE

XX Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1948.

XX Oestrogen receptor; c-rat; k-ras; bcl-2; ribozyme; cleavage;

KW hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;

KW gene expression modification; cancer; phosphorothioate; endonuclease;

XX anticancer; breast cancer; endometrium cancer; ss.

XX Homo sapiens.

XX

PN WO9954459-A2.

XX

PD

XX 28-OCT-1999.

XX

PF 19-APR-1999; 99WO-US08547.

XX

FR 20-APR-1998; 98US-0082404.

PR 23-JUN-1998; 98US-0103636.

XX

XX (RIBO-) RIBOZYME PHARM INC.

XX

PI Thompson JD, Beigelman L, McSwiggen JA, Karpeisky A, Bellon L;

PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haerberli P;

PI Matulich-Adamic J;

XX

DR WPI; 2000-013248/01.

XX

PT New nucleic acids that interact, and optionally cleave, target

PT sequences, used to treat cancer

XX

PS Claim 77; Page 79; 148pp; English.

XX

CC The present invention describes nucleic acids (A) that interact stably

CC with a target sequence and contain at least one phosphoro(di)thioate

CC link, having endonuclease activity. (A), and more generally any

CC catalytic nucleic acid (A') that modulates expression of the oestrogen

CC receptor gene, are used to treat cancer (particularly of breast or

CC endometrium), in vivo or by transforming cells ex vivo and implanting

CC treated cells, or for other conditions associated with levels of

CC oestrogen receptor. Because of the high selectivity for targeted RNA, (A)

CC can also be used to correlate inhibition of gene expression with

CC alterations in phenotype, particularly for identification of therapeutic

CC targets, and as research reagents (for RNA, in the same way that

CC restriction endonucleases are used with DNA). The combination of

CC modifications in (A) improves resistance to nucleases, binding affinity

CC and/or activity. AAA23503 to AAA24747 represent oestrogen receptor

CC hammerhead ribozyme sequences, and AAA24748 to AAA25992 represent their

CC corresponding target sequences. AAA25993 to AAA26105 represent oestrogen

CC receptor hairpin ribozyme sequences, and AAA26107 to AAA26218 represent

CC their corresponding target sequences. AAA26219 to AAA26271 represent

CC other ribozyme sequences and antisense oligonucleotides used in the

CC exemplification of the present invention.

XX

SQ Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 1.8e+02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1084 AAAAAAAAAAAAAAAAAA 1100

DB 17 AAAAAAAAAAAAAAAAAA 1

RESULT 244

AAQ34110

ID AAQ34110 standard; DNA; 18 BP.

XX AAQ34110;

AC

XX 25-MAR-2003 (updated)

DT 02-FEB-1993 (first entry)

XX

DE

XX Sequence of a microsatellite from clone TGLA60B.

XX PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;

KW genetic mapping; traits; amplification; ss.

XX Bos taurus.

XX

PN WO9213102-A1.

XX

PD 06-AUG-1992.

XX

PF 15-JAN-1992; 92WO-US00340.

XX

FR 15-JAN-1991; 91US-0642342.

XX

XX (GENM-) GENMARK.

PA

XX

PI Georges M, Massey JM;

XX

XX WPI; 1992-284684/34.

DR

XX Polymorphic bovine DNA markers - used in genetic identification,

PT gene mapping, and selective breeding

XX

XX Table 7; Page 375; 517pp; English.

PS

XX The sequence is that of a bovine microsatellite sequence obtd.

CC by screening a library of bovine MboI DNA fragments of between


```

Db      17 AAAAAAAAAAAAAAAAAA 1
|||||
RESULT 247
AAT94669/C
ID AAT94669 standard; DNA; 18 BP.
XX
AC AAT94669;
XX
DT 27-MAR-1998 (first entry)
XX
DE Anchored poly(T) oligonucleotide polyT-Anch3.
XX
KW Flavonoid 3'-hydroxylase; pigmentation; flower colour;
KW transgenic plant; snapdragon; primer; ss.
XX
OS Synthetic.
XX
PN WO9732023-A1.
XX
PD 04-SEP-1997.
XX
PF 28-FEB-1997; 97WO-AU00124.
XX
PR 01-MAR-1996; 96AU-0008386.
XX
PA (FLOR-) FLORIGENE LTD.
XX
PI Brugliera F, Holton TA, Michael MZ;
XX
WPI; 1997-448691/41.
XX
PT Novel flavonoid 3'-hydroxylase(s) from flowering plants - and
PT corresponding DNA, used in the manipulation of pigmentation in
PT plants
XX
PS Example 15; Page 59; 234pp; English.
XX
CC Anchored poly(T) oligonucleotides polyT-anchA (AAT94667), polyT-anchC
CC (AAT94668) and polyT-anchG (AAT94669) are complementary to the upstream
CC region of a polyadenylation sequence. They were used to prime cDNA
CC synthesis from snapdragon (Antirrhinum majus) petal and leaf RNA,
CC and were also utilised in the PCR amplification of plant
CC cytochrome P450 sequences (see also AAT94670-73). A cDNA clone (see
CC AAT94657) encoding flavonoid 3'-hydroxylase (see AAT94670) was isolated
CC using a differential display approach. This can be used to
CC manipulate the pigmentation of transgenic plants.
XX
SQ Sequence 18 BP; 0 A; 0 C; 1 G; 17 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
|||||
Db 17 AAAAAAAAAAAAAAAAAA 1

RESULT 248
AAV54164/C
ID AAV54164 standard; cDNA; 18 BP.
XX
AC AAV54164;
XX
DT 21-DEC-1998 (first entry)
XX
DE Nucleotide sequence PCR primer 1.
XX
KW PCR; primer; amplification; apoptosis; antibody; inhibition; ss;
KW immunohistological staining.
XX

```

```

OS Synthetic.
XX
PN WO9839437-A1.
XX
PD 11-SEP-1998.
XX
PF 05-MAR-1998; 98WO-JP00905.
XX
PR 05-MAR-1997; 97JP-0050302.
XX
PA (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI Sakaki Y;
XX
WPI; 1998-495844/42.
XX
PT Novel apoptosis-related DNAs and proteins - for diagnosis,
PT preventing or treating diseases associated with apoptosis
XX
PS Example 1; Page 47; 70pp; Japanese.
XX
CC This is the nucleotide sequence of a PCR primer used in the method
CC of the invention, involving the use of novel apoptosis-related DNAs
CC and proteins. The inventions can be used as diagnostic reagents for
CC apoptosis e.g. (monoclonal) antibodies for the protein, as a reagent
CC in immunohistological staining, as apoptosis inhibitors. It can also
CC be used for treatment of apoptosis-related diseases.
XX
SQ Sequence 18 BP; 2 A; 0 C; 1 G; 15 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1082 TTAATAAAAAAAAAAAAAA 1098
|||||
Db 18 TTAATAAAAAAAAAAAAAA 2

RESULT 249
AAV07750
ID AAV07750 standard; DNA; 18 BP.
XX
AC AAV07750;
XX
DT 02-DEC-1998 (first entry)
XX
DE Phosphorothioate oligodeoxynucleotide.
XX
KW phosphorothioate; electrospray ionisation-Fourier transform;
KW mass spectrometry; off-resonance excitation; ss.
XX
OS Synthetic.
XX
PI Key Location/Qualifiers
FT misc_difference 1..18
FT /*tag= a
FT /note= "phosphorothioate internucleotide linkages"
XX
PN WO9840520-A1.
XX
PD 17-SEP-1998.
XX
PF 12-MAR-1998; 98WO-US04919.
XX
PR 14-MAR-1997; 97US-0040717.
XX
PA (HYBR-) HYBRIDON INC.
XX
PI Wang BH;
XX
WPI; 1998-520830/44.
XX

```

PT Determining the nucleotide sequence of a nucleic acid analyte -
 XX using electro-spray ionisation
 PS Example 1; Figure 3A; 25pp; English.
 XX
 CC The invention relates to an analytical method for determining the
 CC nucleotide sequence of nucleic acid analytes, including chemically
 CC modified oligonucleotides. This new method utilises electrospray
 CC ionisation-Fourier transform mass spectrometry. The ions are excited by
 CC sustained off-resonance excitation with single shot excitation, and the
 CC target fragmented by collisionally activated dissociation by a neutral
 CC gas, e.g. carbon dioxide. Alternatively, the excitation and dissociation
 CC can be nozzle skimmer dissociation. The method is used in molecular
 CC biology and biomedical applications. The method, utilising electrospray
 CC ionisation-Fourier transform ion cyclotron resonance mass spectrometry,
 CC is extremely rapid and acts directly on the oligonucleotide. The method
 CC is effective for a variety of nucleic acid analytes, particularly
 CC chemically modified oligonucleotides which have not previously been
 CC successfully sequenced. The present sequence represents a
 CC phosphorothioate oligodeoxynucleotide.
 XX
 SQ Sequence 18 BP; 17 A; 0 C; 0 G; 1 T; 0 other;
 Query Match 1.5%; Score 17; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1084 AAAAAAAAAAAAAAAAAA 1100
 DB 1 AAAAAAAAAAAAAAAAAA 17
 RESULT 250
 AAV37712
 ID AAV37712 standard; cDNA; 18 BP.
 AC AAV37712;
 XX
 DT 25-MAR-2003 (updated)
 DT 07-SEP-1998 (first entry)
 XX
 DE Human protein Aq2_li 3'-portion and polyA tail.
 XX
 KW Human; secreted protein; murine adult spleen; human foetal kidney; ovary;
 KW bone marrow; thymus; AE648_li; AE693_li; AK438_li; AK609_li; AM1060_li;
 KW Aq2_li; K433_li; L256_li; prevent; treat; ameliorate; medical; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO9820130-A2.
 XX
 PD 14-MAY-1998.
 XX
 PF 31-OCT-1997; 97WO-US19857.
 XX
 PR 01-NOV-1996; 96US-0742973.
 PR 29-OCT-1997; 97US-0960024.
 XX
 PA (GEMY) GENETICS INST INC.
 XX
 PI Agostino MJ, Jacobs K, Lavallie ER, McCoy JM, Merberg D;
 PI Racie LA, Spaulding V, Treacy M;
 XX
 DR WPI; 1998-286946/25.
 XX
 CC New secreted proteins and associated polynucleotides - obtained from
 PT murine adult spleen, human foetal kidney, human ovary, murine bone
 PT marrow and murine adult thymus
 XX
 PS Disclosure; Page 58; 75pp; English.
 XX
 CC The present invention describes novel proteins isolated from cDNA
 CC clones: AE648_li; AE693_li; AK438_li; AK609_li; AM1060_li; Aq2_li;

CC K433_li; or L256_li, deposited as ATCC 98237. The present sequence
 CC represents the 3'-portion of Aq2_li isolated from a human ovary cDNA
 CC library. The proteins from the present invention may be administered
 CC in a composition to prevent, treat or ameliorate a medical condition.
 CC The proteins may exhibit biological activities such as nutritional
 CC activity, cytokine and cell proliferation/differentiation activity,
 CC immune stimulating or suppressing activity, haematopoiesis regulating
 CC activity, tissue growth activity, activin/inhibin activity,
 CC chemotactic/chemokinetic activity, haemostatic and thrombotic activity,
 CC receptor/ligand activity, anti-inflammatory activity, cachectin/tumour
 CC invasion suppressor activity, tumour inhibition activity and other
 CC activities.
 CC (Updated on 25-MAR-2003 to correct PR field.)
 XX
 SQ Sequence 18 BP; 17 A; 0 C; 1 G; 0 U; 0 other;
 Query Match 1.5%; Score 17; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1084 AAAAAAAAAAAAAAAAAA 1100
 DB 2 AAAAAAAAAAAAAAAAAA 18
 RESULT 251
 AAV21970/c
 ID AAV21970 standard; DNA; 18 BP.
 XX
 AC AAV21970;
 XX
 DT 14-JUL-1998 (first entry)
 XX
 DE Nuclease resistant antisense oligo NBT 13 targeted against (T)18.
 XX
 KW Nuclease resistant; bacterial infection; antibiotic; target;
 KW veterinary medicine; treatment; human; industrial process;
 KW bacterial control; ss.
 XX
 OS Synthetic.
 XX
 PN WO9803533-A1.
 XX
 PD 29-JAN-1998.
 XX
 PF 23-JUL-1997; 97WO-US12961.
 XX
 PR 24-JUL-1996; 96US-0685575.
 XX
 PA (OLIG-) OLIGOS ETC & OLIGOS THERAPEUTICS INC.
 XX
 PI Arrow A, Pale RMK, Thompson TL;
 XX
 DR WPI; 1998-120687/11.
 XX
 PT Treating bacterial infections in humans or animals with
 PT oligo:nucleotide(s) - resistant to nuclease and targeted to
 PT bacterial nucleic acid or proteins, also conjugates of these
 PT oligo:nucleotide(s) with antibiotics
 XX
 PS Claim 49; Page 87; 163pp; English.
 XX
 CC This antisense oligonucleotide is nuclease resistant and can be used in
 CC the treatment of animals, including humans, having a bacterial infection.
 CC The treatment comprises administration of such nuclease resistant
 CC oligonucleotides, targeted to a nucleic acid or protein of the bacterium,
 CC and formulated with a carrier. A compound comprising this nuclease
 CC resistant oligonucleotide can be covalently linked to an antibiotic. The
 CC method is used to treat infections by a wide variety of Gram-positive and
 CC Gram-negative, or acid-fast, bacteria, in human and veterinary medicine.
 CC The methods are particularly used in immuno-compromised individuals
 CC (e.g. patients with acquired immunodeficiency syndrome or those receiving
 CC chemotherapy or radiation therapy), optionally in combination with, or

CC fused to, antiviral or other antimicrobial oligonucleotides. Apart from
 CC therapeutic use, the oligonucleotides can be used to control bacteria
 CC in laboratory cultures, foods, beverages and industrial processes. The
 CC oligonucleotides are specific for bacteria, without affecting metabolism
 CC in mammalian cells. They may also activate RNase H and have a general,
 CC non-specific immune-stimulating effect. The oligonucleotides can be
 CC administered orally, intranasally, rectally, topically or by injection,
 CC optionally coupled to an agent (e.g. carbohydrate or polyamine) that
 CC enhances cellular uptake.

XX Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 18;

Best Local Similarity 100.0%; Pred.No.1.9e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084

AAAAAAAAAAAAAAAA 1100

18 AAAAAAAAAAAAAAAAAA 2

RESULT 252

AAAX19942

ID AAX19942 standard; DNA; 18 BP.

XX AC AAX19942;

XX DT 14-JUN-1999 (first entry)

XX DE Primer SEQ ID NO:2 from JP11075880.

XX KW Primer; oligonucleotide; labelling; detection; self-priming; PCR; ss.

XX OS Synthetic.

XX PN JP11075880-A.

XX PD 23-MAR-1999.

XX PF 10-JUL-1998; 98JP-0195719.

XX PR 14-JUL-1997; 97JP-0205378.

XX PA (KAGA) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.

XX DR WPI; 1999-257710/22.

XX PT Labelling of an oligonucleotide - useful for detecting genes

XX PS Example 1; Page 7; 10pp; Japanese.

XX CC A method has been developed for labelling an oligonucleotide having a
 CC repeated sequence of (XY)_n (where X and Y consists of a combination of
 CC adenine and thymine or uracil or guanine and cytosine, and n is an
 CC integer of 1 or more) at the 3'-terminal side in which the repeated
 CC sequence is added and extended using a labelled body of the nucleotide
 CC constituting the repeated sequence and a DNA polymerase lacking in 5' to
 CC 3' exonuclease activity. The method can be used for detecting a gene.
 CC The method can detect a gene in a sensitivity up to ten times higher
 CC than prior art methods. The present sequence represents a primer used
 CC in an example from the present invention.

XX SQ Sequence 18 BP; 18 A; 0 C; 0 G; 0 U; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 18;

Best Local Similarity 100.0%; Pred.No.1.9e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084

AAAAAAAAAAAAAAAA 1100

1 AAAAAAAAAAAAAAAAAA 17

RESULT 253

AAAX19943/c

ID AAX19943 standard; DNA; 18 BP.

XX AC AAX19943;

XX DT 14-JUN-1999 (first entry)

XX DE Primer SEQ ID NO:3 from JP11075880.

XX KW Primer; oligonucleotide; labelling; detection; self-priming; PCR; ss.

XX OS Synthetic.

XX PN JP11075880-A.

XX PD 23-MAR-1999.

XX PF 10-JUL-1998; 98JP-0195719.

XX PR 14-JUL-1997; 97JP-0205378.

XX PA (KAGA) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.

XX DR WPI; 1999-257710/22.

XX PT Labelling of an oligonucleotide - useful for detecting genes

XX PS Example 1; Page 7; 10pp; Japanese.

XX CC A method has been developed for labelling an oligonucleotide having a
 CC repeated sequence of (XY)_n (where X and Y consists of a combination of
 CC adenine and thymine or uracil or guanine and cytosine, and n is an
 CC integer of 1 or more) at the 3'-terminal side in which the repeated
 CC sequence is added and extended using a labelled body of the nucleotide
 CC constituting the repeated sequence and a DNA polymerase lacking in 5' to
 CC 3' exonuclease activity. The method can be used for detecting a gene.
 CC The method can detect a gene in a sensitivity up to ten times higher
 CC than prior art methods. The present sequence represents a primer used
 CC in an example from the present invention.

XX SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 18;

Best Local Similarity 100.0%; Pred.No.1.9e+02; Mismatches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084

AAAAAAAAAAAAAAAA 1100

18 AAAAAAAAAAAAAAAAAA 2

RESULT 254

AAAX18373/c

ID AAX18373 standard; DNA; 18 BP.

XX AC AAX18373;

XX DT 11-MAY-1999 (first entry)

XX DE RT-PCR primer of the invention SEQ ID 14.

XX KW RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.

XX OS Synthetic.

XX PN JP11032765-A.

XX PD 09-FEB-1999.

XX PF 18-JUL-1997; 97JP-0208312.

XX PR 18-JUL-1997; 97JP-0208312.

XX PA (TAKI) TAKARA SHUZO CO LTD.
 XX WPI; 1999-183822/16.
 DR PT Peptides having at least two new nucleotides - useful as primers in
 PT RT-PCR
 XX PS Disclosure; Page 11; 19pp; Japanese.
 XX CC This sequence represents a primer of the invention. The invention relates
 CC to sequences of at least two nucleotides of formula:
 CC (X)m5'-(alpha)n-beta-N3'; or (X)m5'-(gamma)k-delta-N3'; where
 CC X = a labelled compound and/or a nucleotide with voluntary sequence;
 CC m = 0 or 1; alpha = thymine; n = natural number indicating the repetition
 CC of alpha; beta, delta = V or N; V = adenine, guanine or cytosine;
 CC N = adenine, guanine, cytosine or thymine; gamma = thymine;
 CC k = natural number of 3 or over indicating the repetition of gamma, in
 CC which thymine expressed by gamma is composed of 1/3 or less of adenine,
 CC guanine and/or cytosine. The new nucleotides are useful as primers for
 CC RT-PCR and determination of base sequences. The new sequences allow for
 CC reproductive and highly efficient analysis of gene sequences.
 XX CC Sequence 18 BP; 1 A; 0 C; 0 G; 17 T; 0 other;
 SQ Query Match 1.5%; Score 17; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1083 TAAAAAATAAAAAA 1099
 DB 17 TAAAAAATAAAAAA 1
 RESULT 255
 ID AAA40563
 AC AAA40563 standard; cDNA; 18 BP.
 XX AC AAA40563;
 DT 16-NOV-2000 (first entry)
 XX DE Human adult ovary cDNA fragment AQ2_11 #2.
 XX KW Secreted protein; cytosolic; immunostimulatory; antimicrobial;
 KW antiviral; immunosuppressive; antiinflammatory; vulnary; cytokine;
 KW cell proliferation; differentiation; regulator; treatment; tumor;
 KW autoimmune disease; inflammatory disorder; wound; microbial infection;
 KW viral disease; graft versus host reaction suppression; ss.
 XX OS Homo sapiens.
 XX PN WO200037630-A1.
 XX PD 29-JUN-2000.
 XX PF 22-DEC-1999; 99WO-US31005.
 XX PR 23-DEC-1998; 98US-0220876.
 XX PA (GEMY) GENETICS INST INC.
 XX PI Jacobs K, McCoy JM, LaVallie ER, Collins-Racie LA, Evans C;
 PI Merberg D, Treacy M, Bowman MR;
 XX P-PSDB; AAB10274.
 DR WPI; 2000-442661/38.
 XX Secreted human proteins AS296-1i and AS34-1i, useful for treating
 PT tumors, autoimmune diseases, inflammatory disorders, wounds, microbial
 PT infections and viral diseases -
 XX PS Disclosure; Page 269; 293pp; English.

XX CC This invention describes novel secreted human proteins (I) which have
 CC cytostatic, immunostimulatory, antimicrobial, antiviral,
 CC immunosuppressive, antiinflammatory and vulnary activity and which act
 CC as cytokine, cell proliferation or differentiation regulators. (I)
 CC is useful for treating tumors, autoimmune diseases, inflammatory
 CC disorders, wounds, microbial infections and viral diseases. (I) is also
 CC useful for suppressing graft versus host reaction. AAA40490-AA0580
 CC represent cDNA fragments that encode the secreted proteins
 CC AAB10226-B10288 described in the method of the invention.
 XX CC Sequence 18 BP; 17 A; 0 C; 1 G; 0 U; 0 other;
 SQ Query Match 1.5%; Score 17; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1084 AAAAAAATAAAAAA 1100
 DB 2 AAAAAAATAAAAAA 18
 RESULT 256
 ID AAZ90646/c
 XX ID AAZ90646 standard; DNA; 18 BP.
 AC AAZ90646;
 XX DT 13-JUN-2000 (first entry)
 XX DE Human adipose tissue gene amplifying primer #7.
 XX KW Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;
 KW arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.
 XX OS Homo sapiens.
 XX PN JP2000037190-A.
 XX PD 08-FEB-2000.
 XX PF 23-JUL-1998; 98JP-0225228.
 XX PR 23-JUL-1998; 98JP-0225228.
 XX PA (NIBS) JAPAN TOBACCO INC.
 DR WPI; 2000-306578/27.
 XX PT A physiologically active protein specifically derived from mammal
 PT tissue -
 XX PS Example 2; Page 18; 50pp; Japanese.
 XX CC The invention relates to identification of genes and proteins of adipose
 CC tissue relating to obesity, particularly complications of visceral
 CC obesity including diabetes, hyperlipemia, hypertension,
 CC arteriosclerosis, hyperuricemia and sleep apnea syndrome. The genes
 CC (AAZ90631-633) and the proteins (AAZ90631-633) are used in the genetic
 CC diagnosis, prevention and treatment of adipose tissue related diseases.
 CC Sequences AAZ90640-51 represent PCR primers amplifying the human adipose
 CC tissue genes.
 XX CC Sequence 18 BP; 2 A; 0 C; 1 G; 15 T; 0 other;
 SQ Query Match 1.5%; Score 17; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1082 TTAATAAATAAAAAA 1098
 DB 18 TTAATAAATAAAAAA 2

RESULT 257
AAZ87161
ID AAZ87161 standard; RNA; 18 BP.
XX AC
XX AAZ87161;
XX DT 08-MAY-2000 (first entry)
XX DE Oligoarabinonucleotide SEQ ID NO:2.
XX KW Beta-D-arabinose; antisense; inhibition;
XX KW transcription; expression; reverse transcription;
XX KW viral replication; RNase H cleavage; triple helix formation; ss.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT modified_base 1..18
XX FT /*tag= a
XX FT /note= "Ribose moiety replaced by beta-D-arabinose"
XX PN WO9967378-A1.
XX PD 29-DEC-1999.
XX PF 17-JUN-1999; 99WO-CA00571.
XX PR 19-JUN-1998; 98CA-2241361.
XX PA (UYMC-) UNIV MCGILL.
XX PI Damha MJ, Parniak MA, Noronha AM, Wilds C, Borkow G, Arion D;
XX DR WPI; 2000-160584/14.
XX PT Therapeutic composition containing antisense oligonucleotides that
XX PT include arabinose sugars, particularly for inhibiting viral replication
XX PS Example 1; Page 29; 91pp; English.
XX The invention relates to a new composition for selective, sequence-
CC specific inhibition of gene transcription and expression in a host. The
CC composition comprises oligonucleotides containing arabinose sugars that
CC can hybridize to either a single-stranded (ss) RNA to induce RNase H
CC cleavage activity, or to a DNA/DNA or DNA/RNA duplex to form a triple
CC helix, thereby inhibiting DNA replication and/or transcription. The
CC oligoarabinonucleotides are used for antisense inhibition of gene
CC expression or to prevent DNA replication, or reverse transcription of
CC RNA by retroviruses. The compositions are therefore particularly used to
CC inhibit retroviral replication. The oligoarabinonucleotides can also be
CC used, in combination with RNase H, as reagents for sequence-specific
CC cleavage or RNA mapping, and additionally for the study and control of
CC gene expression in cells. The oligoarabinonucleotides have excellent
CC affinity for RNA, increased resistance to nucleases and show little if
CC any non-specific binding to cellular or serum proteins. They target ss
CC RNA, but not complementary ss DNA, so may be useful for targeting
CC retroviral genomic RNA to inhibit the early stages of viral replication.
CC Oligoarabinonucleotides containing pyrimidine bases form triple helices
CC with significantly higher thermal stability than those produced by
CC normal oligonucleotides. Sequences AAZ87160-287164 represent
CC oligoarabinonucleotides containing beta-D-arabinose used in an
CC exemplification of the present invention.
XX SQ Sequence 18 BP; 18 A; 0 C; 0 G; 0 U; 0 other;
Query Match 1.5%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1084 AAAAAAAAAAAAAAAAAA 1100
|||||

Db 1 AAAAAAAAAAAAAAAAAA 17
RESULT 258
AAZ87162/C
ID AAZ87162 standard; RNA; 18 BP.
XX AC
XX AAZ87162;
XX DT 08-MAY-2000 (first entry)
XX DE Oligoarabinonucleotide SEQ ID NO:3.
XX KW Beta-D-arabinose; antisense; inhibition;
XX KW transcription; expression; reverse transcription;
XX KW viral replication; RNase H cleavage; triple helix formation; ss.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT modified_base 1..18
XX FT /*tag= a
XX FT /note= "Ribose moiety replaced by beta-D-arabinose"
XX PN WO9967378-A1.
XX PD 29-DEC-1999.
XX PF 17-JUN-1999; 99WO-CA00571.
XX PR 19-JUN-1998; 98CA-2241361.
XX PA (UYMC-) UNIV MCGILL.
XX PI Damha MJ, Parniak MA, Noronha AM, Wilds C, Borkow G, Arion D;
XX DR WPI; 2000-160584/14.
XX PT Therapeutic composition containing antisense oligonucleotides that
XX PT include arabinose sugars, particularly for inhibiting viral replication
XX PS Example 1; Page 29; 91pp; English.
XX The invention relates to a new composition for selective, sequence-
CC specific inhibition of gene transcription and expression in a host. The
CC composition comprises oligonucleotides containing arabinose sugars that
CC can hybridize to either a single-stranded (ss) RNA to induce RNase H
CC cleavage activity, or to a DNA/DNA or DNA/RNA duplex to form a triple
CC helix, thereby inhibiting DNA replication and/or transcription. The
CC oligoarabinonucleotides are used for antisense inhibition of gene
CC expression or to prevent DNA replication, or reverse transcription of
CC RNA by retroviruses. The compositions are therefore particularly used to
CC inhibit retroviral replication. The oligoarabinonucleotides can also be
CC used, in combination with RNase H, as reagents for sequence-specific
CC cleavage or RNA mapping, and additionally for the study and control of
CC gene expression in cells. The oligoarabinonucleotides have excellent
CC affinity for RNA, increased resistance to nucleases and show little if
CC any non-specific binding to cellular or serum proteins. They target ss
CC RNA, but not complementary ss DNA, so may be useful for targeting
CC retroviral genomic RNA to inhibit the early stages of viral replication.
CC Oligoarabinonucleotides containing pyrimidine bases form triple helices
CC with significantly higher thermal stability than those produced by
CC normal oligonucleotides. Sequences AAZ87160-287164 represent
CC oligoarabinonucleotides containing beta-D-arabinose used in an
CC exemplification of the present invention.
XX SQ Sequence 18 BP; 0 A; 0 C; 0 G; 0 U; 0 other;
Query Match 1.5%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1084 AAAAAAAAAAAAAA 1100
    |||||
Db 18 AAAAAAAAAAAAAA 2

RESULT 259
AAZ87166/c
ID AAZ87166 standard; DNA; 18 BP.
XX
AC AAZ87166;
XX
DT 08-MAY-2000 (first entry)
XX
DE Deoxyarabinonucleotide SEQ ID NO:7.
XX
KW 2'-deoxy-2'-fluoro-beta-D-arabinose; antisense; inhibition;
transcription; expression; reverse transcription;
KW viral replication; RNase H cleavage; triple helix formation; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..18
FT /*tag= a
FT /*note= "Deoxyribose moiety replaced by 2'-deoxy-2'-
FT fluoro-beta-D-arabinose"
XX
PN WO9967378-A1.
XX
PD 29-DEC-1999.
XX
PF 17-JUN-1999; 99WO-CA00571.
XX
PR 19-JUN-1998; 98CA-2241361.
XX
PA (UYMC-) UNIV MCGILL.
XX
PI Damha MJ, Parniak MA, Noronha AM, Wilds C, Borkow G, Arion D;
XX WPI; 2000-160594/14.
XX
PT Therapeutic composition containing antisense oligonucleotides that
include arabinose sugars, particularly for inhibiting viral replication
-
PS Example 2; Page 31; 91pp; English.
XX
CC The invention relates to a new composition for selective, sequence-
specific inhibition of gene transcription and expression in a host. The
composition comprises oligonucleotides containing arabinose sugars that
can hybridise to either a single-stranded (ss) RNA to induce RNase H
cleavage activity, or to a DNA/DNA or DNA/RNA duplex to form a triple
helix, thereby inhibiting DNA replication and/or transcription. The
oligoarabinonucleotides are used for antisense inhibition of gene
expression or to prevent DNA replication, or reverse transcription of
RNA by retroviruses. The compositions are therefore particularly used to
inhibit retroviral replication. The oligoarabinonucleotides can also be
used, in combination with RNase H, as reagents for sequence-specific
cleavage or RNA mapping, and additionally for the study and control of
gene expression in cells. The oligoarabinonucleotides have excellent
affinity for RNA, increased resistance to nucleases and show little if
any non-specific binding to cellular or serum proteins. They target ss
retroviral genomic RNA to inhibit the early stages of viral replication.
Oligoarabinonucleotides containing pyrimidine bases form triple helices
with significantly higher thermal stability than those produced by
normal oligonucleotides. Sequences AAZ87165-287169 represent
oligodeoxyarabinonucleotides containing 2'-deoxy-2'-fluoro-beta-D-
arabinose used in an exemplification of the present invention.
XX
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 other;
1.5%; Score 17; DB 1; Length 18;

Query Match
```

```
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1100
    |||||
Db 18 AAAAAAAAAAAAAA 2

RESULT 260
AAZ87167
ID AAZ87167 standard; DNA; 18 BP.
XX
AC AAZ87167;
XX
DT 08-MAY-2000 (first entry)
XX
DE Deoxyarabinonucleotide SEQ ID NO:8.
XX
KW 2'-deoxy-2'-fluoro-beta-D-arabinose; antisense; inhibition;
transcription; expression; reverse transcription;
KW viral replication; RNase H cleavage; triple helix formation; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..18
FT /*tag= a
FT /*note= "Deoxyribose moiety replaced by 2'-deoxy-2'-
FT fluoro-beta-D-arabinose"
XX
PN WO9967378-A1.
XX
PD 29-DEC-1999.
XX
PF 17-JUN-1999; 99WO-CA00571.
XX
PR 19-JUN-1998; 98CA-2241361.
XX
PA (UYMC-) UNIV MCGILL.
XX
PI Damha MJ, Parniak MA, Noronha AM, Wilds C, Borkow G, Arion D;
XX WPI; 2000-160584/14.
XX
PT Therapeutic composition containing antisense oligonucleotides that
include arabinose sugars, particularly for inhibiting viral replication
-
PS Example 2; Page 31; 91pp; English.
XX
CC The invention relates to a new composition for selective, sequence-
specific inhibition of gene transcription and expression in a host. The
composition comprises oligonucleotides containing arabinose sugars that
can hybridise to either a single-stranded (ss) RNA to induce RNase H
cleavage activity, or to a DNA/DNA or DNA/RNA duplex to form a triple
helix, thereby inhibiting DNA replication and/or transcription. The
oligoarabinonucleotides are used for antisense inhibition of gene
expression or to prevent DNA replication, or reverse transcription of
RNA by retroviruses. The compositions are therefore particularly used to
inhibit retroviral replication. The oligoarabinonucleotides can also be
used, in combination with RNase H, as reagents for sequence-specific
cleavage or RNA mapping, and additionally for the study and control of
gene expression in cells. The oligoarabinonucleotides have excellent
affinity for RNA, increased resistance to nucleases and show little if
any non-specific binding to cellular or serum proteins. They target ss
retroviral genomic RNA to inhibit the early stages of viral replication.
Oligoarabinonucleotides containing pyrimidine bases form triple helices
with significantly higher thermal stability than those produced by
normal oligonucleotides. Sequences AAZ87165-287169 represent
oligodeoxyarabinonucleotides containing 2'-deoxy-2'-fluoro-beta-D-
arabinose used in an exemplification of the present invention.
XX
```

SQ Sequence 18 BP; 18 A; 0 C; 0 G; 0 U; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
 |||||
 Db 1 AAAAAAAAAAAAAAAAAA 17

RESULT 261
 AAD20091
 ID AAD20091 standard; mRNA; 18 BP.
 XX
 AC AAD20091;
 XX
 XX
 DT 03-JAN-2002 (first entry)
 XX
 DE mRNA fragment used in 3' end PCR/IVT method of the invention.
 XX
 KW RNA polymerase; RNAP; RNA detection; IVT; in vitro transcription; ss.
 XX
 OS Unidentified.
 XX
 PN US6271002-B1.
 XX
 PD 07-AUG-2001.
 XX
 PF 04-OCT-1999; 99US-0411074.
 XX
 PR 04-OCT-1999; 99US-0411074.
 XX
 PA (ROSE-) ROSETTA INPHARMATICS INC.
 XX
 PI Linsley PS, Schelter JM;
 XX
 DR WPI; 2001-624273/72.
 XX
 PT Amplifying and detecting RNA derived from a population of cells by
 PT employing a primer that contains an RNA polymerase promoter in a
 PT polymerase chain reaction -
 XX
 XX Example 3; Fig 1; 29pp; English.
 CC The invention relates to methods and kits for amplification of mRNA
 CC using a primer in PCR that contains an RNA polymerase (RNAP) promoter.
 CC The invention provides methods for amplification and detection of RNA
 CC derived from a population of cells, preferably eukaryotic cells and
 CC most preferably mammalian cells, which methods preserve fidelity with
 CC respect to sequence and transcript representation and additionally
 CC enable amplification of extremely small amounts of mRNA. The method
 CC and kit are useful for amplifying and detecting RNA derived from a
 CC population of cells, especially eukaryotic cells like mammals. The
 CC RNAs generated are useful for profiling gene expression in different
 CC populations of cells. The present sequence is a mRNA fragment used
 CC in 3' end PCR/IVT (in vitro transcription) method of the invention.
 XX
 SQ Sequence 18 BP; 17 A; 0 C; 0 G; 0 U; 1 other;

Query Match 1.5%; Score 17; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
 |||||
 Db 2 AAAAAAAAAAAAAAAAAA 18

RESULT 262
 AAF82472/c
 ID AAF82472 standard; DNA; 18 BP.
 XX

AA82472;
 29-JUN-2001 (first entry)
 Phagemid vector PCR2.1 polylinker oligonucleotide #6.
 Phagemid vector; PCR2.1; rat; secreted factor; P00210D09; cardiant;
 nephrotropic; antiinflammatory; gene therapy; cardiac disease;
 renal disease; inflammatory disease; polylinker; ss.
 Synthetic.
 WO200123419-A2.
 05-APR-2001.
 27-SEP-2000; 2000WO-US26592.
 27-SEP-1999; 99US-0156277.
 (SCIO-) SCIOS INC.
 Stanton LW, Kapoun AM;
 WPI; 2001-328177/34.
 Novel secreted factor encoded by clone P00210D09 useful for diagnosing,
 treating and/or preventing various cardiac, renal and inflammatory
 diseases -
 Example 1; Page 41; 69pp; English.
 The present sequence corresponds to polylinker DNA of the phagemid
 vector PCR2.1. It was used in the construction of a normalised rat cDNA
 library, which was used in an example demonstrating differential
 expression of a rat gene referred to as clone P00210D09. The invention
 relates to a polypeptide comprising a sequence of at least 80% identity
 to residues 22-122 of the present sequence, or a sequence encoded by a
 nucleic acid hybridising under stringent conditions to the complement of
 the coding region comprising 1031 nucleotides, and having at least one
 biological activity of the polypeptide encoded by clone P00210D09. The
 polypeptides and polynucleotides of the invention are useful for the
 treatment of cardiac, renal and inflammatory diseases. The
 polynucleotides are useful in antisense mediated gene inhibition and in
 gene therapy. The polypeptides are useful in assays for identifying lead
 compounds that may be used as therapeutic agents in the treatment of
 cardiac, kidney or inflammatory diseases.
 Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
 |||||
 Db 18 AAAAAAAAAAAAAAAAAA 2

RESULT 263
 AAD03565/c
 ID AAD03565 standard; DNA; 18 BP.
 XX
 AC AAD03565;
 XX
 XX 19-JUN-2001 (first entry)
 XX
 DE Oligonucleotide #6 used for the preparation of normalised cDNA libraries.
 XX
 KW Rat; secreted factor; clone P00188 D12; cardiant; antiinflammatory;
 antiarhythmic; antiarteriosclerotic; antiatherosclerotic; nephropathic;
 antidiabetic; immunosuppressive; antiasthmatic; antirheumatoid;
 antibacterial; osteopathic; cerebroprotective; vasotropic; antitumor;

KW nootropic; neuroprotective; congestive heart failure; myocarditis;
 KW hypertrophic cardiomyopathy; angina pectoris; myocardial infarction;
 KW kidney disease; acute renal failure; renal glucosuria; renal infarction;
 KW polycystic kidney disease; hereditary nephritis; inflammatory disease;
 KW tumour angiogenesis; osteoarthritis; toxic shock syndrome; psoriasis;
 KW stroke; neural trauma; cerebral malaria; Crohn's disease; osteoporosis;
 KW ulcerative colitis; Alzheimer's disease; gene therapy; ss.

XX Rattus norvegicus.

XX WO200123564-A1.

XX 05-APR-2001.

XX 27-SEP-2000; 2000WO-US26544.

XX 27-SEP-1999; 99US-0156280.

XX (SCIO-) SCIOS INC.

XX Stanton LW, Kapoun AM;

XX WPI; 2001-266159/27.

XX Novel secreted factor encoded by clone P00188D12 which is
 PT differentially expressed in certain disease states, useful in
 PT diagnosing and treating cardiac, renal or inflammatory diseases -

XX Example 1; Page 42; 71pp; English.

XX The patent discloses novel secreted factor protein encoded by clone
 CC P00188 D12. The secreted factor is differentially expressed in certain
 CC disease states. Secreted protein, its antibodies, antagonists or
 CC compositions comprising them are useful in the diagnosis and treatment
 CC of cardiac diseases such as congestive heart failure, myocarditis,
 CC hypertrophic cardiomyopathy, angina pectoris, myocardial infarction,
 CC cardiac arrhythmia, arteriosclerosis, kidney diseases such as acute
 CC renal failure, renal glucosuria, renal infarction, nephrogenic
 CC diabetes insipidus, polycystic kidney disease, hereditary nephritis
 CC and inflammatory diseases such as asthma, autoimmune diabetes, tumour
 CC syndrome, aschma, stroke, neural trauma, psoriasis, cerebral malaria,
 CC osteoporosis, Crohn's disease, ulcerative colitis, Alzheimer's disease.
 CC Secreted protein DNA is useful in antisense-mediated gene inhibition
 CC and in gene therapy. An array comprising one or more oligonucleotides
 CC complementary to reference RNA or DNA encoding the secreted factor is
 CC useful for detecting cardiac, kidney and inflammatory disease.
 CC The present DNA sequence is an oligonucleotide which is used in the
 CC preparation of a normalised cDNA library containing secreted factor
 CC DNAs. The normalised cDNA libraries are used in the identification
 CC of differentially expressed rat secreted factor P00188_D12 gene.

XX Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1084 AAAAAAAAAAAAAAAAAA 1100

Db 18 AAAAAAAAAAAAAAAAAA 2

RESULT 264

AAF99708/C

ID AAF99708 standard; DNA; 18 BP.

XX AAF99708;

XX 12-JUN-2001 (first entry)

XX Immunostimulatory nucleic acid #824.

KW

KW

KW

KW

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
 immunostimulatory; tumour; viral infection; bacterial infection;
 fungal infection; parasitic infection; cancer; asthma;
 infectious disease; allergy; immune deficiency; phosphorothioate; ss.
 Synthetic.

XX WO200122972-A2.

XX 05-APR-2001.

XX 25-SEP-2000; 2000WO-US26383.

XX 25-SEP-1999; 99US-0156113.

XX 27-SEP-1999; 99US-0156135.

XX 23-AUG-2000; 2000US-0227436.

XX (IOWA) UNIV IOWA RES FOUND.

XX (COLE-) COLEY PHARM GMBH.

XX Krieg AM, Schetter C, Vollmer J;

XX WPI; 2001-273485/28.

XX Vaccinating against tumors, infectious diseases, allergies and asthma
 using immunostimulatory Py-rich and TG nucleic acids -

XX Claim 101; Page 56; 338pp; English.

XX The present invention relates to a method for stimulating an immune
 response. The method comprises administering an immunostimulatory nucleic
 acid to a non-rodent subject in sufficient quantity to stimulate an
 immune response. The present sequence is one such immunostimulatory
 nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
 (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
 against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
 and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
 haemophilus, campylobacter, clostridium, Escherichia coli and/or
 staphylococcus), fungal antigens and/or parasitic antigens. The method is
 also useful for preventing cancer, asthma, infectious disease, allergy or
 immune deficiency. The present sequence can also be used to redirect a
 Th2 to a Th1 immune response and to activate immune cells.
 Note: the present sequence may have a phosphorothioate backbone.

XX Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1084 AAAAAAAAAAAAAAAAAA 1100

Db 18 AAAAAAAAAAAAAAAAAA 2

RESULT 265

AAF99734/C

ID AAF99734 standard; DNA; 18 BP.

XX AAF99734;

XX 12-JUN-2001 (first entry)

XX Immunostimulatory nucleic acid #850.

Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
 immunostimulatory; tumour; viral infection; bacterial infection;
 fungal infection; parasitic infection; cancer; asthma;
 infectious disease; allergy; immune deficiency; phosphorothioate; ss.
 Synthetic.

XX WO200122972-A2.


```

XX PD 05-APR-2001.
XX PF 25-SEP-2000; 2000WO-US26383.
XX XX
XX 25-SEP-1999; 99US-0156113.
XX 27-SEP-1999; 99US-0156135.
XX PR 23-AUG-2000; 2000US-0227436.
XX XX
XX (IOWA ) UNIV IOWA RES FOUND.
XX PA (COLE-) COLEY PHARM GMBH.
XX PI Krieg AM, Schetter C, Vollmer J;
XX XX WPI; 2001-273485/28.
XX DR
XX XX
XX Vaccinating against tumors, infectious diseases, allergies and asthma
XX PT using immunostimulatory Py-rich and TG nucleic acids -
XX PS Claim 101; Page 56; 338pp; English.
XX XX
XX The present invention relates to a method for stimulating an immune
XX CC response. The method comprises administering an immunostimulatory nucleic
XX CC acid to a non-rodent subject in sufficient quantity to stimulate an
XX CC immune response. The present sequence is one such immunostimulatory
XX CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
XX CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
XX CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
XX CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
XX CC haemophilus, campylobacter, clostridium, Escherichia coli and/or
XX CC staphylococcus), fungal antigens and/or parasitic antigens. The method is
XX CC also useful for preventing cancer, asthma, infectious disease, allergy or
XX CC immune deficiency. The present sequence can also be used to redirect a
XX CC Th2 to a Th1 immune response and to activate immune cells.
XX CC Note: the present sequence may have a phosphorothioate backbone.
XX XX
XX Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 other;
XX SQ
    Query Match 1.5%; Score 17; DB 1; Length 18;
    Best Local Similarity 100.0%; Pred. No. 1.9e-02;
    Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
Db 18 AAAAAAAAAAAAAAAAAA 2

RESULT 266
AADI17014
ID AADI17014 standard; DNA; 18 BP.
XX AC
XX AADI17014;
XX AC
XX 29-NOV-2001 (first entry)
XX DT
XX DE Oligonucleotide A18-2PEG linker.
XX XX
XX Scaffold protein; antibody mimic; fibronectin type III domain;
XX KW randomised loop; randomised beta-sheet; diagnostic purpose;
XX KW protein designing; ss.
XX XX
XX Unidentified.
XX OS
XX XX
XX Key Location/Qualifiers
XX PF misc_feature 18
XX FT /*tag= a
XX FT /note= "Linked to (PEG)2CCPuromycin"
XX XX
XX WO200164942-A1.
XX PN
XX 07-SEP-2001.
XX PD
XX 28-FEB-2001; 2001WO-US06414.
XX PF

```

```

XX 29-FEB-2000; 2000US-0515260.
XX XX
XX (PHYL-) PHYLOS INC.
XX XX
XX Lipovsek D, Wagner RW, Kuimelis RG;
XX XX
XX WPI; 2001-557782/62.
XX XX
XX Fibronectin scaffold protein array for obtaining a protein/compound
XX PT which binds to a compound/protein, comprises a fibronectin type III
XX PT domain having a randomised loop, a randomised beta-sheet or their
XX PT combination -
XX XX
XX Disclosure; Page 25; 67pp; English.
XX XX
XX The present invention relates to an array of proteins (antibody mimics)
XX CC comprising a fibronectin type III domain having a randomised loop, a
XX CC randomised beta-sheet, or their combination, and has the capacity to
XX CC bind to a compound that is not bound by a corresponding naturally-
XX CC occurring fibronectin, immobilised onto a solid support. The antibody
XX CC mimics is useful for detecting a compound preferably a protein, in a
XX CC biological sample. It is also useful to detect one or more different
XX CC analytes simultaneously in a sample. Hence is useful for diagnostic
XX CC purposes. It is also useful for the purpose of designing proteins
XX CC capable of binding to virtually any compound of interest. The present
XX CC sequence is an oligonucleotide A18-2PEG linker used in an
XX CC exemplification of the invention.
XX XX
XX Sequence 18 BP; 18 A; 0 C; 0 G; 0 U; 0 other;
XX SQ
    Query Match 1.5%; Score 17; DB 1; Length 18;
    Best Local Similarity 100.0%; Pred. No. 1.9e-02;
    Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
Db 1 AAAAAAAAAAAAAAAAAA 17

RESULT 267
ABS78429/c
ID ABS78429 standard; DNA; 18 BP.
XX AC
XX ABS78429;
XX XX
XX 13-DEC-2002 (first entry)
XX DT
XX DE Angiogenesis inhibitory oligonucleotide #913.
XX XX
XX Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
XX KW tumour metastasis; precancerous lesion; rheumatoid arthritis;
XX KW psoriasis; diabetic retinopathy; retinopathy of prematurity;
XX KW macular degeneration; corneal graft rejection; neovascular glaucoma;
XX KW retrolental fibroplasia; rubeosis; Osler-Weber Syndrome;
XX KW myocardial angiogenesis; plaque neovascularisation; telangiectasia;
XX KW haemophilic joint; angiofibroma; wound granulation;
XX KW intestinal adhesion; atherosclerosis; scleroderma; hypertrophic scar.
XX XX
XX Synthetic.
XX OS
XX WO200253141-A2.
XX PN
XX 11-JUL-2002.
XX PD
XX 14-DEC-2001; 2001WO-US48458.
XX PF
XX 14-DEC-2000; 2000US-255534P.
XX PR
XX (COLE-) COLEY PHARM GROUP INC.
XX PA
XX Bratzler RL;
XX PI
XX

```

DR WPI; 2002-566690/60.

XX Inhibiting angiogenesis in a subject, involves administering at least

PT one antiangiogenic nucleic acid molecule to the subject -

XX

PS Claim 2; Page 35; 276pp; English.

XX

CC The invention relates to inhibiting angiogenesis in a subject, comprising

CC administering at least one antiangiogenic nucleic acid molecule.

CC Also included is a kit comprising a first container housing the

CC antiangiogenic nucleic acids, and instructions for administering them to

CC a subject having a condition characterised by unwanted angiogenesis.

CC The method is useful for inhibiting angiogenesis associated with solid

CC tumour growth, tumour metastasis, precancerous lesion, rheumatoid

CC arthritis, psoriasis, diabetic retinopathy, retinopathy of prematurity,

CC macular degeneration, corneal graft rejection, neovascular glaucoma,

CC retrolental fibroplasia, rubeosis, Osler-Webber Syndrome, myocardial

CC angiogenesis, plaque neovascularisation, telangiectasia, haemophilic

CC joints, angiofibroma, wound granulation, intestinal adhesions,

CC atherosclerosis, scleroderma and hypertrophic scars. The present

CC sequence is an antiangiogenic nucleic acid of the invention.

XX

SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.9e+02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1100

DB 18 AAAAAAAAAAAAAA 2

RESULT 268

ABST8455/C

ID ABS78455 standard; DNA; 18 BP.

XX

AC ABS78455;

XX

DT 13-DEC-2002 (first entry)

XX

DE Angiogenesis inhibitory oligonucleotide #939.

XX

KW Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;

KW tumour metastasis; precancerous lesion; rheumatoid arthritis;

KW psoriasis; diabetic retinopathy; retinopathy of prematurity;

KW macular degeneration; corneal graft rejection; neovascular glaucoma;

KW retrolental fibroplasia; rubeosis; Osler-Webber Syndrome;

KW myocardial angiogenesis; plaque neovascularisation; telangiectasia;

KW haemophilic joint; angiofibroma; wound granulation;

KW intestinal adhesion; atherosclerosis; scleroderma; hypertrophic scar.

XX

OS Synthetic.

XX

PN WO200253141-A2.

XX

PD 11-JUL-2002.

XX

PF 14-DEC-2001; 2001WO-US48458.

XX

PR 14-DEC-2000; 2000US-255534P.

XX

PA (COLE-) COLEY PHARM GROUP INC.

XX

PI Bratzler RL;

XX

DR WPI; 2002-566690/60.

XX

XX Inhibiting angiogenesis in a subject, involves administering at least

PT one antiangiogenic nucleic acid molecule to the subject -

XX

PS Claim 2; Page 36; 276pp; English.

XX

CC The invention relates to inhibiting angiogenesis in a subject, comprising

CC administering at least one antiangiogenic nucleic acid molecule.

CC Also included is a kit comprising a first container housing the

CC antiangiogenic nucleic acids, and instructions for administering them to

CC a subject having a condition characterised by unwanted angiogenesis.

CC The method is useful for inhibiting angiogenesis associated with solid

CC tumour growth, tumour metastasis, precancerous lesion, rheumatoid

CC arthritis, psoriasis, diabetic retinopathy, retinopathy of prematurity,

CC macular degeneration, corneal graft rejection, neovascular glaucoma,

CC retrolental fibroplasia, rubeosis, Osler-Webber Syndrome, myocardial

CC angiogenesis, plaque neovascularisation, telangiectasia, haemophilic

CC joints, angiofibroma, wound granulation, intestinal adhesions,

CC atherosclerosis, scleroderma and hypertrophic scars. The present

CC sequence is an antiangiogenic nucleic acid of the invention.

XX

SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.9e+02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1100

DB 18 AAAAAAAAAAAAAA 2

RESULT 269

ABST53437/C

ID ABS53437 standard; DNA; 18 BP.

XX

AC ABS53437;

XX

DT 29-NOV-2002 (first entry)

XX

DE Poly d(T) primer.

XX

KW Terminal continuation; TC; ss; second strand cDNA synthesis;

KW primer; poly d(T).

XX

OS Synthetic.

XX

PN WO200265093-A2.

XX

PD 22-AUG-2002.

XX

PF 14-FEB-2002; 2002WO-US05713.

XX

PR 14-FEB-2001; 2001US-268645P.

PR 14-FEB-2001; 2001US-268664P.

PR 18-JUL-2001; 2001US-306216P.

PR 07-NOV-2001; 2001US-344557P.

PR 07-NOV-2001; 2001US-348242P.

PR 09-NOV-2001; 2001US-350176P.

XX

PA (BAY) BAYLOR COLLEGE MEDICINE.

PA (REMB-) RES FOUND MENTAL HYGIENE INC.

XX

PI Ginsberg SD, Che S;

XX

DR WPI; 2002-567050/60.

XX

PT Increasing efficiency of second strand cDNA synthesis using terminal

PT continuation model before performing further RNA amplification by RNA

PT transcription -

XX

PS Example 7; Page 80; 128pp; English.

XX

CC This invention relates to a novel method for increasing the efficiency

CC of second strand cDNA synthesis through a mechanism of terminal

CC continuation. In the method an RNA molecule is obtained and a first

CC primer is added that comprises a region that hybridises to a

CC complementary region of the molecule before a second primer is added

CC comprising at least one riboguanine at the 3' end of the primer. A first

CC arthritis, osteoarthritis, stroke, psoriasis, restenosis, graft versus
CC host reaction, Crohn's disease, ulcerative colitis and Alzheimer's
CC disease. Sequences AAS94693-AAS94745 represent cDNA clones, which encode
CC the secreted factor polypeptides of the invention, and oligonucleotide
CC probes and PCR primers.

XX Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
| | | | | | | | | | | | | | | | | |
DB 18 AAAAAAAAAAAAAAAAAA 2

RESULT 272

ABA93239/C
ID ABA93239 standard; DNA; 18 BP.

XX ABA93239;

DT 18-APR-2002 (first entry)

XX Adaptor oligonucleotide SEQ ID NO:2.

DE Detection; comparative detection; adaptor; ss.

XX Synthetic.

PN JP2001333800-A.

XX 04-DEC-2001.

PF 30-MAY-2000; 2000JP-0160324.

XX 30-MAY-2000; 2000JP-0160324.

FR (UNIT-) UNITECH CO LTD.

XX WPI; 2002-135950/18.

XX Comparative detection of the amounts of RNA and DNA -

PS Disclosure; Page 9; 9pp; Japanese.

XX The present invention describes a method for the comparative detection
CC of the amount of an RNA. The method comprises: (a) cDNAs obtained by
CC transcribing respectively from at least two tissue RNAs are respectively
CC fragmented by using a same restriction enzyme; (b) each different adaptor
CC and a common adaptor are added to each of the cDNA fragments derived from
CC the same or different tissues by the step (a); (c) the resultant adaptor-
CC added cDNAs are mixed together; (d) an adaptor primer having the common
CC sequence to said different adaptor and a gene-specific adaptor are used
CC to amplify said adaptor-added cDNAs containing no region derived from
CC polyadenylic acid of the mRNA before the addition of the adaptor among
CC the adaptor-added cDNAs prepared by the step (b); (e) the ratios of the
CC cDNA amounts are measured between the tissues; (f) the RNA is detected
CC from the measured result; (g) each different adaptor and a common adaptor
CC are added to each of the genomic DNA fragments derived from a same or
CC different individuals; (h) the resultant adaptor-added genomic DNAs are
CC mixed together; (i) the adaptor-added genomic DNAs are amplified by using
CC an adaptor primer having the common sequence to the different adaptor and
CC a sequence-specific adaptor; and (j) the ratios of the amplified amounts
CC of the genomic DNAs are measured between the individuals. The method is
CC used for the detection of the amounts of RNA and DNA. The present
CC sequence represents an oligonucleotide which is used in the
CC exemplification of the present invention.

XX Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 other;

Query Match

1.5%; Score 17; DB 1; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
| | | | | | | | | | | | | | | | | |
DB 18 AAAAAAAAAAAAAAAAAA 2

RESULT 273

ABL39401/C
ID ABL39401 standard; DNA; 18 BP.

XX ABL39401;

DT 16-APR-2002 (first entry)

XX Immunostimulatory nucleic acid SEQ ID NO: 837.

XX Antibody-induced cell lysis; cancer; immunostimulatory; CD20;
XX angiogenesis; metastasis; cytostatic; ss.

OS Synthetic.

XX Key Location/Qualifiers

FT modified_base 1..18

FT /*tag= a

FT /mod_base= OTHER

FT /note= "phosphorothioate backbone"

XX WO200197843-A2.

XX 27-DEC-2001.

XX 22-JUN-2001; 2001WO-US20154.

XX 22-JUN-2000; 2000US-213346P.

XX (IOWA) UNIV IOWA RES FOUND.

XX Weiner G, Hartmann G;

XX WPI; 2002-154611/20.

XX Treating or preventing cancer, such as basal cell carcinoma, comprises
XX administering immunostimulatory nucleic acids that induce expression of
XX cell surface antigens and antibodies to a subject having or at risk of
XX developing cancer -

XX Disclosure; Page 308; 312pp; English.

XX The present invention relates to methods for treating or preventing
XX cancer, involving administering to a subject having or at risk of
XX developing cancer immunostimulatory nucleic acids that induce expression
XX of cell surface antigens and antibodies. The methods are useful for
XX treating or preventing cancer such as basal cell carcinoma, bladder
XX cancer, bone cancer, brain and central nervous system (CNS) cancer,
XX breast cancer, cervical cancer, colon and rectum cancer, connective
XX tissue cancer, oesophageal cancer, eye cancer, kidney cancer, larynx
XX cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma,
XX non-Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian
XX cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin
XX cancer, stomach cancer, testicular cancer, and uterine cancer. The
XX present sequence is an immunostimulatory oligonucleotide described in
XX the exemplification of the invention.

XX Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 other;

Query Match

1.5%; Score 17; DB 1; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
| | | | | | | | | | | | | | | | | |

CC the prepared aggregates of the double-stranded cDNAs with restriction
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC separate lanes. The method can be used to analyse gene expression
CC rapidly and easily.

XX Sequence 19 BP; 0 A; 2 C; 0 G; 17 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 19;

Best Local Similarity 100.0%; Pred. No. 2e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100

DB 17 AAAAAAAAAAAAAAAAAA 1

RESULT 277

AAQ75549/c

ID AAQ75549 standard; DNA; 19 BP.

XX AC

XX AAQ75549;

XX DT

XX 04-AUG-1995 (first entry)

XX Reverse transcription primer used in cDNA analysis technique.

DE Analysis; gene expression; reverse transcription; primer; cDNA;

KW aggregate; restriction enzyme; ss.

XX OS

XX Synthetic.

XX PN

XX JP06303997-A.

XX PD

XX 01-NOV-1994.

XX PF

XX 16-APR-1993; 93JP-0112515.

XX PR

XX 16-APR-1993; 93JP-0112515.

XX PA

XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

XX WPI; 1995-018287/03.

XX DT

XX Analysis of cDNA and gene expression - by amplification of mRNA

PT followed by digestion with restriction enzymes

XX Disclosure; Page 5; 11pp; Japanese.

XX A method for the analysis of cDNA comprises (a) preparing an

CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs

CC and a plural type of labelled reverse transcription primers

CC (GENESQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the

CC template for each reverse transcription primer; (b) digesting each of

CC the prepared aggregates of the double-stranded cDNAs with restriction

CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in

CC separate lanes. The method can be used to analyse gene expression

CC rapidly and easily.

XX Sequence 19 BP; 0 A; 0 C; 1 G; 18 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 19;

Best Local Similarity 100.0%; Pred. No. 2e+02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100

DB 17 AAAAAAAAAAAAAAAAAA 1

RESULT 278

AAQ75550/c

ID AAQ75550 standard; DNA; 19 BP.

XX AC

XX AAQ75550;

XX DT

XX 04-AUG-1995 (first entry)

XX Reverse transcription primer used in cDNA analysis technique.

KW Analysis; gene expression; reverse transcription; primer; cDNA;

XX aggregate; restriction enzyme; ss.

XX OS

XX Synthetic.

XX PN

XX JP06303997-A.

XX PD

XX 01-NOV-1994.

XX PF

XX 16-APR-1993; 93JP-0112515.

XX PR

XX 16-APR-1993; 93JP-0112515.

XX PA

XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

AC AAQ75550;

XX DT

XX 04-AUG-1995 (first entry)

XX Reverse transcription primer used in cDNA analysis technique.

XX Analysis; gene expression; reverse transcription; primer; cDNA;

KW aggregate; restriction enzyme; ss.

XX OS

XX Synthetic.

XX PN

XX JP06303997-A.

XX PD

XX 01-NOV-1994.

XX PF

XX 16-APR-1993; 93JP-0112515.

XX PR

XX 16-APR-1993; 93JP-0112515.

XX PA

XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

XX WPI; 1995-018287/03.

XX DT

XX Analysis of cDNA and gene expression - by amplification of mRNA

PT followed by digestion with restriction enzymes

XX Disclosure; Page 5; 11pp; Japanese.

XX A method for the analysis of cDNA comprises (a) preparing an

CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs

CC and a plural type of labelled reverse transcription primers

CC (GENESQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the

CC template for each reverse transcription primer; (b) digesting each of

CC the prepared aggregates of the double-stranded cDNAs with restriction

CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in

CC separate lanes. The method can be used to analyse gene expression

CC rapidly and easily.

XX Sequence 19 BP; 0 A; 1 C; 1 G; 17 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 19;

Best Local Similarity 100.0%; Pred. No. 2e+02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100

DB 17 AAAAAAAAAAAAAAAAAA 1

RESULT 279

AAQ75547/c

ID AAQ75547 standard; DNA; 19 BP.

XX AC

XX AAQ75547;

XX DT

XX 04-AUG-1995 (first entry)

XX Reverse transcription primer used in cDNA analysis technique.

KW Analysis; gene expression; reverse transcription; primer; cDNA;

XX aggregate; restriction enzyme; ss.

XX OS

XX Synthetic.

XX PN

XX JP06303997-A.

XX PD

XX 01-NOV-1994.

XX PF

XX 16-APR-1993; 93JP-0112515.

XX PR

XX 16-APR-1993; 93JP-0112515.

XX PA

XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

XX WPI; 1995-018287/03.
 XX Analysis of cDNA and gene expression - by amplification of mRNA
 PT followed by digestion with restriction enzymes
 XX Disclosure; Page 5; 11pp; Japanese.
 XX
 XX A method for the analysis of cDNA comprises (a) preparing an
 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
 CC and a plural type of labelled reverse transcription primers
 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
 CC template for each reverse transcription primer; (b) digesting each of
 CC the prepared aggregates of the double-stranded cDNAs with restriction
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
 CC separate lanes. The method can be used to analyse gene expression
 CC rapidly and easily.
 XX
 SQ Sequence 19 BP; 0 A; 0 C; 2 G; 17 T; 0 other;
 Query Match 1.5%; Score 17; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1084 AAAAAAAAAAAAAAAAAA 1100
 Db 17 AAAAAAAAAAAAAAAAAA 1
 RESULT 280
 AAT10757/c
 ID AAT10757 standard; RNA; 19 BP.
 AC AAT10757;
 XX
 DT 09-SEP-1996 (first entry)
 XX
 DE Oligonucleotide probe, T-2.
 XX
 KW Electronically self-addressable device; ED; electrode;
 KW current source; attachment layer; permeable; counterion;
 KW genetic typing; probe; detection; ss.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT modified_base 1
 FT /*tag= a
 FT /note= "5'-amino terminus"
 XX
 PN WO9601836-A1.
 XX
 XX 25-JAN-1996.
 XX
 XX 05-JUL-1995; 95WO-US08570.
 XX
 XX 07-JUL-1994; 94US-0271882.
 XX
 XX (NANO-) NANOGEN INC.
 XX
 PI Evans GA, Heller MJ, Sosnowski RG, Tu E;
 XX
 XX WPI; 1996-097582/10.
 XX
 XX Electronically self-addressable device - used for electronic control
 PT of, e.g. nucleic acid hybridisation
 XX
 XX Example 1; Page 61; 155pp; English.
 XX
 XX The sequences given in AAT10742-67 are synthetic oligonucleotides
 CC which are used in the construction of the electronically self-
 CC addressable device (ED) of the invention. The ED comprises a
 CC substrate, an electrode or opt. a number of electrodes supported by

CC the substrate, a current source operatively connected to the
 CC electrode and an attachment layer adjacent to the electrode which is
 CC permeable to a counterion but not permeable to a molecule capable of
 CC insulating or binding to the electrode. The attachment layer is
 CC capable of attaching a macromolecule. The ED is used for genetic
 CC typing and comprises a number of electronically addressable
 CC locations each comprising an electrode, and a binding entity, such
 CC as one of these probes, attached to each of the locations capable
 CC of detecting the presence of a genetic sequence.
 XX
 SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 other;
 Query Match 1.5%; Score 17; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1084 AAAAAAAAAAAAAAAAAA 1100
 Db 19 AAAAAAAAAAAAAAAAAA 3
 RESULT 281
 AAV07878/c
 ID AAV07878 standard; DNA; 19 BP.
 AC AAV07878;
 XX
 DT 14-DEC-1998 (first entry)
 XX
 DE Aminoxy-modified oligonucleotide.
 XX
 KW phosphorothioate; ras gene; malignant cell growth; aminoxy-modified;
 KW nuclease resistance; reporter group; ss.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT modified_base 15..18
 FT /*tag= a
 FT /note= "5-methyl, 2'-aminoxyethoxy-thymidine"
 XX
 PN WO9835978-A1.
 XX
 XX 20-AUG-1998.
 XX
 XX 13-FEB-1998; 98WO-US02405.
 XX
 XX 30-JAN-1998; 98US-0016520.
 XX
 XX 14-FEB-1997; 97US-0037143.
 XX
 XX (ISIS-) ISIS PHARM INC.
 XX
 XX Cook PD, Kawasaki AM, Manoharan M;
 XX
 XX WPI; 1998-568232/48.
 XX
 XX New aminoxy-modified oligonucleotides - which can show improved
 PT binding to complementary strands and improved resistance to nuclease
 XX
 XX Disclosure; Page 84; 131pp; English.
 XX
 XX The invention relates to aminoxy-modified(oligo)nucleotides or
 CC nucleosides which are useful as therapeutics, diagnostics, and research
 CC reagents. They may be used, e.g., for modulation of the ras gene and may
 CC be able to modulate the process of transformation from normal to
 CC malignant cell growth. They may be prepared using known methods.
 CC Inclusion of the aminoxy moieties can improve binding of
 CC oligonucleotides to complementary strands. The moieties can also provide
 CC conjugation sites useful for conjugation of useful ligands (e.g. reporter
 CC groups and groups for modifying uptake, distribution or other
 CC pharmacodynamic properties) to oligonucleotides. The present sequence
 CC represents an example of an aminoxy-modified oligonucleotide disclosed
 CC in the specification.

```
XX
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 other;

Query Match          1.5%; Score 17; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
DB 19 AAAAAAAAAAAAAAAAAA 3

RESULT 282
AAV06820/c
ID AAV06820 standard; DNA; 19 BP.
XX
AC AAV06820;
XX
DT 13-OCT-1998 (first entry)
XX
DE Oligonucleotide containing modified internucleotide linkage.
XX
KW oligonucleotide; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 16..18
FT /*tag= a
FT /note= "these T residues are formed as part of a
FT conventional phosphoramidite oligonucleotide synthesis
FT process but using as the reactant a thymosine nucleoside
FT having at the 3'-position a group of formula
FT -CH2-P(OCH2CH2CN)-N(iPr)2"
XX
PN WO9747636-A2.
XX
PD 18-DEC-1997.
XX
PF 03-JUN-1997; 97WO-GB01490.
XX
PR 13-JUN-1996; 96GB-0012600.
XX
PA (NOVS) NOVARTIS AG.
XX
PI Altmann K, Collingwood SP, Douglas ME, Moser HE;
XX
DR WPI; 1998-052233/05.
XX
PT New tetrahydrofuran derivatives - useful in the synthesis of
PT oligonucleotides
XX
PS Example 12; Page 29; 37pp; English.
XX
CC The invention relates, inter alia, to a method of preparing an
CC oligonucleotide by coupling (1) a new nucleoside having a protected
CC 5'-hydroxy group and at the 3'-position a group of formula
CC -CH2-P(OR3)-NR4R5, with (2) a nucleoside or oligonucleotide having a
CC free 5'-hydroxy group, to give (3) a precursor having an
CC internucleoside linkage of formula -CH2-P(OR3)-O-; and converting this
CC to a linkage of formula -CH2-P(OR3)-(X)-O- (where X = S or O).
CC The present sequence is a specific example of an oligonucleotide so
CC prepared.
XX
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 other;

Query Match          1.5%; Score 17; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
DB 19 AAAAAAAAAAAAAAAAAA 3

RESULT 283
AAZ01358/c
ID AAZ01358 standard; DNA; 19 BP.
XX
AC AAZ01358;
XX
DT 27-SEP-1999 (first entry)
XX
DE PCR primer for PGI biallelic marker 4-4-187.
XX
KW PGI gene; biallelic marker; PCR primer; PGI-related biallelic marker;
KW cancer; prostate cancer; diagnosis; therapy; prostate specific antigen;
KW PSA; human; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 16..18
FT /*tag= a
FT /note= "these T residues are formed as part of a
FT conventional phosphoramidite oligonucleotide synthesis
FT process but using as the reactant a thymosine nucleoside
FT having at the 3'-position a group of formula
FT -CH2-P(OCH2CH2CN)-N(iPr)2"
XX
PN WO9932644-A2.
XX
PD 01-JUL-1999.
XX
PF 22-DEC-1998; 98WO-IB02133.
XX
PR 09-SEP-1998; 98US-0099658.
XX
PR 22-DEC-1997; 97US-0996306.
XX
PA (GEST) GENSET.
XX
PI Blumenfeld M, Bougueleret L, Chumakov I, Cohen D;
XX
DR WPI; 1999-405178/34.
XX
PT Use of a prostate cancer associated gene and biallelic markers
PT derived from it
XX
PS Claim 4; Page 374; 385pp; English.
XX
CC The invention relates to a mammalian PGI gene and protein, and a set of
CC PGI biallelic markers. The PGI polynucleotide and biallelic markers are
CC used in a hybridisation assay, a sequencing assay, or in an
CC allele-specific amplification assay for determining the identity of a
CC nucleotide at a PGI-related biallelic marker. The methods can be used to
CC detect and to assess the risk of developing cancer or prostate cancer.
CC Early-stage diagnosis of prostate cancer relies on prostate specific
CC antigen (PSA) dosage. However, the effectiveness of this is limited due
CC to its inability to discriminate between malignant and non-malignant
CC affections of the organ. A need exists for both a reliable diagnostic
CC procedure which would enable early-stage diagnosis, and for preventative
CC and curative treatments of the disease. The PGI gene can be used for
CC detection of prostate cancer, and the risk of developing it in the
CC future, and can also be used to determine therapies for the disease.
XX
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 other;

Query Match          1.5%; Score 17; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
DB 19 AAAAAAAAAAAAAAAAAA 3

RESULT 284
AAAX81927/c
ID AAX81927 standard; DNA; 19 BP.
XX
AC AAX81927;
XX
DT 07-SEP-1999 (first entry)
XX
```


DE Polynucleotide strand with amino groups.
 XX Enzyme-specific cleavable polynucleotide substrate;
 KW quenched fluorescent moiety; biological assay; detection;
 KW identification; microorganism; sterilization assurance; nuclease; ss.
 XX Synthetic.
 OS
 XX
 FH Key Location/Qualifiers
 FT modified_base 7
 FT /*tag= a
 FT /note= "amine-modified C6 derivative of
 FT deoxythymidine (dtr)"
 FT modified_base 9
 FT /*tag= b
 FT /note= "amine-modified C6 derivative of
 FT deoxythymidine (dtr)"
 FT modified_base 11
 FT /*tag= c
 FT /note= "amine-modified C6 derivative of
 FT deoxythymidine (dtr)"
 FT modified_base 13
 FT /*tag= d
 FT /note= "amine-modified C6 derivative of
 FT deoxythymidine (dtr)"
 FT
 PN WO9935288-A1.
 XX
 XX 15-JUL-1999.
 XX
 XX 20-AUG-1998; 98WO-US17311.
 XX
 XX 09-JAN-1998; 98US-0005260.
 XX
 XX (MINN) MINNESOTA MINING & MFG CO.
 XX
 XX Mach PA, Wei A;
 XX
 XX WPI; 1999-419356/35.
 XX
 XX An enzyme-specific cleavable polynucleotide substrate bearing
 XX quenched fluorescent moieties
 XX
 XX Example 2; Page 20; 34pp; English.
 XX
 XX The specification describes an enzyme-specific cleavable polynucleotide
 XX substrate bearing quenched fluorescent moieties. The enzyme-specific
 XX cleavable polynucleotide substrate is useful in biological assays for
 XX detection and identification of microorganisms, sterilization assurance,
 XX pharmaceutical discovery, enzyme assays, immunoassays and other
 XX biological assays. The method provides a rapid and convenient approach
 XX for detection and identification of microorganisms. It can be adapted to
 XX sequence-dependent or sequence-independent tests. The invention provides
 XX improved accuracy, faster detection, and overall lower cost in detection
 XX and identification of microorganisms. The presence of nuclease is
 XX measured more accurately and sensitively by red-shifting the emission
 XX wavelength from far UV region (350-400 nm) to the 500-600 nm region of
 XX the electromagnetic spectrum and reducing the effect of background signal
 XX levels of intact reagents. The present sequence is used in the
 XX course of the invention.
 XX
 SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 other;
 Query Match 1.5%; Score 17; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
 |||||
 Db 19 AAAAAAAAAAAAAAAAAA 3

RESULT 285

AA81316/c
 ID AAX81316 standard; DNA; 19 BP.
 XX
 AC AAX81316;
 XX
 DT 20-AUG-1999 (first entry)
 XX
 DE 5' amino oligonucleotide probe T-2.
 XX
 KW Microelectronic device; multi-step reaction; microscopic format;
 KW ion-permeable permeation layer; electrode; electrical control;
 KW transport; attachment; binding; DNA/RNA hybrid; probe; ss.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT misc_feature 1
 FT /*tag= a
 FT /note= "amino group attached at 5' terminal"
 FT
 PN WO9929711-A1.
 XX
 XX 17-JUN-1999.
 XX
 XX 01-DEC-1998; 98WO-US25475.
 XX
 XX 05-DEC-1997; 97US-0986065.
 XX
 XX (NANO-) NANOGEN INC.
 XX
 XX Butler WF, Edman CF, Heller MJ, Nerenberg MI, Sosnowski RG;
 XX Tu E;
 XX
 XX WPI; 1999-385567/32.
 XX
 XX New microelectronic device designed to carry out and control
 XX multi-step and multiplex molecular biological reactions in
 XX microscopic format
 XX
 XX Example 1; Page 90; 179pp; English.
 XX
 XX The specification describes a self-addressable, self-assembling
 XX microelectronic device which is designed to actively carry out and
 XX control multi-step and multiplex molecular biological reactions in
 XX microscopic formats. A key aspect of this invention is played by the
 XX ion-permeable permeation layer which overlies the electrode. This
 XX permeation layer allows attachment of nucleic acids to permit
 XX immobilization but also separates the attached oligonucleotides and
 XX hybridized target DNA sequences from the highly reactive electrochemical
 XX environment generated immediately at the electrode surface. The
 XX microelectronic device is designed and fabricated to actively carry
 XX out and control reactions such as nucleic acid hybridizations,
 XX antibody/antigen reactions, sample preparation, diagnostics and
 XX biopolymer synthesis. The device can electronically control the
 XX transport and attachment of specific binding entities, such as nucleic
 XX acids and polypeptides, to specific micro-locations. The device can
 XX subsequently control the transport and reaction of analytes or reactants
 XX at the addressed specific micro-locations. The device is able to
 XX concentrate analytes and reactants, remove non-specifically bound
 XX molecules, provide stringency control for DNA hybridization reactions
 XX and improve the detection of analytes. The present sequence
 XX represents a probe used to exemplify the invention.
 XX
 SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 other;
 Query Match 1.5%; Score 17; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
 |||||
 Db 19 AAAAAAAAAAAAAAAAAA 3

```
RESULT 286
AA88947/c
ID AAA88947 standard; DNA; 19 BP.
XX
XX AAA88947;
AC
XX
XX
DT 05-MAR-2001 (first entry)
XX
XX Oligonucleotide ISIS 22110.
XX
XX Oligonucleotide; nuclease resistance; psoriasis; antipsoriatic;
KW dermatological; cytostatic; virucide; antibacterial; fungicide;
KW therapy; diagnosis; ss.
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FH modified_base 16
FT /tag= a
FT /mod_base= OTHER
FT /note= "3'-O-(2-methoxyethyl)thymidine"
FT
FT modified_base 17
FT /tag= b
FT /mod_base= OTHER
FT /note= "3'-O-(2-methoxyethyl)thymidine"
FT
FT modified_base 18
FT /tag= c
FT /mod_base= OTHER
FT /note= "3'-O-(2-methoxyethyl)thymidine"
FT
FT modified_base 19
FT /tag= d
FT /mod_base= OTHER
FT /note= "3'-O-(2-methoxyethyl)thymidine"
XX
XX WO200066609-A1.
XX
XX 09-NOV-2000.
XX
XX 03-MAY-2000; 2000WO-US11913.
XX
XX 03-MAY-1999; 99US-0303586.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Manoharan M, Mohan V;
XX
XX WPI; 2000-672833/65.
XX
XX New oligonucleotides containing sequences with A and B geometry, used
PT to treat and diagnose e.g. psoriasis, skin cancers and viral, fungal
PT and bacterial infections, bind to single stranded RNA or DNA -
XX
XX Example 54; Page 69; 132pp; English.
XX
XX Oligonucleotide ISIS 22110 contains a phosphodiester backbone and
CC has 3'-O-(2-methoxyethyl) chemistry. It was used in experiments
CC to determine the effects of snake venom phosphodiesterase and
CC liver homogenate on the stability of oligonucleotides. Novel
CC oligonucleotides of the invention have both A- and B-form
CC conformational geometries. The A-form geometry modulates the binding
CC affinity and nuclease resistance of the oligonucleotide. The B-form
CC geometry allows the oligonucleotide to serve as substrate for
CC RNase-H when bound to a target nucleic acid strand. The
CC oligonucleotides can be used to treat psoriasis and other
CC inflammatory skin conditions, skin cancers and viral, bacterial and
CC fungal infections, and in various diagnostic applications.
XX
XX Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 other;
SQ
Query Match 1.5%; Score 17; DB 1; Length 19;
Best Local Similarity 100.0%; Pred.No. 2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1084 AAAAAAAAAAAAAAAAAA 1100
DB 19 AAAAAAAAAAAAAAAAAA 3
XX
XX
XX
XX AAA88948;
XX
XX 05-MAR-2001 (first entry)
XX
XX Oligonucleotide ISIS 22111.
XX
XX Oligonucleotide; nuclease resistance; psoriasis; antipsoriatic;
KW dermatological; cytostatic; virucide; antibacterial; fungicide;
KW therapy; diagnosis; DNA-RNA hybrid; ss.
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FH modified_base 16
FT /tag= a
FT /mod_base= OTHER
FT /note= "2'-O-(2-methoxyethyl)thymidine"
FT
FT modified_base 17
FT /tag= b
FT /mod_base= OTHER
FT /note= "2'-O-(2-methoxyethyl)thymidine"
FT
FT modified_base 18
FT /tag= c
FT /mod_base= OTHER
FT /note= "2'-O-(2-methoxyethyl)thymidine"
FT
FT modified_base 19
FT /tag= d
FT /mod_base= OTHER
FT /note= "2'-O-(2-methoxyethyl)uridine"
XX
XX misc_RNA 19
FT /tag= e
FT /label= RNA
XX
XX WO200066609-A1.
XX
XX 09-NOV-2000.
XX
XX 03-MAY-2000; 2000WO-US11913.
XX
XX 03-MAY-1999; 99US-0303586.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Manoharan M, Mohan V;
XX
XX WPI; 2000-672833/65.
XX
XX New oligonucleotides containing sequences with A and B geometry, used
PT to treat and diagnose e.g. psoriasis, skin cancers and viral, fungal
PT and bacterial infections, bind to single stranded RNA or DNA -
XX
XX Example 54; Page 69; 132pp; English.
XX
XX Oligonucleotide ISIS 22111 contains a phosphodiester backbone and
CC has 2'-O-(2-methoxyethyl) chemistry. It was used in experiments
CC to determine the effects of snake venom phosphodiesterase and
CC liver homogenate on the stability of oligonucleotides. Novel
CC oligonucleotides of the invention have both A- and B-form
CC conformational geometries. The A-form geometry modulates the binding
CC affinity and nuclease resistance of the oligonucleotide. The B-form
CC geometry allows the oligonucleotide to serve as substrate for
CC RNase-H when bound to a target nucleic acid strand. The
CC oligonucleotides can be used to treat psoriasis and other
```

CC inflammatory skin conditions, skin cancers and viral, bacterial and
 CC fungal infections, and in various diagnostic applications.

XX Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 2e+02; 0;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1100
 |||||
 DB 19 AAAAAAAAAAAAAA 3

RESULT 288

AAA88949/c

ID AAA88949 standard; DNA; 19 BP.

XX AC AAA88949;

XX DT 05-MAR-2001 (first entry)

XX DE Oligonucleotide ISIS 22112.

XX KW Oligonucleotide; nuclease resistance; psoriasis; antipsoriatic;
 KW dermatological; cytostatic; virucide; antibacterial; fungicide;
 KW therapy; diagnosis; ss.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT modified_base 16

FT /*tag= a

FT /mod_base= OTHER

FT /*note= "3'-O-(2-methoxyethyl)thymidine"

FT modified_base 17

FT /*tag= b

FT /mod_base= OTHER

FT /*note= "3'-O-(2-methoxyethyl)thymidine"

FT modified_base 18

FT /*tag= c

FT /mod_base= OTHER

FT /*note= "3'-O-(2-methoxyethyl)thymidine"

FT modified_base 19

FT /*tag= d

FT /mod_base= OTHER

FT /*note= "3'-O-(2-methoxyethyl)thymidine"

FT modified_base 1.119

FT /*tag= e

FT /*note= "phosphorothioate linkage"

XX WO200066609-A1.

XX PN

XX PD

XX PF

XX PF 03-MAY-2000; 2000WO-US11913.

XX PR 03-MAY-1999; 99US-0303586.

XX PA (ISIS-) ISIS PHARM INC.

XX PI Manoharan M, Mohan V;

XX PN WPI; 2000-672833/65.

XX XX

XX XX

XX XX

XX New oligonucleotides containing sequences with A and B geometry, used
 to treat and diagnose e.g. psoriasis, skin cancers and viral, fungal
 and bacterial infections, bind to single stranded RNA or DNA -

PS Example 54; Page 69; 132pp; English.

XX Oligonucleotide ISIS 22112 contains a phosphorothioate backbone and
 CC has 3'-O-(2-methoxyethyl) chemistry. It was used in experiments

CC to determine the effects of snake venom phosphodiesterase and
 CC liver homogenate on the stability of oligonucleotides. Novel
 CC oligonucleotides of the invention have both A- and B-form
 CC conformational geometry. The A-form geometry modulates the binding
 CC affinity and nuclease resistance of the oligonucleotide. The B-form
 CC geometry allows the oligonucleotide to serve as substrate for
 CC RNase-H when bound to a target nucleic acid strand. The
 CC oligonucleotides can be used to treat psoriasis and other
 CC inflammatory skin conditions, skin cancers and viral, bacterial and
 CC fungal infections, and in various diagnostic applications.

XX Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 19;

Best Local Similarity 100.0%; Pred. No. 2e+02; 0;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1100

|||||

DB 19 AAAAAAAAAAAAAA 3

RESULT 289

AAA88950/c

ID AAA88950 standard; DNA; 19 BP.

XX AC AAA88950;

XX DT 05-MAR-2001 (first entry)

XX DE Oligonucleotide ISIS 22113.

XX KW Oligonucleotide; nuclease resistance; psoriasis; antipsoriatic;
 KW dermatological; cytostatic; virucide; antibacterial; fungicide;
 KW therapy; diagnosis; DNA-RNA hybrid; ss.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT modified_base 16

FT /*tag= a

FT /mod_base= OTHER

FT /*note= "2'-O-(2-methoxyethyl)thymidine"

FT modified_base 17

FT /*tag= b

FT /mod_base= OTHER

FT /*note= "2'-O-(2-methoxyethyl)thymidine"

FT modified_base 18

FT /*tag= c

FT /mod_base= OTHER

FT /*note= "2'-O-(2-methoxyethyl)thymidine"

FT modified_base 19

FT /*tag= d

FT /mod_base= OTHER

FT /*note= "2'-O-(2-methoxyethyl)uridine"

FT misc_RNA 19

FT /*tag= e

FT /label= RNA

FT modified_base 1.119

FT /*tag= f

FT /*note= "phosphorothioate linkage"

XX WO200066609-A1.

XX PN

XX XX

XX PD

XX XX

XX PF 03-MAY-2000; 2000WO-US11913.

XX XX

XX PR 03-MAY-1999; 99US-0303586.

XX XX

XX PA (ISIS-) ISIS PHARM INC.

XX XX

XX PI Manoharan M, Mohan V;

```
XX WPI; 2000-672833/65.
XX
XX New oligonucleotides containing sequences with A and B geometry, used
XX to treat and diagnose e.g. psoriasis, skin cancers and viral, fungal
XX and bacterial infections, bind to single stranded RNA or DNA -
XX
XX Example 54; Page 69; 132pp; English.
XX
XX Oligonucleotide ISIS 22113 contains a phosphorothioate backbone and
XX has 2'-O-(2-methoxyethyl) chemistry. It was used in experiments
XX to determine the effects of snake venom phosphodiesterase and
XX liver homogenate on the stability of oligonucleotides. Novel
XX oligonucleotides of the invention have both A- and B-form
XX conformational geometry. The A-form geometry modulates the binding
XX affinity and nuclease resistance of the oligonucleotide. The B-form
XX geometry allows the oligonucleotide to serve as substrate for
XX RNase-H when bound to a target nucleic acid strand. The
XX oligonucleotides can be used to treat psoriasis and other
XX inflammatory skin conditions, skin cancers and viral, bacterial and
XX fungal infections, and in various diagnostic applications.
XX
XX Sequence 19 BP; 0 A; 0 C; 0 G; 0 T; 0 other;
XX
XX Query Match 1.5%; Score 17; DB 1; Length 19;
XX Best Local Similarity 100.0%; Pred. No. 2e+02;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1084 AAAAAAAAAAAAAAAAAA 1100
XX | | | | | | | | | | | | | | | |
XX Db 19 AAAAAAAAAAAAAAAAAA 3
XX
XX RESULT 290
XX AAA88951/c
XX ID AAA88951 standard; DNA; 19 BP.
XX AC AAA88951;
XX
XX DT 05-MAR-2001 (first entry)
XX
XX DE Oligonucleotide ISIS 22114.
XX
XX KW Oligonucleotide; nuclease resistance; psoriasis; antipsoriatic;
XX dermatological; cytostatic; virucide; antibacterial; fungicide;
XX therapy; diagnosis; ss.
XX
XX OS Synthetic.
XX
XX FH Key Location/Qualifiers
XX modified_base 16
XX /tag= a
XX /mod_base= OTHER
XX /note= "3'-O-(2-methoxyethyl)thymidine"
XX modified_base 17
XX /tag= b
XX /mod_base= OTHER
XX /note= "3'-O-(2-methoxyethyl)thymidine"
XX modified_base 18
XX /tag= c
XX /mod_base= OTHER
XX /note= "3'-O-(2-methoxyethyl)thymidine"
XX modified_base 19
XX /tag= d
XX /mod_base= OTHER
XX /note= "3'-O-(2-methoxyethyl)thymidine"
XX modified_base 1.15
XX /tag= e
XX /note= "phosphorothioate linkage"
XX
XX PN WO200066609-A1.
XX
XX PD 09-NOV-2000.
```

```
XX 03-MAY-2000; 2000WO-US11913.
XX
XX 03-MAY-1999; 99US-0303586.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Manoharan M, Mohan V;
XX
XX WPI; 2000-672833/65.
XX
XX New oligonucleotides containing sequences with A and B geometry, used
XX to treat and diagnose e.g. psoriasis, skin cancers and viral, fungal
XX and bacterial infections, bind to single stranded RNA or DNA -
XX
XX Example 54; Page 69; 132pp; English.
XX
XX Oligonucleotide ISIS 22114 contains a mixed phosphodiester and
XX phosphorothioate backbone and has 3'-O-(2-methoxyethyl) chemistry.
XX It was used in experiments to determine the effects of snake venom
XX phosphodiesterase and liver homogenate on the stability of
XX oligonucleotides. Novel oligonucleotides of the invention have
XX both A- and B-form conformational geometry. The A-form geometry
XX modulates the binding affinity and nuclease resistance of the
XX oligonucleotide. The B-form geometry allows the oligonucleotide to
XX serve as substrate for RNase-H when bound to a target nucleic acid
XX strand. The oligonucleotides can be used to treat psoriasis and other
XX inflammatory skin conditions, skin cancers and viral, bacterial and
XX fungal infections, and in various diagnostic applications.
XX
XX Sequence 19 BP; 0 A; 0 C; 0 G; 0 T; 0 other;
XX
XX Query Match 1.5%; Score 17; DB 1; Length 19;
XX Best Local Similarity 100.0%; Pred. No. 2e+02;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1084 AAAAAAAAAAAAAAAAAA 1100
XX | | | | | | | | | | | | | | | |
XX Db 19 AAAAAAAAAAAAAAAAAA 3
XX
XX RESULT 291
XX AAA88952/c
XX ID AAA88952 standard; DNA; 19 BP.
XX AC AAA88952;
XX
XX DT 05-MAR-2001 (first entry)
XX
XX DE Oligonucleotide ISIS 22115.
XX
XX KW Oligonucleotide; nuclease resistance; psoriasis; antipsoriatic;
XX dermatological; cytostatic; virucide; antibacterial; fungicide;
XX therapy; diagnosis; DNA-RNA hybrid; ss.
XX
XX OS Synthetic.
XX
XX FH Key Location/Qualifiers
XX modified_base 16
XX /tag= a
XX /mod_base= OTHER
XX /note= "2'-O-(2-methoxyethyl)thymidine"
XX modified_base 17
XX /tag= b
XX /mod_base= OTHER
XX /note= "2'-O-(2-methoxyethyl)thymidine"
XX modified_base 18
XX /tag= c
XX /mod_base= OTHER
XX /note= "2'-O-(2-methoxyethyl)thymidine"
XX modified_base 19
XX /tag= d
XX /mod_base= OTHER
```

```

FT      /note= "2'-O-(2-methoxyethyl)uridine"
FT      19
FT      /tag= e
FT      /label= RNA
FT      modified_base
FT      1..15
FT      /tag= f
FT      /note= "phosphorothioate linkage"
FT      XX
FT      DN
FT      WO200066509-A1.
FT      XX
FT      09-NOV-2000.
FT      XX
FT      03-MAY-2000; 2000WO-US11913.
FT      XX
FT      03-MAY-1999; 99US-0303586.
FT      XX
FT      (ISIS-) ISIS PHARM INC.
FT      PA
FT      Manoharan M, Mohan V;
FT      XX
FT      WPI; 2000-672833/65.
FT      DR
FT      XX
FT      New oligonucleotides containing sequences with A and B geometry, used
FT      to treat and diagnose e.g. psoriasis, skin cancers and viral, fungal
FT      and bacterial infections, bind to single stranded RNA or DNA -
FT      XX
FT      Example 54; Page 69; 132pp; English.
FT      XX
FT      CC
FT      Oligonucleotide ISIS 22115 contains a mixed phosphodiester and
FT      phosphorothioate backbone and has 2'-O-(2-methoxyethyl) chemistry.
FT      It was used in experiments to determine the effects of snake venom
FT      phosphodiesterase and liver homogenate on the stability of
FT      oligonucleotides. Novel oligonucleotides of the invention have
FT      both A- and B-form conformational geometry. The A-form geometry
FT      modulates the binding affinity and nuclease resistance of the
FT      oligonucleotide. The B-form geometry allows the oligonucleotide to
FT      serve as substrate for RNase-H when bound to a target nucleic acid
FT      strand. The oligonucleotides can be used to treat psoriasis and other
FT      inflammatory skin conditions, skin cancers and viral, bacterial and
FT      fungal infections, and in various diagnostic applications.
FT      XX
FT      XX
FT      Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 other;
FT      XX
FT      Query Match      1.5%; Score 17; DB 1; Length 19;
FT      Best Local Similarity 100.0%; Pred. No. 2e+02;
FT      Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
FT      QY      1084 AAAAAAAAAAAAAA 1100
FT      Db      19 AAAAAAAAAAAAAA 3
FT      RESULT 292
FT      AAA88965/c
FT      ID      AAA88965 standard; DNA; 19 BP.
FT      XX
FT      AC      AAA88965;
FT      XX
FT      DT      05-MAR-2001 (first entry)
FT      XX
FT      2'-Modified chimeric oligonucleotide.
FT      DE
FT      XX
FT      Oligonucleotide; nuclease resistance; psoriasis; antipsoriatic;
FT      dermatological; cytostatic; virucide; antibacterial; fungicide;
FT      therapy; diagnosis; ss.
FT      XX
FT      OS      Synthetic.
FT      XX
FT      Key      Location/Qualifiers
FT      modified_base 16
FT      /tag= a
FT      /mod_base= OTHER
FT      /note= "2'-modified thymidine, i.e. -S-Me, -Me,

```

```

FT      2'-ara-(F), 2'-ara-(OH), -2'-ara-(OMe)"
FT      17
FT      /tag= b
FT      /mod_base= OTHER
FT      /note= "2'-modified thymidine, i.e. -S-Me, -Me,
FT      2'-ara-(F), 2'-ara-(OH), -2'-ara-(OMe)"
FT      18
FT      /tag= c
FT      /mod_base= OTHER
FT      /note= "2'-modified thymidine, i.e. -S-Me, -Me,
FT      2'-ara-(F), 2'-ara-(OH), -2'-ara-(OMe)"
FT      19
FT      /tag= d
FT      /mod_base= OTHER
FT      /note= "2'-modified thymidine, i.e. -S-Me, -Me,
FT      2'-ara-(F), 2'-ara-(OH), -2'-ara-(OMe)"
FT      XX
FT      WO200066509-A1.
FT      PN
FT      09-NOV-2000.
FT      XX
FT      03-MAY-2000; 2000WO-US11913.
FT      XX
FT      03-MAY-1999; 99US-0303586.
FT      PR
FT      (ISIS-) ISIS PHARM INC.
FT      XX
FT      Manoharan M, Mohan V;
FT      PI
FT      WPI; 2000-672833/65.
FT      DR
FT      XX
FT      New oligonucleotides containing sequences with A and B geometry, used
FT      to treat and diagnose e.g. psoriasis, skin cancers and viral, fungal
FT      and bacterial infections, bind to single stranded RNA or DNA -
FT      XX
FT      Example 86; Page 102; 132pp; English.
FT      XX
FT      This sequence represents 2'-modified chimeric oligonucleotides
FT      containing 2'-modified T. The nucleotides were used to examine
FT      the effects of the modifications on nuclease resistance. Novel
FT      oligonucleotides of the invention have both A- and B-form
FT      conformational geometry. The A-form geometry modulates the binding
FT      affinity and nuclease resistance of the oligonucleotide. The B-form
FT      geometry allows the oligonucleotide to serve as substrate for
FT      RNase-H when bound to a target nucleic acid strand. The
FT      oligonucleotides can be used to treat psoriasis and other
FT      inflammatory skin conditions, skin cancers and viral, bacterial and
FT      fungal infections, and in various diagnostic applications.
FT      CC
FT      XX
FT      Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 other;
FT      XX
FT      Query Match      1.5%; Score 17; DB 1; Length 19;
FT      Best Local Similarity 100.0%; Pred. No. 2e+02;
FT      Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
FT      QY      1084 AAAAAAAAAAAAAA 1100
FT      Db      19 AAAAAAAAAAAAAA 3
FT      RESULT 293
FT      AAC62422/c
FT      ID      AAC62422 standard; DNA; 19 BP.
FT      XX
FT      AC      AAC62422;
FT      XX
FT      DT      07-FEB-2001 (first entry)
FT      XX
FT      DE      T19 diester for use in nuclease stability assay.
FT      XX
FT      KW      T19 diester; nuclease stability assay; polymerase chain reaction;
FT      PCR; molecular cloning; disease diagnosis; disease treatment; ss.
FT      XX

```

OS Synthetic.
 PN US6127124-A.
 XX
 PD 03-OCT-2000.
 XX
 PF 20-JAN-1999; 99US-0234237.
 XX
 PR 20-JAN-1999; 99US-0234237.
 XX
 PA (ISIS-) ISIS PHARM INC.
 PI Leeds JM, Cummins LJ;
 XX WPI; 2000-637737/61.
 DR
 XX
 PT Determining the nuclease stability and relative binding affinity of an
 PT oligomeric compound comprises capillary gel electrophoresis using
 PT laser-induced fluorescence -
 XX
 PS Example 3; column 19-20; 14pp; English.
 XX
 CC The present invention is concerned with methods of determining the
 CC nuclease stability of oligomeric compounds using capillary-gel
 CC electrophoresis and laser-induced fluorescence. The methods are useful in
 CC the polymerase chain reaction (PCR), molecular cloning and disease
 CC diagnosis and treatment. The present sequence was used in a demonstration
 CC of the methods of the invention.
 XX
 SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 other;
 XX
 Query Match 1.5%; Score 17; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 QY 1084 AAAAAAAAAAAAAAAAAA 1100
 DB 19 AAAAAAAAAAAAAAAAAA 3
 XX
 RESULT 294
 AAC62454/c
 ID AAC62454 standard; DNA; 19 BP.
 XX
 AC AAC62454;
 XX
 DT 07-FEB-2001 (first entry)
 XX
 DE Cleavage of nucleic acids from solid supports assay oligonucleotide #3.
 XX
 KW Nucleic acid cleavage; solid support; DNA-RNA hybrid;
 KW affinity chromatography; sequencing; mutagenesis; DNA preparation;
 KW nucleic acid purification; ss.
 XX
 OS Synthetic.
 FH Key Location/Qualifiers
 FT misc_RNA 10
 FT /tag= a
 XX
 PN WO200058329-A1.
 XX
 PD 05-OCT-2000.
 XX
 PF 28-MAR-2000; 2000WO-GH01190.
 XX
 PR 29-MAR-1999; 99GB-0007245.
 XX
 PA (GOLD/) GOLDSBOROUGH A.
 XX
 DR WPI; 2000-664908/64.
 XX
 PT Detaching nucleic acid molecule comprising unconventional nucleotide

PT incorporated at predetermined site from a solid support involves
 PT cleaving the nucleic acid molecule at the site of unconventional
 XX nucleotide -
 PS Example 3; Page 34; 47pp; English.
 XX
 CC The present invention is concerned with the cleavage of nucleic acids
 CC from solid supports. This is carried out by adding a non-conventional
 CC nucleotide into the nucleic acid attached to the support, so that it is
 CC recognised and cleaved by a specific DNA glycosylase and the sequence is
 CC released. This is useful in many molecular biological procedures such as
 CC sequencing, in vitro amplifications, cDNA and template preparation,
 CC DNA-based assays, mutagenesis procedures, nucleic acid purification and
 CC affinity chromatography. The present sequence is an oligonucleotide used
 CC in assays to demonstrate the methods of the invention.
 XX
 SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 1 U; 0 other;
 XX
 Query Match 1.5%; Score 17; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 QY 1084 AAAAAAAAAAAAAAAAAA 1100
 DB 19 AAAAAAAAAAAAAAAAAA 3
 XX
 RESULT 295
 AAA71630/c
 ID AAA71630 standard; DNA; 19 BP.
 XX
 AC AAA71630;
 XX
 DT 14-DEC-2000 (first entry)
 XX
 DE Phosphorothioate 20-mer primer DNA #1.
 XX
 KW Phosphorothioate; primer; oligomer synthesis; antisense therapy; ss.
 XX
 OS Synthetic.
 FH Key Location/Qualifiers
 FT modified_base 1..20
 FT /tag= a
 FT /mod_base= OTHER
 FT /note= "phosphorothioate linkage"
 XX
 PN EP1028124-A2.
 XX
 PD 16-AUG-2000.
 XX
 PF 06-SEP-1999; 99EP-0307066.
 XX
 PR 04-FEB-1999; 99US-0118564.
 PR 09-APR-1999; 99US-0288679.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Ravikumar VT, Manoharan M, Capaldi DC, Krotz A, Cole DL, Guzaev A;
 XX WPI; 2000-500332/45.
 DR
 XX
 PT Novel method for the production of oligomers with reduced exocyclic
 PT adducts comprises treatment with deprotecting and cleaving reagents -
 XX
 PS Example 2; Page 17; 33pp; English.
 XX
 CC This invention describes a novel synthetic method (M) comprising: (a)
 CC providing a sample comprising a number of oligomers of formula (1); (b)
 CC contacting the sample with a deprotecting agent to remove R t groups from
 CC the oligomers; and (c) reacting the oligomer with a cleaving reagent.
 CC The method is used to produce oligomeric compounds for use in antisense
 CC and oligonucleotide therapies. The method enables the synthesis of

CC oligomers with a reduction in the number acrylonitrile groups attached.
 CC Acrylonitrile has been demonstrated to be a potent carcinogen in rats.
 CC This sequence represents a phosphorothioate 20-mer primer which is used
 CC in the method of the invention.

XX SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAA 1100
 |||||
 Db 19 AAAAAAAAAAAAAAAA 3

RESULT 296
 AAA06839/C
 ID AAA06839 standard; DNA; 19 BP.

XX AC AAA06839;

XX DT 19-JUN-2000 (first entry)

XX DE Modified T-containing oligonucleotide, SEQ ID NO:14.

XX KW Modified nucleoside; aminoxy group;

XX KW 2'-deoxy-erythro-pentofuranosyl sugar moiety; nuclease resistant;

XX KW hybridisation; binding affinity; ss.

XX OS Synthetic.

XX FH Key Location/Qualifiers
 XX FT modified_base 16..19
 XX FT /*tag= a
 XX FT /note= "These nucleotides are substituted with 2'-O-(2-[N-(2-amino)ethyl-N-(methyl)aminoxyethyl] group"

XX PN WO200008042-A1.

XX PD 17-FEB-2000.

XX PF 09-AUG-1999; 99WO-US17988.

XX PR 07-AUG-1998; 98US-0130973.

XX PA (ISIS-) ISIS PHARM INC.

XX PI Manoharan M, Cook PD, Prakash TP, Kawasaki AM;

XX DR WPI; 2000-224020/19.

XX PT Aminoxy-modified nucleosides and oligonucleotides useful in
 XX PT diagnostic, therapeutic and research reagents and for modulating the
 XX PT expression of protein in organisms -

XX PS Example 99; Page 120; 195pp; English.

XX CC The invention relates to aminoxy-modified nucleosides and
 XX CC oligonucleotides and to oligonucleotides that elicit RNase H for cleavage
 XX CC in a complementary nucleic acid strand. It also relates to
 XX CC oligonucleotides wherein at least some of the nucleotides are
 XX CC functionalised to be nuclease resistant, at least some of the nucleotides
 XX CC include a substituent that potentiates hybridisation of the
 XX CC oligonucleotide to a complementary strand, and at least some of the
 XX CC nucleotides include a 2'-deoxy-erythro-pentofuranosyl sugar moiety. The
 XX CC inclusion of one or more aminoxy moieties in such oligonucleotides
 XX CC provides for improved binding of such oligonucleotides to a complementary
 XX CC strand. The oligonucleotides of the invention are used as diagnostic,
 XX CC therapeutic or research reagents, and can be used to modulate gene
 XX CC expression in organisms. The oligonucleotides containing the modified
 XX CC nucleosides have increased nuclease resistance and increased binding

CC affinity to a complementary strand. The present sequence represents
 CC an oligonucleotide containing nucleotides substituted with a 2'-O-(2-[N-(2-amino)ethyl-N-(methyl)aminoxyethyl] group.

XX SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAA 1100
 |||||
 Db 19 AAAAAAAAAAAAAAAA 3

RESULT 297
 AAZ61390/C
 ID AAZ61390 standard; DNA; 19 BP.

XX AC AAZ61390;

XX DT 19-JUN-2000 (first entry)

XX DE Uniform phosphodiester oligonucleotide.

XX KW Oligomeric compound; 2'-O-modified ribosyl nucleoside;

XX KW 3' endo geometry; nuclease resistance; phosphodiester; ss.

XX OS Synthetic.

XX FH Key Location/Qualifiers
 XX FT modified_base 16
 XX FT /*tag= a
 XX FT /note= "2'-modified T"
 XX FT modified_base 17
 XX FT /*tag= b
 XX FT /note= "2'-modified T"
 XX FT modified_base 18
 XX FT /*tag= c
 XX FT /note= "2'-modified T"
 XX FT modified_base 19
 XX FT /*tag= d
 XX FT /note= "2'-modified T"

XX PN WO200008044-A1.

XX PD 17-FEB-2000.

XX PF 06-AUG-1999; 99WO-US17895.

XX PR 07-AUG-1998; 98US-0130566.

XX PA (ISIS-) ISIS PHARM INC.

XX PI Manoharan M, Cook PD;

XX DR WPI; 2000-2056668/18.

XX PT Novel 2'-O-aminoethylloxethyl modified nucleosides and oligonucleotides
 XX PT used in diagnostic, therapeutic and research reagents -

XX PS Disclosure; Page 44; 60pp; English.

XX CC The present sequence represents an uniform phosphodiester
 XX CC oligonucleotide. The specification describes oligomeric compounds
 XX CC containing 2'-O-modified ribosyl nucleosides. The 2'-O-modified
 XX CC nucleosides include ring structures that position the sugar moiety of
 XX CC the nucleosides preferentially in 3' endo geometries. The modified
 XX CC oligomeric compounds have increased binding affinity and increased
 XX CC nuclease resistance. The oligomeric compounds can be used in diagnostic,
 XX CC therapeutic and research reagents.

XX SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1100
| | | | | | | | | | | | | | | | | | | | |
DB 19 AAAAAAAAAAAAAA 3

RESULT 298
AAZ61404/C
ID AAZ61404 standard; DNA; 19 BP.

XX AC AAZ61404;
XX XX
DT 19-JUN-2000 (first entry)
XX XX
DE 2'-O-modified ribosyl oligonucleotide with phosphodiester linkages.
XX XX
KW Oligomeric compound; 2'-O-modified ribosyl nucleoside;
XX 3' endo geometry; nuclease resistance; phosphorothioate; ss.
XX OS Synthetic.
XX XX

Key Location/Qualifiers
FT misc_feature 1..19 /*tag= a
FT /*note= "nucleosides linked by phosphodiester linkages"
FT modified_base 16..19 /*tag= b
FT /*note= "2'-O-[2-N-dimethylaminoethyl]oxyethyl-5-methyl uridine"

WO200008044-A1.
17-FEB-2000.

XX PF 06-AUG-1999; 99WO-US17895.
XX XX
XX PF 07-AUG-1998; 98US-0130566.
XX XX
XX PA (ISIS-) ISIS PHARM INC.
XX PI Manoharan M, Cook PD;
XX DR WPI; 2000-205668/18.
XX XX

Novel 2'-O-aminoethyloxyethyl modified nucleosides and oligonucleotides used in diagnostic, therapeutic and research reagents -
Disclosure; Page 51; 60pp; English.

CC The present sequence represents an oligomeric compound containing 2'-O-modified ribosyl nucleosides. The oligomeric compound contains phosphodiester linkages. The 2'-O-modified nucleosides include ring structures that position the sugar moiety of the nucleosides preferentially in 3' endo geometries. The modified oligomeric compounds have increased binding affinity and increased nuclease resistance. The oligomeric compounds can be used in diagnostic, therapeutic and research reagents.

XX SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1100
| | | | | | | | | | | | | | | | | | | | |
DB 19 AAAAAAAAAAAAAA 3

RESULT 299
AAZ95240/C
ID AAZ95240 standard; DNA; 19 BP.

XX AC AAZ95240;
XX XX
DT 05-JUN-2000 (first entry)
XX XX
DE Modified oligonucleotide #3 ISIS # 22110.
XX XX
KW Antisense oligonucleotide; phosphorothioate; gene therapy; ISIS # 22110;
XX research reagent; therapeutic; ss.
XX OS Synthetic.
XX XX

Key Location/Qualifiers
FT misc_feature 1..15 /*tag= a
FT /*note= "Phosphorothioate internucleotide linkage"
FT misc_feature 15..19 /*tag= d
FT /*note= "Optionally all phosphorothioate internucleotide linkages"
FT modified_base 16..19 /*tag= c
FT /*mod_base= OTHER
FT /*note= "Optionally all 3'-O-(2-methoxyhexyl) or all 2'-O-(2-methoxyethyl)"

WO200004189-A1.
27-JAN-2000.

XX PF 13-JUL-1999; 99WO-US15886.
XX XX
XX PR 14-JUL-1998; 98US-0115043.
XX XX
XX PA (ISIS-) ISIS PHARM INC.
XX PI Manoharan M, Cook PD;
XX DR WPI; 2000-182445/16.
XX XX

Novel modified oligonucleotides, useful in antisense methodologies, diagnostics, therapeutics and as research reagents -
Example 54; Page 59; 75pp; English.

CC This sequence represents a modified oligonucleotide used in the course of the invention. The invention relates to oligonucleotides comprising CC nucleotides covalently linked together by internucleotide linkages where CC at least 1 nucleotide is linked to adjacent nucleotide by a CC 2',5'-internucleotide linkage and bears a 3'-substituent. The CC oligonucleotides can be used in gene therapy and are also useful in CC antisense methodologies, diagnostics, therapeutics and as research CC reagents.

XX SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1100
| | | | | | | | | | | | | | | | | | | | |
DB 19 AAAAAAAAAAAAAA 3

RESULT 300
AAZ95241/C
ID AAZ95241 standard; DNA; 19 BP.

XX XX


```
AC AAZ95241;
XX
DT 05-JUN-2000 (first entry)
XX
DE Modified oligonucleotide #3 ISIS # 22111.
XX
KW Antisense oligonucleotide; phosphorothioate; gene therapy; ISIS # 22111;
XX research reagent; therapeutic; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_feature 1..15
FT /tag= a
FT /note= "Phosphorothioate internucleotide linkage"
FT misc_feature 15..19
FT /tag= d
FT /note= "Optionally all phosphorothioate internucleotide
FT linkages"
FT modified_base 16..19
FT /tag= c
FT /mod_base= OTHER
FT /note= "Optionally all 3'-O-(2-methoxyhexyl) or all
FT 2'-O-(2-methoxyethyl)"
FT misc_RNA 19
FT /tag= d
XX
XX WO200004189-A1.
XX
XX 27-JAN-2000.
XX
XX 13-JUL-1999; 99WO-US15886.
XX
XX 14-JUL-1998; 98US-0115043.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Manoharan M, Cook PD;
XX
XX WPI; 2000-182445/16.
XX
XX Novel modified oligonucleotides, useful in antisense methodologies,
XX diagnostics, therapeutics and as research reagents -
XX
XX Example 54; Page 59; 75pp; English.
XX
XX This sequence represents a modified oligonucleotide used in the course of
XX the invention. The invention relates to oligonucleotides comprising
XX nucleotides covalently linked together by internucleotide linkages where
XX at least 1 nucleotide is linked to adjacent nucleotide by a
XX 2',5'-internucleotide linkage and bears a 3'-substituent. The
XX oligonucleotides can be used in gene therapy and are also useful in
XX antisense methodologies, diagnostics, therapeutics and as research
XX reagents.
XX
XX Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 1 U; 0 other;
XX
XX Query Match 1..5%; Score 17; DB 1; Length 19;
XX Best Local Similarity 100.0%; Pred. No. 2e+02;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1084 AAAAAAAAAAAAAAAAAA 1100
XX |||||
XX DB 19 AAAAAAAAAAAAAAAAAA 3
XX
XX RESULT 301
XX AAH46460/c
XX ID AAH46460 standard; DNA; 19 BP.
XX
XX AC AAH46460;
XX
XX 14-SEP-2001 (first entry)
XX
```

```
XX Oligonucleotide #8.
XX
XX Phosphorothioate; anti-viral therapy; stereochemical pathway; ss.
XX
XX Synthetic.
XX
XX FH Key Location/Qualifiers
XX modified_base 1..19
XX /tag= a
XX /mod_base= "OTHER"
XX /note= "All bases are phosphorothioate"
XX modified_base 1
XX /tag= b
XX /mod_base= "OTHER"
XX /note= "Modified with 2'-O-methoxyethyl"
XX
XX US6242591-B1.
XX
XX 05-JUN-2001.
XX
XX 11-JAN-2000; 2000US-0481486.
XX
XX 15-OCT-1997; 97US-0950779.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Cole DL, Ravikumar VT, Cheruvallath ZS;
XX
XX WPI; 2001-407218/43.
XX
XX Preparing sulfurized 2' substituted phosphorothioate oligonucleotides
XX useful in biological research, comprises phosphorylating the
XX 5'-hydroxyl of a nucleic acid having a nucleoside with a 2'
XX modification -
XX
XX Example 12; Column 7; 7pp; English.
XX
XX The present invention relates to a method for preparing phosphorothioate
XX oligonucleotides having at least one nucleoside with a 2' modification.
XX The method comprises phosphorylating the 5'-hydroxyl of a nucleic acid
XX group having at least one nucleoside with a 2' modification in an
XX acetonitrile. The present sequence was used to illustrate the method of
XX the present invention. The method is useful for synthesizing sulphurised
XX 2' substituted phosphorothioate oligonucleotides, which may be used in
XX molecular biological research, in applications such as anti-viral
XX therapy, and for determining the stereochemical pathways of certain
XX enzymes which recognise nucleic acids.
XX
XX Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 other;
XX
XX Query Match 1..5%; Score 17; DB 1; Length 19;
XX Best Local Similarity 100.0%; Pred. No. 2e+02;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1084 AAAAAAAAAAAAAAAAAA 1100
XX |||||
XX DB 19 AAAAAAAAAAAAAAAAAA 3
XX
XX RESULT 302
XX AAH25737/c
XX ID AAH25737 standard; DNA; 19 BP.
XX
XX AC AAH25737;
XX
XX 14-AUG-2001 (first entry)
XX
XX Human type II RNase H substrate oligonucleotide #4.
XX
XX Human; RNase H type II; RNase H1 cleavage substrate; antisense therapy;
XX gene therapy; primer; phosphorothioate backbone; ss.
XX
```



```
XX PT Guanidinium functionalized oligomers prepared from corresponding
PT monomer units, are hybridizable with a specific RNA or DNA sequence,
PT useful for diagnostic and therapeutic purposes -
XX PS Example 26; Page 54; 108pp; English.
XX CC The present invention relates to nucleotide oligomers comprising
CC monomer units. Oligomers modulate gene expression when hybridized by a
CC single- or double-stranded nucleic acid. They are useful for
CC gene therapy, diagnostic and investigative purposes.
XX SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 other;
    Query Match 1.5%; Score 17; DB 1; Length 19;
    Best Local Similarity 100.0%; Pred. No. 2e+02;
    Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1084 AAAAAAAAAAAAAAAAAA 1100
Db 19 AAAAAAAAAAAAAAAAAA 3

RESULT 305
AAF31564/c
ID AAF31564 standard; DNA; 19 BP.
XX AC AAF31564;
XX DT 09-APR-2001 (first entry)
XX KW DNA/RNA hybrid; oligomer; C3' methylene hydrogen phosphate;
XX KW AIDS; atherosclerosis; ss.
XX OS Synthetic.
XX PN DNA/RNA hybrid; oligomer; C3' methylene hydrogen phosphate;
XX PN AIDS; atherosclerosis; ss.
XX PN Synthetic.
XX PN WO200102419-A1.
XX PN 11-JAN-2001.
XX PF 05-JUL-2000; 2000WO-US40304.
XX PR 07-JUL-1999; 99US-0349033.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Cook PD, Manoharan M, Maier M, An H;
XX DR WPI; 2001-138117/14.
XX CC New oligomers for use as research reagent, for treating disease caused
XX CC by undesired production of proteins, and for diagnosing and treating
XX CC AIDS, atherosclerosis -
XX PS Example 46; Page 74; 110pp; English.
XX CC The present invention relates to C3' methylene hydrogen phosphate
XX CC oligomers. The oligomers may be used as research reagents, for
XX CC treating disease caused by undesired production of proteins
XX CC and for diagnosing and treating AIDS and atherosclerosis.
XX SQ Sequence 19 BP; 0 A; 0 C; 0 G; 15 T; 4 U; 0 other;
    Query Match 1.5%; Score 17; DB 1; Length 19;
    Best Local Similarity 100.0%; Pred. No. 2e+02;
    Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1084 AAAAAAAAAAAAAAAAAA 1100
Db 19 AAAAAAAAAAAAAAAAAA 3

XX PT Guanidinium functionalized oligomers prepared from corresponding
PT monomer units, are hybridizable with a specific RNA or DNA sequence,
PT useful for diagnostic and therapeutic purposes -
XX PS Example 26; Page 54; 108pp; English.
XX CC The present invention relates to nucleotide oligomers comprising
CC monomer units. Oligomers modulate gene expression when hybridized by a
CC single- or double-stranded nucleic acid. They are useful for
CC gene therapy, diagnostic and investigative purposes.
XX SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 other;
    Query Match 1.5%; Score 17; DB 1; Length 19;
    Best Local Similarity 100.0%; Pred. No. 2e+02;
    Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1084 AAAAAAAAAAAAAAAAAA 1100
Db 19 AAAAAAAAAAAAAAAAAA 3

RESULT 306
AAC83664/c
ID AAC83664 standard; DNA; 19 BP.
XX AC AAC83664;
XX DT 02-MAR-2001 (first entry)
XX DE 2'-O-N-[2-(dimethylamino)ethylacetamido]-modified oligo ISIS #32335.
XX KW 2'-O-acetamido; diagnostic; kinase modulator; nuclease resistance;
XX KW tumour formation; cancer; protein kinase C expression;
XX KW cell adhesion molecule expression; multidrug resistance; ss.
XX OS Synthetic.
XX FH Key Location/Qualifiers
FT modified_base 16..19
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-O-N-[2-(dimethylamino)ethylacetamido]5Meu"
XX PN US6147200-A.
XX PD 14-NOV-2000.
XX PF 19-AUG-1999; 99US-0378568.
XX PR 19-AUG-1999; 99US-0378568.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Manoharan M, Cook PD, Fraser AS, Prakash TP, Kawasaki AM;
XX DR WPI; 2001-069824/08.
XX CC New 2'-O-acetamido modified nucleosides (I) used to produce
XX CC oligonucleotides which have enhanced nuclease resistance and superior
XX CC hybridization properties than prior art.
XX PS Example 12; Column 28; 29pp; English.
XX CC The present sequence is a modified oligonucleotide.
XX CC 2'-O-acetamido-modified nucleosides were used to produce oligonucleotides
XX CC which have enhanced nuclease resistance and superior hybridisation
XX CC properties than prior art. The oligomeric compounds are useful for
XX CC identification or quantification of ribonucleic acid and deoxyribonucleic
XX CC acid or for modulating the activity of an ribonucleic acid or
XX CC deoxyribonucleic acid molecule. They have a modified nucleoside monomer
XX CC and are specifically hybridisable with a preselected nucleotide sequence
XX CC of a single-stranded or double-stranded target deoxyribonucleic acid or
XX CC ribonucleic acid molecule. The oligomers are further useful in a
XX CC ras-luciferase fusion system using ras-luciferase transactivation. They
XX CC are useful in abnormal cell proliferation and tumour formation and
XX CC modulation of expression of protein kinase C and cell adhesion
XX CC molecules such as ICAM. They are useful in the modulation of proteins
XX CC related to multidrug resistance and viral genomic nucleic acids such as
XX CC HIV, herpes viruses, Epstein-Barr virus, cytomegalovirus, papillomavirus,
XX CC hepatitis C virus and influenza virus.
XX SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 other;
    Query Match 1.5%; Score 17; DB 1; Length 19;
    Best Local Similarity 100.0%; Pred. No. 2e+02;
    Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1084 AAAAAAAAAAAAAAAAAA 1100
Db 19 AAAAAAAAAAAAAAAAAA 3

RESULT 307
```

```

AAD41998/c
ID AAD41998 standard; DNA; 19 BP.
XX
AC AAD41998;
XX
DT 04-NOV-2002 (first entry)
DE
DE Oligonucleotide #1 used to illustrate the method of the invention.
XX
XX Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity;
KW nuclear resistance; alkylation; therapeutic; diagnostic; ss.
XX
OS Unidentified.
XX
XX Key Location/Qualifiers
FH modified_base 15..18
FT /tag= a
FT /mod_base= OTHER
FT /note= "5-methyl, 2'-aminoxyethoxy (2'-AOE) residues"
XX
XX US6403779-B1.
XX
XX 11-JUN-2002.
XX
XX 08-JAN-1999; 99US-0227782.
XX
XX 08-JAN-1999; 99US-0227782.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Kawasaki AM, Fraser AS, Manoharan M, Cook PD, Prakash TP;
XX WPI; 2002-546338/58.
XX
XX Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside
XX used for preparation of 2'-O-alkylated compounds comprises dissolving
XX nucleoside in aprotic solvent, cooling, treating with base, warming,
XX cooling and reacting with ester -
XX
XX Example 46; Column 31; 24pp; English.
XX
XX The present invention relates to a novel method of selective alkylation
XX of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside.
XX The method involves dissolving the nucleoside in at least one aprotic
XX solvent, cooling, treating with base, warming, cooling and reacting with
XX a reactive ester. The method is useful for the preparation of 2'-O-alkyl
XX nucleotides, nucleosides and nucleoside surrogates used for preparation
XX of oligomeric compounds having improved hybridisation affinity and
XX nuclear resistance, which are useful as therapeutics, diagnostics and
XX research reagents. The present sequence is a modified oligonucleotide
XX used to illustrate the method of the invention.
XX
XX Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 other;
SQ
Query Match 1.5%; Score 17; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
Db 19 AAAAAAAAAAAAAAAAAA 3

RESULT 308
AAD41999/c
ID AAD41999 standard; DNA; 19 BP.
XX
XX AAD41999;
XX
DT 04-NOV-2002 (first entry)
DE
DE Oligonucleotide #2 used to illustrate the method of the invention.
XX
XX Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity;
KW nuclear resistance; alkylation; therapeutic; diagnostic; ss.
XX
OS Unidentified.
XX
XX Key Location/Qualifiers
FH modified_base 15..18
FT /tag= a
FT /mod_base= OTHER
FT /note= "5-methyl, 2'-aminoxyethoxy (2'-AOE) residues"
XX
XX US6403779-B1.
XX
XX 11-JUN-2002.
XX
XX 08-JAN-1999; 99US-0227782.
XX
XX 08-JAN-1999; 99US-0227782.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Kawasaki AM, Fraser AS, Manoharan M, Cook PD, Prakash TP;
XX WPI; 2002-546338/58.
XX
XX Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside
XX used for preparation of 2'-O-alkylated compounds comprises dissolving
XX nucleoside in aprotic solvent, cooling, treating with base, warming,
XX cooling and reacting with ester -
XX
XX Example 46; Column 31; 24pp; English.
XX
XX The present invention relates to a novel method of selective alkylation
XX of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside.
XX The method involves dissolving the nucleoside in at least one aprotic
XX solvent, cooling, treating with base, warming, cooling and reacting with
XX a reactive ester. The method is useful for the preparation of 2'-O-alkyl
XX nucleotides, nucleosides and nucleoside surrogates used for preparation
XX of oligomeric compounds having improved hybridisation affinity and
XX nuclear resistance, which are useful as therapeutics, diagnostics and
XX research reagents. The present sequence is a modified oligonucleotide
XX used to illustrate the method of the invention.
XX
XX Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 other;
SQ
Query Match 1.5%; Score 17; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
Db 19 AAAAAAAAAAAAAAAAAA 3

RESULT 309
AAD42000/c
ID AAD42000 standard; DNA; 19 BP.
XX
XX AAD42000;
XX
DT 04-NOV-2002 (first entry)
DE
DE Oligonucleotide #3 used to illustrate the method of the invention.
XX
XX Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity;
KW nuclear resistance; alkylation; therapeutic; diagnostic; ss.
XX
OS Unidentified.
XX
XX Key Location/Qualifiers
FH modified_base 15..18
FT /tag= a

```

```

FT /mod_base= OTHER
FT /note= "2'-methoxyethoxy (MOE) residues"
PN US6403779-B1.
XX 11-JUN-2002.
XX
XX 08-JAN-1999; 99US-0227782.
XX
XX 08-JAN-1999; 99US-0227782.
XX (ISIS-) ISIS PHARM INC.
XX
XX Kawasaki AM, Fraser AS, Manoharan M, Cook PD, Prakash TP;
XX WPI; 2002-546338/58.
XX
XX Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside
XX used for preparation of 2'-O-alkylated compounds comprises dissolving
XX nucleoside in aprotic solvent, cooling, treating with base, warming,
XX cooling and reacting with ester -
XX
XX Example 46; Column 31; 24pp; English.
XX
XX The present invention relates to a novel method of selective alkylation
XX of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside.
XX The method involves dissolving the nucleoside in at least one aprotic
XX solvent, cooling, treating with base, warming, cooling and reacting with
XX a reactive ester. The method is useful for the preparation of 2'-O-alkyl
XX nucleotides, nucleosides and nucleoside surrogates used for preparation
XX of oligomeric compounds having improved hybridisation affinity and
XX nuclear resistance, which are useful as therapeutics, diagnostics and
XX research reagents. The present sequence is a modified oligonucleotide
XX used to illustrate the method of the invention.
XX
XX Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 other;
XX
Query Match 1.5%; Score 17; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1084 AAAAAAAAAAAAAAAAAA 1100
Db 19 AAAAAAAAAAAAAAAAAA 3
RESULT 310
AAD2001/c
ID AAD42001 standard; DNA; 19 BP.
XX
XX AAD42001;
XX
XX 04-NOV-2002 (first entry)
XX
XX Oligonucleotide #4 used to illustrate the method of the invention.
XX
XX Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity;
XX nuclear resistance; alkylation; therapeutic; diagnostic; ss.
XX
XX Unidentified.
XX
XX Key Location/Qualifiers
XX modified_base 16..19
XX /*tag= a
XX /mod_base= OTHER
XX /note= "5-methyl, 2'-dimethylaminoxyethyl residues"
XX
XX US6403779-B1.
XX
XX 11-JUN-2002.
XX
XX 08-JAN-1999; 99US-0227782.
XX
XX 08-JAN-1999; 99US-0227782.
XX (ISIS-) ISIS PHARM INC.
XX
XX Kawasaki AM, Fraser AS, Manoharan M, Cook PD, Prakash TP;
XX WPI; 2002-546338/58.
XX
XX Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside

```

```

PR 08-JAN-1999; 99US-0227782.
XX (ISIS-) ISIS PHARM INC.
XX
XX Kawasaki AM, Fraser AS, Manoharan M, Cook PD, Prakash TP;
XX WPI; 2002-546338/58.
XX
XX Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside
XX used for preparation of 2'-O-alkylated compounds comprises dissolving
XX nucleoside in aprotic solvent, cooling, treating with base, warming,
XX cooling and reacting with ester -
XX
XX Example 46; Column 31; 24pp; English.
XX
XX The present invention relates to a novel method of selective alkylation
XX of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside.
XX The method involves dissolving the nucleoside in at least one aprotic
XX solvent, cooling, treating with base, warming, cooling and reacting with
XX a reactive ester. The method is useful for the preparation of 2'-O-alkyl
XX nucleotides, nucleosides and nucleoside surrogates used for preparation
XX of oligomeric compounds having improved hybridisation affinity and
XX nuclear resistance, which are useful as therapeutics, diagnostics and
XX research reagents. The present sequence is a modified oligonucleotide
XX used to illustrate the method of the invention.
XX
XX Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 other;
XX
Query Match 1.5%; Score 17; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1084 AAAAAAAAAAAAAAAAAA 1100
Db 19 AAAAAAAAAAAAAAAAAA 3
RESULT 311
AAD42002/c
ID AAD42002 standard; DNA; 19 BP.
XX
XX AAD42002;
XX
XX 04-NOV-2002 (first entry)
XX
XX Oligonucleotide #5 used to illustrate the method of the invention.
XX
XX Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity;
XX nuclear resistance; alkylation; therapeutic; diagnostic; ss.
XX
XX Unidentified.
XX
XX Key Location/Qualifiers
XX modified_base 16..19
XX /*tag= a
XX /mod_base= OTHER
XX /note= "5-methyl, 2'-methoxyethyl residues"
XX
XX US6403779-B1.
XX
XX 11-JUN-2002.
XX
XX 08-JAN-1999; 99US-0227782.
XX
XX 08-JAN-1999; 99US-0227782.
XX (ISIS-) ISIS PHARM INC.
XX
XX Kawasaki AM, Fraser AS, Manoharan M, Cook PD, Prakash TP;
XX WPI; 2002-546338/58.
XX
XX Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside

```



```

Query Match      1.5%; Score 17; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
   |||||
DB 19 AAAAAAAAAAAAAAAAAA 3

RESULT 314
AAD42005/c
ID AAD42005 standard; DNA; 19 BP.
XX
AC AAD42005;
XX
DT 04-NOV-2002 (first entry)
XX
DE Oligonucleotide #8 used to illustrate the method of the invention.
XX
KW Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity;
XX nuclear resistance; alkylation; therapeutic; diagnostic; ss.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT modified_base 18
FT /tag= a
FT /mod_base= OTHER
FT /note= "5-methyl, 2'-methoxyethyl residues"
XX
PN US6403779-B1.
XX
PD 11-JUN-2002.
XX
PF 08-JAN-1999; 99US-0227782.
XX
PR 08-JAN-1999; 99US-0227782.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Kawasaki AM, Fraser AS, Manoharan M, Cook PD, Prakash TP;
XX WPI; 2002-546338/58.
XX
PT Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside
XX used for preparation of 2'-O-alkylated compounds comprises dissolving
XX nucleoside in aprotic solvent, cooling, treating with base, warming,
XX cooling and reacting with ester -
XX
PS Example 46; Column 33; 24pp; English.
XX
CC The present invention relates to a novel method of selective alkylation
XX of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside.
XX The method involves dissolving the nucleoside in at least one aprotic
XX solvent, cooling, treating with base, warming, cooling and reacting with
XX a reactive ester. The method is useful for the preparation of 2'-O-alkyl
XX nucleotides, nucleosides and nucleoside surrogates used for preparation
XX of oligomeric compounds having improved hybridisation affinity and
XX nuclear resistance, which are useful as therapeutics, diagnostics and
XX research reagents. The present sequence is a modified oligonucleotide
XX used to illustrate the method of the invention.
XX
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 other;

Query Match      1.5%; Score 17; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
   |||||
DB 19 AAAAAAAAAAAAAAAAAA 3

RESULT 314
AAD42005/c
ID AAD42005 standard; DNA; 19 BP.
XX
AC AAD42005;
XX
DT 04-NOV-2002 (first entry)
XX
DE Oligonucleotide #8 used to illustrate the method of the invention.
XX
KW Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity;
XX nuclear resistance; alkylation; therapeutic; diagnostic; ss.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT modified_base 18
FT /tag= a
FT /mod_base= OTHER
FT /note= "5-methyl, 2'-methoxyethyl residues"
XX
PN US6403779-B1.
XX
PD 11-JUN-2002.
XX
PF 08-JAN-1999; 99US-0227782.
XX
PR 08-JAN-1999; 99US-0227782.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Kawasaki AM, Fraser AS, Manoharan M, Cook PD, Prakash TP;
XX WPI; 2002-546338/58.
XX
PT Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside
XX used for preparation of 2'-O-alkylated compounds comprises dissolving
XX nucleoside in aprotic solvent, cooling, treating with base, warming,
XX cooling and reacting with ester -
XX
PS Example 46; Column 33; 24pp; English.
XX
CC The present invention relates to a novel method of selective alkylation
XX of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside.
XX The method involves dissolving the nucleoside in at least one aprotic
XX solvent, cooling, treating with base, warming, cooling and reacting with
XX a reactive ester. The method is useful for the preparation of 2'-O-alkyl
XX nucleotides, nucleosides and nucleoside surrogates used for preparation
XX of oligomeric compounds having improved hybridisation affinity and
XX nuclear resistance, which are useful as therapeutics, diagnostics and
XX research reagents. The present sequence is a modified oligonucleotide
XX used to illustrate the method of the invention.
XX
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 other;

Query Match      1.5%; Score 17; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
   |||||
DB 19 AAAAAAAAAAAAAAAAAA 3

RESULT 315
AAD42009/c
ID AAD42009 standard; DNA; 19 BP.
XX
AC AAD42009;
XX
DT 04-NOV-2002 (first entry)
XX
DE Oligonucleotide #12 used to illustrate the method of the invention.
XX
KW Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity;
XX nuclear resistance; alkylation; therapeutic; diagnostic; ss.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT modified_base 15..18
FT /tag= a
FT /mod_base= OTHER
FT /note= "2'-dimethylaminoxyethyl thymidine (T-2'DMAOE)"
XX
PN US6403779-B1.
XX
PD 11-JUN-2002.
XX
PF 08-JAN-1999; 99US-0227782.
XX
PR 08-JAN-1999; 99US-0227782.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Kawasaki AM, Fraser AS, Manoharan M, Cook PD, Prakash TP;
XX WPI; 2002-546338/58.
XX
PT Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside
XX used for preparation of 2'-O-alkylated compounds comprises dissolving
XX nucleoside in aprotic solvent, cooling, treating with base, warming,
XX cooling and reacting with ester -
XX
PS Example 46; Column 35; 24pp; English.
XX
CC The present invention relates to a novel method of selective alkylation
XX of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside.
XX The method involves dissolving the nucleoside in at least one aprotic
XX solvent, cooling, treating with base, warming, cooling and reacting with
XX a reactive ester. The method is useful for the preparation of 2'-O-alkyl
XX nucleotides, nucleosides and nucleoside surrogates used for preparation
XX of oligomeric compounds having improved hybridisation affinity and
XX nuclear resistance, which are useful as therapeutics, diagnostics and
XX research reagents. The present sequence is a modified oligonucleotide
XX used to illustrate the method of the invention.
XX
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 other;

Query Match      1.5%; Score 17; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
   |||||
DB 19 AAAAAAAAAAAAAAAAAA 3

RESULT 316
AAD42010/c
ID AAD42010 standard; DNA; 19 BP.
XX
AC AAD42010;
XX
DT 04-NOV-2002 (first entry)
XX

```

| | | |
|------------|--|--|
| OS | Unidentified. | |
| XX | | |
| Key | Location/Qualifiers | |
| FH | 16..19 | |
| FT | /*tag= a | |
| FT | /mod_base= OTHER | |
| FT | /note= "2'-dimethylaminoxyethyl thymidine (T-2'DMAOE)" | |
| FT | | |
| XX | | |
| FN | US6403779-B1. | |
| XX | | |
| PD | 11-JUN-2002. | |
| XX | | |
| PF | 08-JAN-1999; 99US-0227782. | |
| XX | | |
| PR | 08-JAN-1999; 99US-0227782. | |
| XX | | |
| FA | (ISIS-) ISIS PHARM INC. | |
| XX | | |
| PI | Kawasaki AM, Fraser AS, Manoharan M, Cook PD, Prakash TP; | |
| DR | WPI; 2002-546338/58. | |
| XX | | |
| PT | Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside | |
| PT | used for preparation of 2'-O-alkylated compounds comprises dissolving | |
| PT | nucleoside in aprotic solvent, cooling, treating with base, warming, | |
| PT | cooling and reacting with ester - | |
| XX | | |
| PS | Example 46; Column 37; 24pp; English. | |
| XX | | |
| CC | The present invention relates to a novel method of selective alkylation | |
| CC | of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside. | |
| CC | The method involves dissolving the nucleoside in at least one aprotic | |
| CC | solvent, cooling, treating with base, warming, cooling and reacting with | |
| CC | a reactive ester. The method is useful for the preparation of 2'-O-alky- | |
| CC | nucleotides, nucleosides and nucleoside surrogates used for preparation | |
| CC | of oligomeric compounds having improved hybridisation affinity and | |
| CC | nuclear resistance, which are useful as therapeutics, diagnostics and | |
| CC | research reagents. The present sequence is a modified oligonucleotide | |
| CC | used to illustrate the method of the invention. | |
| XX | | |
| SQ | Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 other; | |
| | | |
| | Query Match 1.5%; Score 17; DB 1; Length 19; | |
| | Best Local Similarity 100.0%; Pred.No. 2e+02; | |
| | Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps | |
| | | |
| Qy | 1084 AAAAAAAAAAAAAAAAAA 1100 | |
| | | |
| Db | 19 AAAAAAAAAAAAAAAAAA 3 | |
| | | |
| RESULT 318 | | |
| AAD42020/c | | |
| ID | AAD42020 standard; DNA; 19 BP. | |
| XX | | |
| AC | AAD42020; | |
| XX | | |
| DT | 04-NOV-2002 (first entry) | |
| XX | | |
| DE | Oligonucleotide #23 used to illustrate the method of the invention. | |
| XX | | |
| KW | Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity; | |
| KW | nuclear resistance; alkylation; therapeutic; diagnostic; ss. | |
| XX | | |
| OS | Unidentified. | |
| XX | | |
| Key | Location/Qualifiers | |
| FH | 15..18 | |
| FT | /*tag= a | |
| FT | /mod_base= OTHER | |
| FT | /note= "2'-O-methyleneiminoxyethyl thymidine" | |
| FT | | |
| XX | | |
| PN | US6403779-B1. | |


```

XX PD 11-JUN-2002.
XX PF 08-JAN-1999; 99US-0227782.
XX PR 08-JAN-1999; 99US-0227782.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Kawasaki AM, Fraser AS, Manoharan M, Cook PD, Prakash TP;
XX WPI; 2002-546338/58.
XX Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside
PT used for preparation of 2'-O-alkylated compounds comprises dissolving
PT nucleoside in aprotic solvent, cooling, treating with base, warming,
PT cooling and reacting with ester -
XX Example 46; Column 41; 24pp; English.
XX The present invention relates to a novel method of selective alkylation
CC of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside.
CC The method involves dissolving the nucleoside in at least one aprotic
CC solvent, cooling, treating with base, warming, cooling and reacting with
CC a reactive ester. The method is useful for the preparation of 2'-O-alkyl
CC nucleotides, nucleosides and nucleoside surrogates used for preparation
CC of oligomeric compounds having improved hybridisation affinity and
CC nuclear resistance, which are useful as therapeutics, diagnostics and
CC research reagents. The present sequence is a modified oligonucleotide
CC used to illustrate the method of the invention.
XX Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 other;
SQ
Query Match 1.5%; Score 17; DB 1; Length 19;
Best Local Similarity 100.0%; Pred.No. 2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1084 AAAAAAAAAAAAAAAAAA 1100
DB 19 AAAAAAAAAAAAAAAAAA 3
RESULT 319
ID ABK94423 standard; DNA; 19 BP.
XX AC ABK94423;
XX 27-AUG-2002 (first entry)
XX Human MLH1 DNA mismatch repair gene, exon 12, PCR primer 12.1F.
XX hMLH1; DNA mismatch repair; BRCA1; ss; PCR; primer; BRCA1;
XX breast and ovarian cancer susceptibility gene; TGDS; human;
XX two-dimensional DNA electrophoresis; tumour suppressor gene;
XX breast cancer; ovarian cancer; tumour.
XX Homo sapiens.
XX WO200236819-A1.
XX 10-MAY-2002.
XX 06-NOV-2000; 2000WO-IB01607.
XX 06-NOV-2000; 2000WO-IB01607.
XX (SCSC-) ACAD APPLIED SCI.
XX Vijg J;
XX WPI; 2002-471507/50.
XX
PT Detecting mutations in the BRCA1 and hMLH1 gene comprises subjecting
PT amplification products to 2-dimensional gel electrophoresis to produce
PT a characteristic spot pattern for a specific mutation in either the
PT BRCA1 or the hMLH1 gene -
XX Claim 6; Page 21; 57pp; English.
XX The invention relates to detecting mutations in the BRCA1 and hMLH1 gene
CC comprising subjecting a set of amplification products to two-dimensional
CC DNA electrophoresis (TGDS) to produce a characteristic spot pattern for a
CC specific mutation in either the BRCA1 or the hMLH1 gene.
CC Also included are test kits for enabling BRCA1 or hMLH1 gene testing
CC comprising short PCR primers given in the specification, mixed in 20 mM
CC of Tris-HCl, 50 mM KCl, 25 micro M of dNTP, and 5 % formamide.
CC The method is useful for detecting mutations in the BRCA1 (breast
CC and ovarian cancer susceptibility gene, a tumour suppressor gene) and
CC hMLH1 gene (a DNA mismatch repair gene). The present sequence is a
CC PCR primer specific to hMLH1 used in the method of the invention.
XX Sequence 19 BP; 4 A; 1 C; 0 G; 14 T; 0 other;
SQ
Query Match 1.5%; Score 17; DB 1; Length 19;
Best Local Similarity 100.0%; Pred.No. 2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1080 TATTAAAAAAAAAAAA 1096
DB 17 TATTAAAAAAAAAAAA 1
RESULT 320
ID ABL51520/C
XX AC ABL51520;
XX 01-JUL-2002 (first entry)
XX Tailing reaction related exemplary primer biotin-dT18U SEQ ID NO:1.
XX Tailing reaction; tailed primer; primer; probe; identification;
XX detection; linear amplification scheme; chain extending enzyme;
XX telomerase; ss.
XX Synthetic.
XX Key Location/Qualifiers
XX modified_base 1 /*tag= a
XX FT /mod_base= OTHER
XX FT /note= "biotinylated"
XX FT misc_RNA 19
XX US2002031776-A1.
XX 14-MAR-2002.
XX 26-JUL-2001; 2001US-0917138.
XX 28-MAY-1999; 99US-136545P.
XX 25-MAY-2000; 2000US-0580358.
XX (TULL/) TULLIS R H.
XX (STRE/) STREIFEL J A.
XX Tullis RH, Streifel JA;
XX WPI; 2002-361176/39.
XX Identifying and detecting nucleic acids, particularly DNA hybridization
PT probes, involves employing chain extending enzymes (e.g. telomerase) to
PT elongate probes to render them readily detectable -

```


PF 20-AUG-1999; 99US-0378665.
 XX 20-AUG-1999; 99US-0378665.
 PR (ISIS-) ISIS PHARM INC.
 PA Fraser AS, Manoharan M, Cook PD, Jung ME, Kawasaki AM;
 XX WPI; 2002-235143/29.
 DR Alkylation of alcohols, amines, or thiols, useful for preparing
 XX nucleosides that are precursors for preparation of oligomeric compounds
 PT beneficial as therapeutics, involves use of cyclic sulfate
 PT intermediates -
 XX Example 15; Column 35; 45pp; English.
 PS The present sequence is that of a chimeric oligonucleotide having
 XX some 2'-methyl thioethyl modifications. This was compared with
 CC oligonucleotides with methoxyethoxy (see ABA91950) and
 CC dimethylaminopropyl (see ABA91951) modifications for resistance to
 CC snake venom phosphodiesterase. The assay revealed the nuclease
 CC resistance of the modified oligomers. The invention provides
 CC methods for the alkylation of alcohols, amines, thiols and their
 CC derivatives by cyclic sulfate intermediates. In particular, methods
 CC for the alkylation of the 2', 3' or 5'-hydroxy position of
 CC nucleosides and their analogues with cyclic sulfates to form the
 CC 2', 3' or 5'-O-alkyl sulfate modified compounds are disclosed.
 CC Displacement of the 2', 3' or 5'-O-sulfate with a nucleophile
 CC provides 2', 3' or 5'-O-modified nucleosides and their analogues.
 CC The methods are especially useful for the preparation of
 CC 2'-O-alkyl nucleotides, nucleosides and nucleoside surrogates that
 CC are precursors for the preparation of oligomeric compounds useful
 CC as therapeutics, diagnostics and research reagents.
 XX Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 other;
 SQ Query Match 1.5%; Score 17; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1084 AAAAAAAAAAAAAAAAAA 1100
 DB 19 AAAAAAAAAAAAAAAAAA 3
 RESULT 323
 ABA91950/C
 ID ABA91950 standard; DNA; 19 BP.
 XX ABA91950;
 AC 23-MAY-2002 (first entry)
 XX Methoxyethoxy modified oligonucleotide.
 DE 2'-O-alkyl oligonucleotide; nuclease resistance; diagnosis; therapy;
 XX ss.
 KW Synthetic.
 XX Key Location/Qualifiers
 FH modified_base 16
 FT /*tag= a
 FT /mod_base= "OTHER"
 FT /note= "2'-methoxyethoxy thymidine"
 FT modified_base 17
 FT /*tag= b
 FT /mod_base= "OTHER"
 FT /note= "2'-methoxyethoxy thymidine"
 FT modified_base 18
 FT /*tag= c
 FT /mod_base= "OTHER"

FT modified_base 19
 FT /note= "2'-methoxyethoxy thymidine"
 FT /*tag= d
 FT /mod_base= "OTHER"
 FT /note= "2'-methoxyethoxy thymidine"
 XX US6277982-B1.
 PN 21-AUG-2001.
 XX 20-AUG-1999; 99US-0378665.
 XX 20-AUG-1999; 99US-0378665.
 PR (ISIS-) ISIS PHARM INC.
 PA Fraser AS, Manoharan M, Cook PD, Jung ME, Kawasaki AM;
 XX WPI; 2002-235143/29.
 DR Alkylation of alcohols, amines, or thiols, useful for preparing
 XX nucleosides that are precursors for preparation of oligomeric compounds
 PT beneficial as therapeutics, involves use of cyclic sulfate
 PT intermediates -
 XX Example 15; Column 35; 45pp; English.
 PS The present sequence is that of a chimeric oligonucleotide having
 XX some 2'-methoxyethoxy modifications. This was compared with
 CC oligonucleotides with methyl thioethyl (see ABA91949) and
 CC dimethylaminopropyl (see ABA91951) modifications for resistance to
 CC snake venom phosphodiesterase. The assay revealed the nuclease
 CC resistance of the modified oligomers. The invention provides
 CC methods for the alkylation of alcohols, amines, thiols and their
 CC derivatives by cyclic sulfate intermediates. In particular, methods
 CC for the alkylation of the 2', 3' or 5'-hydroxy position of
 CC nucleosides and their analogues with cyclic sulfates to form the
 CC 2', 3' or 5'-O-alkyl sulfate modified compounds are disclosed.
 CC Displacement of the 2', 3' or 5'-O-sulfate with a nucleophile
 CC provides 2', 3' or 5'-O-modified nucleosides and their analogues.
 CC The methods are especially useful for the preparation of
 CC 2'-O-alkyl nucleotides, nucleosides and nucleoside surrogates that
 CC are precursors for the preparation of oligomeric compounds useful
 CC as therapeutics, diagnostics and research reagents.
 XX Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 other;
 SQ Query Match 1.5%; Score 17; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1084 AAAAAAAAAAAAAAAAAA 1100
 DB 19 AAAAAAAAAAAAAAAAAA 3
 RESULT 324
 ABA91951/C
 ID ABA91951 standard; DNA; 19 BP.
 XX ABA91951;
 AC 23-MAY-2002 (first entry)
 XX Dimethylaminopropyl modified oligonucleotide.
 DE 2'-O-alkyl oligonucleotide; nuclease resistance; diagnosis; therapy;
 XX ss.
 KW Synthetic.
 XX Key Location/Qualifiers
 FH modified_base 16
 FT /*tag= a
 FT /mod_base= "OTHER"
 FT /note= "2'-methoxyethoxy thymidine"
 FT modified_base 17
 FT /*tag= b
 FT /mod_base= "OTHER"
 FT /note= "2'-methoxyethoxy thymidine"
 FT modified_base 18
 FT /*tag= c
 FT /mod_base= "OTHER"

```
FT FT /*tag= a
FT FT /mod_base= "OTHER"
FT FT /note= "2'-dimethylaminopropyl thymidine"
FT FT 17
FT FT modified_base
FT FT /*tag= b
FT FT /mod_base= "OTHER"
FT FT /note= "2'-dimethylaminopropyl thymidine"
FT FT 18
FT FT modified_base
FT FT /*tag= c
FT FT /mod_base= "OTHER"
FT FT /note= "2'-dimethylaminopropyl thymidine"
FT FT 19
FT FT modified_base
FT FT /*tag= d
FT FT /mod_base= "OTHER"
FT FT /note= "2'-dimethylaminopropyl thymidine"
XX PN US6277982-B1.
XX XX 21-AUG-2001.
XX XX 20-AUG-1999; 99US-0378665.
XX XX 20-AUG-1999; 99US-0378665.
XX XX (ISIS-) ISIS PHARM INC.
XX XX Fraser AS, Manoharan M, Cook PD, Jung ME, Kawasaki AM;
XX XX WPI; 2002-235143/29.
XX XX Alkylation of alcohols, amines, or thiols, useful for preparing
XX XX nucleosides that are precursors for preparation of oligomeric compounds
XX XX beneficial as therapeutics, involves use of cyclic sulfate
XX XX intermediates -
XX XX Example 15; Column 35; 45pp; English.
XX XX The present sequence is that of a chimeric oligonucleotide having
XX XX some 2'-dimethylaminopropyl modifications. This was compared with
XX XX oligonucleotides with methyl thioethyl (see ABA91949) and
XX XX methoxyethoxy (see ABA91950) modifications for resistance to
XX XX snake venom phosphodiesterase. The assay revealed the nuclease
XX XX resistance of the modified oligomers. The invention provides
XX XX methods for the alkylation of alcohols, amines, thiols and their
XX XX derivatives by cyclic sulfate intermediates. In particular, methods
XX XX for the alkylation of the 2', 3' or 5'-hydroxy position of
XX XX nucleosides and their analogues with cyclic sulfates to form the
XX XX 2', 3' or 5'-O-alkyl sulfate modified compounds are disclosed.
XX XX Displacement of the 2', 3' or 5'-O-sulfate with a nucleophile
XX XX provides 2', 3' or 5'-O-modified nucleosides and their analogues.
XX XX The methods are especially useful for the preparation of
XX XX 2'-O-alkyl nucleotides, nucleosides and nucleoside surrogates that
XX XX are precursors for the preparation of oligomeric compounds useful
XX XX as therapeutics, diagnostics and research reagents.
XX XX Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 other;
SQ Query Match 1.5%; Score 17; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
Db |||||
19 AAAAAAAAAAAAAAAAAA 3

RESULT 325
AAK98526/c
ID AAK98526 standard; DNA; 19 BP.
XX AC AAK98526;
XX XX 16-APR-2002 (first entry)
DT Location/Qualifiers

XX DE Nucleic acid quantitative analysis related oligonucleotide #1.
XX KW Target detection; quantitative analysis; probe; medical diagnosis;
XX KW forensics; bacterial screening; tissue typing; gene expression analysis;
XX KW genotyping; ss.
XX OS Synthetic.
XX XX Key Location/Qualifiers
XX FT modified_base 1
XX FT /*tag= a
XX FT /mod_base= OTHER
XX FT /note= "modified by thiol"
XX XX WO200202810-A2.
XX PN 10-JAN-2002.
XX XX 02-JUL-2001; 2001WO-EP07575.
XX XX 01-JUL-2000; 2000DE-1033334.
XX XX (CLON-) CLONDIAG CHIP TECHNOLOGIES GMBH.
XX XX Bickel R, Ehrlich R, Ellinger T, Ermantraut E, Kaiser T, Schulz T;
XX XX Wagner G;
XX XX WPI; 2002-154760/20.
XX XX Determining targets by interaction with probe array, useful e.g. for
XX XX diagnosis, based on detecting formation of precipitate at specific
XX XX probe sites -
XX XX Example 5; Page 47; 92pp; German.
XX XX The present invention relates to a method for the qualitative and
XX XX quantitative detection of targets in a sample by molecular interaction
XX XX between the target and probes in an array. The method can be used to
XX XX detect interactions between nucleic acids, antigens and antibodies or
XX XX receptor and ligands, particularly in applications such as medical
XX XX diagnosis, forensic science, bacterial screening, tissue typing for
XX XX transplantation, monitoring gene expression, and genotyping. The present
XX XX sequence is a modifying oligonucleotide used in the exemplification of
XX XX the invention.
XX XX Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 other;
SQ Query Match 1.5%; Score 17; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
Db |||||
19 AAAAAAAAAAAAAAAAAA 3

RESULT 326
ABZ75398/c
ID ABZ75398 standard; DNA; 19 BP.
XX AC ABZ75398;
XX XX 07-MAY-2003 (first entry)
DT Synthetic nuclease-resistant oligomeric compound #54.
XX DE Nuclease resistant; ds; pharmaceutical; topical administration;
XX KW transdermal patch; enzymatic degradation resistant.
XX XX Synthetic.
XX XX Key Location/Qualifiers
XX FT Key
```

```
FT modified_base 19 /*tag= a
FT FT /mod_base= "OTHER"
FT FT /note= "phenoxazine"
XX XX
PN WO2003004602-A2.
XX PD 16-JAN-2003.
XX XX
XX 01-JUL-2002; 2002WO-US20934.
XX XX
XX 03-JUL-2001; 2001US-302682P.
XX PR 28-NOV-2001; 2001US-0996292.
XX PR 10-DEC-2001; 2001US-0013295.
XX XX
XX PA (ISIS-) ISIS PHARM INC.
XX XX
XX PI Mancharan M, Maier MA, Prakash TP, Rajeev KG;
XX XX WPI; 2003-247768/25.
XX XX
XX Nuclease-resistant oligomeric compound useful as pharmaceuticals for
FT topocal administration such as transdermal patches
FT PS Disclosure; Page 234; 234pp; English.
XX XX
XX CC The invention relates to novel nuclease-resistant oligomeric compounds.
XX CC The compounds of the invention are useful as pharmaceuticals for topical
XX CC administration such as transdermal patches. The oligomeric compound is
XX CC resistant to enzymatic degradation. The sequences shown in
XX CC ABZ75345-ABZ75399 represent the nuclease-resistant compounds of the
XX CC invention.
XX SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 1 other;
XX
XX Query Match 1.5%; Score 17; DB 1; Length 19;
XX Best Local Similarity 100.0%; Pred. No. 2e+02;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1084 AAAAAAAAAAAAAA 1100
DB 18 AAAAAAAAAAAAAA 2
XX
RESULT 327
ABZ75399/c
ID ABZ75399 standard; DNA; 19 BP.
XX
XX AC ABZ75399;
XX XX
XX DT 07-MAY-2003 (first entry)
XX XX
XX DE Synthetic nuclease-resistant oligomeric compound #55.
XX XX
XX KW Nuclease resistant; ds; pharmaceutical; topical administration;
XX KW transdermal patch; enzymatic degradation resistant.
XX XX
XX OS Synthetic.
XX XX
XX FH Key Location/Qualifiers
XX modified_base 19 /*tag= a
XX FT /mod_base= "OTHER"
XX FT /note= "G-clamp modification"
XX XX
XX PN WO2003004602-A2.
XX XX
XX PD 16-JAN-2003.
XX XX
XX 01-JUL-2002; 2002WO-US20934.
XX XX
XX 03-JUL-2001; 2001US-302682P.
XX PR 28-NOV-2001; 2001US-0996292.
XX PR
```

```
PR 10-DEC-2001; 2001US-0013295.
XX XX
XX PA (ISIS-) ISIS PHARM INC.
XX XX
XX PI Mancharan M, Maier MA, Prakash TP, Rajeev KG;
XX XX WPI; 2003-247768/25.
XX XX
XX Nuclease-resistant oligomeric compound useful as pharmaceuticals for
FT topocal administration such as transdermal patches
FT PS Disclosure; Page 234; 234pp; English.
XX XX
XX CC The invention relates to novel nuclease-resistant oligomeric compounds.
XX CC The compounds of the invention are useful as pharmaceuticals for topical
XX CC administration such as transdermal patches. The oligomeric compound is
XX CC resistant to enzymatic degradation. The sequences shown in
XX CC ABZ75345-ABZ75399 represent the nuclease-resistant compounds of the
XX CC invention.
XX SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 1 other;
XX
XX Query Match 1.5%; Score 17; DB 1; Length 19;
XX Best Local Similarity 100.0%; Pred. No. 2e+02;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1084 AAAAAAAAAAAAAA 1100
DB 18 AAAAAAAAAAAAAA 2
XX
RESULT 328
ABZ58336/c
ID ABZ58336 standard; DNA; 19 BP.
XX
XX AC ABZ58336;
XX XX
XX DT 28-APR-2003 (first entry)
XX XX
XX DE Oligonucleotide with 2'-O- (2- (methylthio)ethyl) -5-methyluridine.
XX KW Oligonucleotide; 2'-O- (2- (methylthio)ethyl) -5-methyluridine.
XX KW antisense; DNA-RNA hybrid; ss.
XX XX
XX OS Synthetic.
XX XX
XX FH Key Location/Qualifiers
XX modified_base 16 /*tag= a
XX FT /mod_base= OTHER
XX FT /note= "2'-O- (2-methylthio)ethyl) -5-methyluridine"
XX modified_base 17 /*tag= b
XX FT /mod_base= OTHER
XX FT /note= "2'-O- (2-methylthio)ethyl) -5-methyluridine"
XX modified_base 18 /*tag= c
XX FT /mod_base= OTHER
XX FT /note= "2'-O- (2-methylthio)ethyl) -5-methyluridine"
XX modified_base 19 /*tag= d
XX FT /mod_base= OTHER
XX FT /note= "2'-O- (2-methylthio)ethyl) -5-methyluridine"
XX XX
XX PN WO2003004603-A2.
XX XX
XX PD 16-JAN-2003.
XX XX
XX 01-JUL-2002; 2002WO-US20940.
XX XX
XX 03-JUL-2001; 2001US-302683P.
XX PR 28-JAN-2002; 2002US-0058740.
XX XX
```

```

PA (ISIS-) ISIS PHARM INC.
XX
XX PI Prakash TP, Manoharan M;
XX WPI; 2003-239204/23.
XX
XX PT Increasing binding of oligomeric compound to proteins useful in
XX preparation of antisense therapeutics, involves use of modified
XX oligomeric compound having oligonucleotide group -
XX
XX PS Example 27; Page 72; 122pp; English.
XX
XX CC The present sequence is an example of an oligonucleotide of the
XX invention containing 2'-O-(2-(methylthio)ethyl)-5-methyluridine
XX (2'-O-(MTE)-5-methyluridine) modifications. In examples of the
XX invention, 2'-O-MTE was incorporated into oligonucleotides and
XX evaluated for antisense properties in comparison with the known
XX 2'-O-(2-methoxyethyl) (2'-O-MOE) modification. The 2'-O-MTE
XX modified oligonucleotides exhibited similar binding affinity to
XX target RNA as their 2'-O-MOE equivalent while binding to human
XX serum albumin was improved. The modification can be used to
XX modulate the pharmacokinetics of oligonucleotides, e.g. in
XX antisense therapy.
XX
XX SQ Sequence 19 BP; 0 A; 0 C; 0 G; 15 T; 4 U; 0 other;
XX
XX Query Match 1.5%; Score 17; DB 1; Length 19;
XX Best Local Similarity 100.0%; Pred. No. 2e+02;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1084 AAAAAAAAAAAAAAAAAA 1100
DB 19 AAAAAAAAAAAAAAAAAA 3
XX
XX RESULT 329
XX AAQ25565/c
XX ID AAQ25565 standard; DNA; 20 BP.
XX AC AAQ25565;
XX
XX DT 25-MAR-2003 (updated)
XX DT 02-DEC-1992 (first entry)
XX
XX DE Dye-coupled 3'-amino modified oligonucleotide.
XX
XX KW DNA synthesis; RNA; antisense strands; detection; ss.
XX
XX OS Synthetic.
XX
XX FH Key Location/Qualifiers
XX modified_base 20
XX /*tag= a
XX /*note= "3-amino modified"
XX
XX PN EP490281-A1.
XX
XX PD 17-JUN-1992.
XX
XX PF 06-DEC-1991; 91EP-0120935.
XX
XX PR 11-DEC-1990; 90DE-4039488.
XX
XX PA (PARH ) HOECHST AG.
XX
XX PI Engels J, Herrlein M, Konrad R, Mag M;
XX WPI; 1992-201578/25.
XX
XX PT New dye-coupled modified nucleosides, nucleotides and
XX oligonucleotides - useful for synthesis of antisense DNA and RNA
XX strands in presence of template, also for in-vivo and in-vitro
XX detection of genetic material
XX

```

```

XX PS Example; Page 9; 17pp; German.
XX
XX CC The sequence is an example of a dye coupled 3'-amino modified oligo-
XX nucleotide, it can be used in the synthesis of DNA and RNA
XX nucleosides, nucleotides and oligonucleotides and for the synthesis
XX of opposite strands in the presence of a template strand and in
XX fluorescence microscopic and macroscopic detection in vivo and in
XX vitro of genetic material. It is labelled with a fluorescent dye.
XX See also AAQ25566 and AAQ25567.
XX (Updated on 25-MAR-2003 to correct PN field.)
XX
XX SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 other;
XX
XX Query Match 1.5%; Score 17; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 2.1e+02;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1084 AAAAAAAAAAAAAAAAAA 1100
DB 20 AAAAAAAAAAAAAAAAAA 4
XX
XX RESULT 330
XX AAQ33554/c
XX ID AAQ33554 standard; DNA; 20 BP.
XX AC AAQ33554;
XX
XX DT 25-MAR-2003 (updated)
XX DT 02-FEB-1993 (first entry)
XX
XX DE Microsatellite sequence from clone AGLA247.
XX
XX KW PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
XX genetic mapping; traits; amplification; ss.
XX
XX OS Bos taurus.
XX
XX PN WO9213102-A1.
XX
XX PD 06-AUG-1992.
XX
XX PF 15-JAN-1992; 92WO-US00340.
XX
XX PR 15-JAN-1991; 91US-0642342.
XX
XX PA (GENM-) GENMARK.
XX
XX PI Georges M, Massey JM;
XX WPI; 1992-284684/34.
XX
XX PT Polymorphic bovine DNA markers - used in genetic identification,
XX gene mapping, and selective breeding
XX
XX PS Table 7; Page 150; 517pp; English.
XX
XX CC The sequence is that of a bovine microsatellite sequence obt'd. by
XX screening a library of bovine MboI DNA fragments of between
XX 250 and 500 bp with an (AC)15 and a (TC)15 oligonucleotide probe.
XX One out of 50 clones cross-hybridised. Assuming independent
XX distribution of microsatellites and MboI sites, the frequency of
XX (T6)n >9 microsatellites in the bovine genome is estimated at >100,
XX 000. The sequence information for ca. 230 such bovine microsatellites
XX is summarised in the specification and indexed herein (see below).
XX The sequences upstream and downstream of the microsatellite sequence
XX were used to generate the required PCR primers for in vitro
XX amplification of the corresp. microsatellite (using the program
XX OPTIPRIM). The microsatellites may be used to identify individuals,
XX for parentage testing, and in the genetic mapping of economic trait
XX loci, or genes involved the determinism of economically important
XX traits esp. in cattle, to allow selective breeding.
XX

```